

DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF000008; EGF_2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
 DR Hydroxylation; Repeat; Serine protease
 DR SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 50.8%; Score 96; DB 11; Length 482;
 Best Local Similarity 36.4%; Pred. No. 3.2e-09;
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCRXKLCSPFXAEXIFRNXXRTROPFWASY 44
 Db 41 ANSFEEFKKGNLERECMEIEICSEFEAREVEFEDNEKTEFWNKY 84

RESULT 7
 ID 054740 PRELIMINARY; PRT; 481 AA.
 AC 054740;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6).
 GN F10 OR F10.
 OS Mus musculus (Mouse).
 OC Plasmod Pbluescript.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RX MEDLINE=98454993; PubMed=9783672;
 RA Heidemann H.H., Kontermann R.E.;
 RT Cloning and recombinant expression of mouse coagulation factor X.";
 RL Thromb. Res. 92:33-41(1998).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

DR EMBL: AJ322677; CAA10933.1; -.
 DR HSSP: P00742; 1XKA.
 DR MEROPS: S01.216; -.
 DR MGD; MGI:103107; F10.
 DR InterPro: IPR000152; Asx_hydroxy1.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
 DR Repeat; Serine protease; Signal.
 DR SIGNAL 1
 FT CHAIN 41 481 COAGULATION FACTOR X.
 SO SEQUENCE 481 AA; 53986 MW; CF702D5EF9D97AE CRC64;

Query Match 49.2%; Score 93; DB 11; Length 481;
 Best Local Similarity 31.8%; Pred. No. 1.1e-08;
 Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCRXKLCSPFXAEXIFRNXXRTROPFWASY 44
 Db 41 ANSFEEFKKGNLERECMEIEICSEFEAREVEFEDNEKTEFWNKY 84

RESULT 8
 ID 099132 PRELIMINARY; PRT; 481 AA.
 AC 099132;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Coagulation factor X.
 GN F10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

DR EMBL: BC003877; AAH03877.1; -.
 DR HSSP: P00742; 1XKA.
 DR MEROPS: S01.216; -.
 DR MGD; MGI:103107; F10.
 DR InterPro: IPR000152; Asx_hydroxy1.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR001438; EGF_11.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00010; EGF_blood.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00001; EGF_like; 2.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.

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RT "Complete sequence of UC72A01."
CC Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL; AF318182; AK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MG1:97771; PROC.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00040; TRYPsin_DOM; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC259D3ED16 CRC64;

Query Match 54.5%; Score 103; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 1.5e-10;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCXXLCSFXXAEXIFRXXXRTROFWVS 44
Db 42 ANSFLEMRPGSLERECMEICDLEFAQEIFQVVDTLAWIKY 85

RESULT 5
O9TR0 PRELIMINARY; PRT; 456 AA.
AC O9TR0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Protein C precursor.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunenberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene.";
RL Mamm. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms.";
RL Anim. Genet. 30:237-238(1999)
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.

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DR EMBL; AF001979; CAA05126.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00040; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_SER; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease; signal.
FT SIGNAL 1 42
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
FT CHAIN
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 52.9%; Score 100; DB 6; Length 456;
Best Local Similarity 43.2%; Pred. No. 5.5e-10;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCXXLCSFXXAEXIFRXXXRTROFWVS 44
Db 43 ANSFLEIRAGSLERECMEICDLEFAKEIFQVVDTLAWWSKY 86

RESULT 6
ID O63207 PRELIMINARY; PRT; 482 AA.
AC O63207;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL; X79807; CAA56202.1; -.
DR HSSP; P00742; IXKA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.

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DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 65.1%; Score 123; DB 4; Length 701;
Best Local Similarity 52.3%; Pred. No. 4,6e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLKRCXXLCSPFXAXEJFRNXXRTQRFVWSY 44
DB 61 ANAFLELRPGSLERCEKCEOCSEFEARELIFKQERTKLFMIST 104

RESULT 2
Q91WN8 PRELIMINARY; PRT; 460 AA.
AC Q91WN8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013896; AA113896.1; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_Ca; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolase; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 011726868FCC274 CRC64;

Query Match 57.7%; Score 109; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 1,2e-11;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLKRCXXLCSPFXAXEJFRNXXRTQRFVWSY 44
DB 42 ANSFLERMPGSLERCEKCEOCSEFEARELIFQNVEDTLAFWIKY 85

RESULT 3
Q61109 PRELIMINARY; PRT; 446 AA.
AC Q61109;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=96276538; PubMed=8701412;
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino P.U.;
RT "Characterization of a cDNA encoding murine coagulation factor VII."
RL Thromb. Haemost. 75:481-487(1996).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY
DR EMBL; U44795; AAC52570.1; -.
DR HSSP; P08709; LEAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Cystealin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00069; EGF-like; 1.
DR SMART; SM00001; EGF_1; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDDA6870 CRC64;

Query Match 56.1%; Score 106; DB 11; Length 446;
Best Local Similarity 47.7%; Pred. No. 4,1e-11;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLKRCXXLCSPFXAXEJFRNXXRTQRFVWSY 44
DB 42 ANSLEELMPGSLERCEKCEOCSEFEARELIFKSERIKQFIWY 85

RESULT 4
Q99PC6 PRELIMINARY; PRT; 460 AA.
AC Q99PC6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anticoagulant protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/
RA Kof I.;
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GenCore version 5.1.4_ps_4578
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OM protein - protein search, using bw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10glu28glu_4
Perfect score: 189
Sequence: 1 ANGFLXXLRGSLXRCRX.....XXAEXIFRXRXTRQFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	65.1	701	4 Q96PQ8	Q96PQ8 homo sapien
2	109	57.7	460	11 Q91WN8	Q91WN8 mus musculu
3	106	56.1	446	11 Q61109	Q61109 mus musculu
4	103	54.5	460	11 Q93PC6	Q93PC6 mus musculu
5	100	52.9	456	6 Q91TR0	Q91TR0 canis fam11
6	96	50.8	482	11 Q63207	Q63207 rattus norv
7	93	49.2	481	11 Q54740	Q54740 mus musculu
8	93	49.2	481	11 Q99132	Q99132 mus musculu
9	93	49.2	481	11 Q88947	Q88947 mus musculu
10	90	47.6	456	4 Q14316	Q14316 homo sapien
11	90	47.6	461	6 Q95ND7	Q95ND7 pan troglod
12	90	47.6	461	6 Q95ND6	Q95ND6 pan troglod
13	89	47.1	469	6 Q9GMD9	Q9GMD9 ornithorhn
14	88	46.6	49	6 Q95ME8	Q95ME8 bos taurus
15	81	42.9	138	6 Q28894	Q28894 sus scrofa
16	80	42.3	433	13 Q90YK1	Q90YK1 brachydanto

17	78	41.3	100	4 Q15253	Q15253 homo sapien
18	77	40.7	608	13 Q9PTW7	Q9PTW7 structio ca
19	77	41.3	648	6 Q29094	Q29094 sus scrofa
20	76	40.2	399	11 Q9CQW3	Q9CQW3 mus musculu
21	73.5	38.9	542	5 Q8TE13	Q8TE13 halocynthia
22	72	38.1	650	4 Q9NSD0	Q9NSD0 homo sapien
23	72	38.1	650	4 Q16519	Q16519 homo sapien
24	71	37.6	179	4 Q8TRA3	Q8TRA3 homo sapien
25	71	37.6	198	11 Q8RI82	Q8RI82 mus musculu
26	66	34.9	607	13 Q91001	Q91001 gallus gall
27	61	32.3	678	4 Q14393	Q14393 homo sapien
28	60	31.7	673	11 Q61592	Q61592 mus musculu
29	60	31.7	674	11 Q99K57	Q99K57 mus musculu
30	58	30.7	25	11 Q9QVH6	Q9QVH6 rattus sp.
31	58	30.7	674	11 Q63772	Q63772 rattus sp.
32	57	30.2	98	13 P82807	P82807 notechis sc
33	50.5	26.7	575	10 Q94E17	Q94E17 oryza sativ
34	50.5	26.7	608	10 Q9XF36	Q9XF36 medicago sa
35	50	26.5	472	13 Q98S05	Q98S05 gaetereoten
36	50	26.5	613	13 Q98S06	Q98S06 gaetereoten
37	50	26.5	910	13 Q98S07	Q98S07 gaetereoten
38	49.5	26.2	196	10 Q04284	Q04284 belaginnella
39	49.5	26.2	567	10 Q8W4J2	Q8W4J2 arabidopsis
40	49.5	26.2	603	10 Q91PC7	Q91PC7 arabidopsis
41	49.5	26.2	606	10 Q9SUG9	Q9SUG9 arabidopsis
42	49.5	26.2	651	10 Q8S218	Q8S218 oryza sativ
43	48.5	25.7	431	10 Q94EY5	Q94EY5 arabidopsis
44	48.5	25.7	492	10 Q9SMJ7	Q9SMJ7 cicor arlet
45	48.5	25.7	543	10 Q9MB23	Q9MB23 arabidopsis

ALIGNMENTS

RESULT 1
Q96PQ8 PRELIMINARY; PRT; 701 AA.
ID Q96PQ8
AC Q96PQ8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunocnjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.",
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL, AF272774; AAKS686.1; -.
DR InterPro, IPR000152; Asx_hydroxyl.
DR InterPro, IPR000561; EGF_hydroxyl.
DR InterPro, IPR000742; EGF_2.
DR InterPro, IPR001881; EGF_1-like.
DR InterPro, IPR003006; EGF.
DR InterPro, IPR001254; Set_protease_Try.
DR InterPro, IPR000294; Vitk_dep_GLA.
DR Pfam, PF00008; EGF_2.
DR Pfam, PF00594; GLA; 1.
DR Pfam, PF00047; Ig_2.
DR Pfam, PF00089; trypsin; 1.
DR SMART, SM00181; EGF; 2.
DR PROSITE, PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE, PS00022; EGF_1; UNKNOWN_1.
DR PROSITE, PS01186; EGF_2; UNKNOWN_1.
DR PROSITE, PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE, PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE, PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE, PS00240; TRYPSIN_DOM; 1.

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FT DOMAIN 125 165 EGF-LIKE 2.
 FT DOMAIN 234 492 SERINE PROTEASE.
 FT ACT SITE 275 275 CHARGE RELAY SYSTEM.
 FT ACT SITE 321 321 CHARGE RELAY SYSTEM.
 FT ACT SITE 418 418 CHARGE RELAY SYSTEM.
 FT MOD RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

Query Match 48.7%; Score 92; DB 1; Length 492;
 Best local similarity 36.4%; Pred. No. 4.1e-09;
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLKRXKCRXXLCSEFXAXEIPFNXXRTQRTQVWST 44
 DB 41 ANSFLFEVKGQNLRECELEBACSLSEAREVEFEDAQTDEFWSKY 84

RESULT 15
 ID FA9 HUMAN STANDARD; PRT; 461 AA.
 AC P00740;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
 GN F9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86000558; PubMed=2994716;
 RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;
 RT "Nucleotide sequence of the gene for human factor IX (antithemophilic factor B).";
 RL Biochemistry 24:3736-3750(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8510593; PubMed=3857619;
 RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
 Graham J.B., Stadford D.W.;
 RT "Evidence for a prevalent dimorphism in the activation peptide of human coagulation factor IX.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84236100; PubMed=6329734;
 RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,
 Huddleston J.A., Brownlee G.G.;
 RT "The gene structure of human anti-haemophilic factor IX.";
 RL EMBO J. 3:1053-1060(1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83220788; PubMed=6687940;
 RA Jaye M., de la Salle H., Schamber F., Ballard A., Kohli V.,
 Finkelstein A., Tolstoshev P., Lecocq J.P.;
 RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-base synthetic oligonucleotide probe deduced from the amino acid sequence of bovine factor IX.";
 RL Nucleic Acids Res. 11:2325-2335(1983).
 RN [5]
 RP SEQUENCE OF 36-326 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=84300526; PubMed=6089157;
 RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;
 RT "Isolation and characterization of human factor IX cDNA"

RT Identification of Tag I polymorphism and regional assignment.";
 RL Somat. Cell Mol. Genet. 10:465-473(1984).
 RN [6]
 RP SEQUENCE OF 290-359 FROM N.A.
 RX MEDLINE=88127096; PubMed=3340835;
 RA Stoffet E.S., Koebel D.D., Sarkar G., Sommer S.S.;
 RT "Genomic amplification with transcript sequencing.";
 RL Science 239:491-494(1988).
 RN [7]
 RP SEQUENCE OF 444-461 FROM N.A.
 RX MEDLINE=94054330; PubMed=8236150;
 RA de la Salle C., Charmanlier J.L., Baas M.J., Schwartz A.,
 Wiesel M.L., Grunbaum L., Cazenave J.-P.;
 RT "A deletion located in the 3' non translated part of the factor IX gene responsible for mild haemophilia B.";
 RL Thromb. Haemost. 70:370-371(1993).
 RN [8]
 RP SEQUENCE OF 47-461 (VARIANT NAGOYA).
 RX MEDLINE=90078229; PubMed=2592373;
 RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
 Ogata K., Kamiya T., Saito H., Niho Y., Iwanaga S.;
 RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by tryptophan and its activation by alpha-chymotrypsin and rat mast cell chymase.";
 RL J. Biol. Chem. 264:21257-21265(1989).
 RN [9]
 RP HYDROXYLATION OF ASP-110.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kisiel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation zymogens.";
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [10]
 RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=78194509; PubMed=659613;
 RA di Scipio R.G., Kurachi K., Davie E.W.;
 RT "Activation of human factor IX (Christmas factor).";
 RL J. Clin. Invest. 61:1528-1538(1978).
 RN [11]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185715; PubMed=6425296;
 RA Morita T., Isaacs B.S., Esmen C.T., Johnson A.E.;
 RT "Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding site that lacks gamma-carboxyglutamic acid.";
 RL J. Biol. Chem. 259:5698-5704(1984).
 RN [12]
 RP ERRATUM.
 RA Morita T., Isaacs B.S., Esmen C.T., Johnson A.E.;
 RL J. Biol. Chem. 260:2583-2583(1985).
 RN [13]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=86189947; PubMed=3009023;
 RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;
 RT "Defective propeptide processing of blood clotting factor IX caused by mutation of arginine to glutamine at position -4.";
 RL Cell 45:343-348(1986).
 RN [14]
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.
 RX MEDLINE=90062160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
 Shimomishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl2-Glc) O-glycosidically linked to a serine residue in the first epidermal growth factor-like domain of human factors VII and IX and protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [15]
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).

RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 RN [5]
 RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE=7305314; PubMed=4264286;
 RA Titani K., Hemmerson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 RL Biochemistry 11:4899-4903(1972).
 RN [7]
 RP PROCESSING.
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Titani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN [8]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN [9]
 RP SULFATION.
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN [10]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
 RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN [11]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Tejleman O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN [12]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1527084;
 RA Selander-Sunnerhagen M., Ullner M., Persson E., Tejleman O.,
 RA Stenflo J., Drakenberg T.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
 RL J. Biol. Chem. 267:19642-19649(1992).
 RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Trewhella J.;
 RT "The relative orientation of Gla and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";

RL Biochemistry 35:11547-11559(1996).
 CC - FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC - CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC - SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC - PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC - PTM: N- AND O-GLYCOSYLATED.
 CC - PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC - MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC - SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, X00673; CAA25286.1; -.
 CC PIR, A00925; EXBO.
 CC PDB, IAP0; 31-JAN-94.
 CC PDB, ICCF; 31-MAY-94.
 CC PDB, 1WHE; 15-MAY-97.
 CC PDB, 1WHF; 15-MAY-97.
 CC MEROPS: S01.216; -.
 CC GlycoSuiteDB: P00743; -.
 CC InterPro: IPR000152; Asx_hydroxyl.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR000742; EGF 2.
 CC InterPro: IPR001881; EGF_Ca.
 CC InterPro: IPR002383; GLA_blood.
 CC InterPro: IPR001254; Ser_protease_Try.
 CC InterPro: IPR000294; VitK_dep_GLA.
 CC Pfam: PF00008; EGF; 2.
 CC Pfam: PF00089; trypsin; 1.
 CC Pfam: PF00594; gla; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00001; GLABLOOD.
 CC SMART: SM00179; EGF_CA; 1.
 CC SMART: SM00001; EGF_like; 1.
 CC SMART: SM00069; GLA; 1.
 CC SMART: SM00020; Tryp_Spc; 1.
 CC PROSITE: PS00010; ASX_HYDROXYL; 1.
 CC PROSITE: PS00022; EGF_1; 1.
 CC PROSITE: PS01186; EGF_2; 2.
 CC PROSITE: PS01187; EGF_CA; 1.
 CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE: PS00240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC GlycoProtein: Hydroxylase; Serine protease; Plasma; Blood coagulation;
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 CC SIGNAL 1 23
 CC PROPEP 24 40
 CC CHAIN 41 180
 CC CHAIN 183 492
 CC PROPEP 183 233
 CC CHAIN 234 492
 CC PROPEP 476 492
 CC DOMAIN 86 122
 CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 CC FACTOR X LIGHT CHAIN.
 CC FACTOR X HEAVY CHAIN.
 CC ACTIVATION PEPTIDE.
 CC ACTIVATED FACTOR XA, HEAVY CHAIN.
 CC MAY BE REMOVED BUT IS NOT NECESSARY FOR
 CC ACTIVATION.
 CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

RL Blood 78:890-894(1991).
 RN [14]
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
 RX MEDLINE=92190481; PubMed=1347706;
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
 Rainville I.R., Long G.L.;
 RT "Protein C/Vermont: symptomatic type II protein C deficiency
 associated with two GLA domain mutations.";
 RL Blood 79:1456-1465(1992).
 RN [15]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Suganara Y., Miura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 a missense mutation.";
 RL Blood 80:126-133(1992).
 RN [16]
 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [17]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [18]
 RP VARIANT GLN-220.
 RX MEDLINE=93250852; PubMed=1301959;
 RA Gandville S., Vidard M., Aisch M., Alhenc-Gelas M., Fischer A.M.,
 Gouault-Heilman M., Toulon P., Fiesinger J.N., Goossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
 deficiency: characterization by denaturing gradient gel
 electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [19]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yamamoto K., Matsushita T., Sugura I., Takamatsu J., Iwasaki E.,
 Wada H., Deguchi K., Shirakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
 RN [20]
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE=93131312; PubMed=8324221;
 RA Gandville S., Alhenc-Gelas M., Gaussem P., Aillaud M.-F., Dupuy E.,
 Juhon-Vague I., Aisch M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 gene in patients presenting with defective protein C anticoagulant
 activity.";
 RL Blood 82:159-168(1993).
 RN [21]
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; T-385; T-388 AND
 V-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
 Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [22]
 RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Miller D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,
 Kakkar V.V., Cooper D.N.;
 RT "A Glu domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 causing type 2 protein C deficiency and recurrent venous

RT thrombosis."; Fibrinolysis 4:345-347(1993).
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [23]
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
 RX MEDLINE=94122329; PubMed=8292730;
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
 Koepfer M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with
 symptomatic type I protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).
 RN [24]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Patrascu P., Gemmati D., Castaman G., Rodeghiero F.,
 Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RL Br. J. Haematol. 84:285-289(1993).
 RN [25]
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
 QY
 Db 1 ANGFLXXLRGSLRXCRXXLCSPFXAEXIFRNXXRTQFW 41
 43 ANSFLELRHSLRRCIEBICDFEAKEIFQVVDTLFW 83
 RESULT 14
 ID FA10 BOVIN STANDARD; PRT; 492 AA.
 AC P00743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-487 FROM N.A.
 RX MEDLINE=84247315; PubMed=6330671;
 RA Pung M.R., Campbell R.M., McGillivray R.T.A.;
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
 containing a prepro leader sequence.";
 RL Nucleic Acids Res. 12:4481-4492(1984).
 RN [2]
 RP SEQUENCE OF 41-180.
 RX MEDLINE=8010563; PubMed=6766735;
 RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
 Titani K.;
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
 factor).";
 RL Biochemistry 19:659-667(1980).
 RN [3]
 RP REVISION TO 103.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kisilel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 K-dependent blood coagulation zymogens.";
 RL Biochem. Res. Commun. 115:8-14(1983).
 RN [4]
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
 Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 chain.";

```
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 103 103 SIMILARITY).
FT ACT_SITE 103 103 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 274 274 CHARGE RELAY SYSTEM.
FT ACT_SITE 320 320 CHARGE RELAY SYSTEM.
FT ACT_SITE 417 417 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 149 BY SIMILARITY.
FT DISULFID 151 164 BY SIMILARITY.
FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 244 BY SIMILARITY.
FT DISULFID 259 275 BY SIMILARITY.
FT DISULFID 368 402 BY SIMILARITY.
FT DISULFID 413 441 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
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Query Match 49.7%; Score 94; DB 1; Length 490;
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Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
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Ddb 41 ANSFLKXKKNLRCMCENCSYEALVEFEDREKTNEMWXY 84
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RESULT 13
PRTC_HUMAN STANDARD; PRT; 461 AA.
AC P04070; O16001; Rel. 03; Created;
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-NOV-2002 (Rel. 41, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Aucoproteombin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
CN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85270390; PubMed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RT "The nucleotide sequence of the gene for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=85269639; PubMed=2991859;
RA Beckmann R.J., Schmidt R.J., Sautter R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNA";
RL Nucleic Acids Res. 13:5233-5247 (1985).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=86120978; PubMed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RT "Evolution and organization of the human protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550 (1986).
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RN [4]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 106-461 FROM N.A.
RA MEDLINE=84272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770 (1984).
RN [6]
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RA MEDLINE=90293094; PubMed=1694179;
RA Miletich J.P., Broze G.J. Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404 (1990).
RN [7]
RP HYDROXYLATION.
RA MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107 (1992).
RN [8]
RP 3D-STRUCTURE MODELING OF 175-450.
RA MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greenard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599 (1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RA MEDLINE=97157472; PubMed=9003757;
RA Wather T., Oganesyan V., Hof P., Huber R., Foundling S., Emon C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RL EMBO J. 15:6822-6831 (1996).
RN [10]
RP REVIEW ON PROC VARIANTS.
RA MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84 (1993).
RN [11]
RP VARIANT CYS-444.
RA MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Hassan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832 (1987).
RN [12]
RP VARIANT TRP-211 (LONDON-1).
RA MEDLINE=90098906; PubMed=2602169;
RA Grundy C.B., Chitcliffe A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513 (1989).
RN [13]
RP VARIANT CYS-272.
RA MEDLINE=91329836; PubMed=1868249;
RA Reitsma P.H., Poort S.R., Allart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";
```


RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RT protein C.";
 RL Biochemistry 25:5098-5102 (1986).
 RP [3]
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RT blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595 (1985).
 RN [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";
 RL Gene 41:311-314 (1986).
 RN [5]
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,
 RT Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884 (1983).
 RN [6]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702 (1984).
 RN [7]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163 (1993).
 RN [8]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.U., Hameedhushan K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519 (1989).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
 RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966 (1993).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635 (1998).
 CC -I- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -I- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.

CC -I- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -I- PTM: N- AND O-GLYCOSYLATED.
 CC -I- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXa (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIa (IN THE EXTRINSIC PATHWAY).
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; K03194; AA52490.1; -;
 CC EMBL; M57285; AA52421.1; -;
 CC EMBL; L29433; AA52764.1; -;
 CC EMBL; L00390; AA52764.1; JOINED.
 CC EMBL; L00391; AA52764.1; JOINED.
 CC EMBL; L00382; AA52764.1; JOINED.
 CC EMBL; L00393; AA52764.1; JOINED.
 CC EMBL; L00394; AA52764.1; JOINED.
 CC EMBL; L00395; AA52764.1; JOINED.
 CC EMBL; L00396; AA52764.1; JOINED.
 CC EMBL; M22613; AA51984.1; -;
 CC EMBL; K01886; AA52486.1; -;
 CC EMBL; M3297; AA52656.1; -;
 CC PIR; A00924; EXHU.
 CC PIR; A25853; A25853.
 CC PIR; A24478; A24478.
 CC PDB; IHCG; 08-MAY-95.
 CC PDB; IFXY; 29-OCT-97.
 CC PDB; IFXY; 17-JUN-98.
 CC PDB; 1XKA; 23-MAR-99.
 CC PDB; 1XKB; 23-MAR-99.
 CC MEROPS; S01.216; -;
 CC GlycoSuiteDB; P00742; -;
 CC Gene; HGNC:3528; F10.
 CC MIM; 134530; -;
 CC MIM; 227600; -;
 CC InterPro; IPR000152; Asx hydroxyl.
 CC InterPro; IPR001314; Chymotrypsin.
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR000742; EGF 2.
 CC InterPro; IPR001881; EGF-Ca.
 CC InterPro; IPR002383; GLA blood.
 CC InterPro; IPR001254; Ser_protease_Try.
 CC InterPro; IPR000294; VltK_dep_GLA.
 CC Pfam; PF00089; EGF; 2.
 CC Pfam; PF00089; clypsin; 1.
 CC Pfam; PF00594; gla; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00179; EGF_CA; 1.
 CC SMART; SM00001; EGF_like; 1.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; Tryp_Spc; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS01187; EGF_CA; 1.
 CC PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE; PS00340; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC GlycoProtein; Hydrolase; Serine protease; Plasma; Blood coagulation.
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 CC SIGNAL 1 31
 CC POTENTIAL.

RN [5]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213513; PubMed=6304092;
 RA Esmon N.L., Debault L.E., Esmon C.T.;
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
 domainless protein C."; J. Biol. Chem. 258:5548-5553(1983).
 RN [6]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213514; PubMed=6406503;
 RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
 RT "Structural changes required for activation of protein C are induced
 by Ca2+ binding to a high affinity site that does not contain gamma-
 carboxyglutamic acid."; J. Biol. Chem. 258:5554-5560(1983).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 and VIIIA.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
 REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 SITE IS NECESSARY FOR THE RECOGNITION OF THE
 THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; K02435; AAA30685.1; -
 DR PIR; A00928; KXBO.
 DR HSSP; P04070; LPCU.
 DR MEROPS; S01.218; -
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrilase; Signal.
 RN NON_TER 1
 FT SIGNAL <1 29
 FT PROPEP 30 39

FT CHAIN 40 194
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 FT DOMAIN 94 129
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 Query Match 51.3%; Score 97; DB 1; Length 456;
 Best Local Similarity 43.2%; Pred. No. 4.6e-10; Indels 0; Gaps 0;
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
 Cy 1 ANGFLXLRGSLXRCRXLLCSFYXAXEYIFRNXXRTQPFVSY 44
 Db 40 ANSLFELRPGNVRBESSEVCEFEARELIFONTEDIMAFWSFY 83
 RESULT 11
 ID FA10_HUMAN STANDARD; PRT; 488 AA.
 AC P00742; Q14340;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stewart factor).
 GN F10.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91216473; PubMed=1902434;
 RA Messler T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
 human coagulation factor X.";
 RL Gene 99:291-294(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87026600; PubMed=3768336;

CC -|- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the
 CC thrombin-chromomodulin complex.
 CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -|- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF191307; AAG28380.1; -.
 CC HSSP: P04070; 1PCU.
 CC MEROPS: S01.218; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0001; GLABLOOD.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00001; EGF-like; 2.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 KW SIGNAL 1 18
 FT PROPEP 19 41
 FT CHAIN 42 459
 FT CHAIN 42 196
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FT MOD_RES 70 70
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 FT DISULFID 146 159
 FT DISULFID 161 174
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 FT DISULFID 240 256
 FT DISULFID 371 385
 FT DISULFID 396 424
 FT CARBOHYD 138 138
 FT CARBOHYD 292 292
 FT CARBOHYD 353 353
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 54.0%; Score 102; DB 1; Length 459;
 Best Local Similarity 45.5%; Pred. No. 5.6e-11;
 Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;
 QY 1 ANGFLXLLREGSLXRXCRXLCSFXAXEIPFNXXRTQRFWSY 44
 DB 42 ANSFLELRPSSLRECKEKTCDFEARERIFONTENTMAFWSKY 85
 RESULT 10
 ID PRTC_BOVIN STANDARD; PRT; 456 AA.
 AC P00745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
 DE (Autoproteolytic cleavage) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV) (Fragment).
 GN PROC.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85014826; PubMed=6091100;
 RA Long G.L., Balagaje R.M., McGillicray R.T.A.;
 RA "Cloning and sequencing of liver cDNA coding for bovine protein C";
 RA Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
 RL [2]
 RP SEQUENCE OF 40-194.
 RX MEDLINE=83007325; PubMed=6896876;
 RA Fernlund P., Stenflo J.;
 RA "Amino acid sequence of the light chain of bovine protein C";
 RA J. Biol. Chem. 257:12170-12179(1982).
 RL [3]
 RP REVISION TO 110.
 RX MEDLINE=83169769; PubMed=6572939;
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
 RA "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";
 RA Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
 RL [4]
 RP SEQUENCE OF 197-456.
 RX MEDLINE=83007326; PubMed=6896877;
 RA Stenflo J., Fernlund P.;
 RA "Amino acid sequence of the heavy chain of bovine protein C";
 RA J. Biol. Chem. 257:12180-12190(1982).
 RL

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FT DOMAIN 87 123 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 128 169 EGF-LIKE 2.
FT DOMAIN 194 446 SERINE PROTEASE.
FT SITE 193 194 CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
ACT SITE 234 234 FACTOR IYA, OR THROMBIN) (BY SIMILARITY).
ACT SITE 283 283 BY SIMILARITY.
ACT SITE 385 385 BY SIMILARITY.
BINDING 379 379 SUBSTRATE (BY SIMILARITY).
DISULFID 58 63 BY SIMILARITY.
DISULFID 91 102 BY SIMILARITY.
DISULFID 96 111 BY SIMILARITY.
DISULFID 113 122 BY SIMILARITY.
DISULFID 132 143 BY SIMILARITY.
DISULFID 139 153 BY SIMILARITY.
DISULFID 155 168 BY SIMILARITY.
DISULFID 176 303 BY SIMILARITY.
DISULFID 200 205 BY SIMILARITY.
DISULFID 219 235 BY SIMILARITY.
DISULFID 351 370 BY SIMILARITY.
DISULFID 381 409 BY SIMILARITY.
MOD RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
MOD RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
MOD RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
MOD RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
MOD RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
MOD RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
MOD RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
MOD RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
MOD RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
MOD RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
MOD RES 104 104 HYDROXYLATION (BY SIMILARITY).
MOD RES 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 446 AA; 50276 MW; 2512E44A45C8C96E CRC64;

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Query Match 56.1%; Score 106; DB 1; Length 446;
Best Local Similarity 47.7%; Pred. No. 9.9e-12;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

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QY 1 ANGFLXXLRGSGSLKRCRXXLCSPXXAEXIFRMXXRTRPFWASY 44
42 ANSLLEELWPGSLERECNEQCSFEAREIFKSPERTKQFWIVY 85

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RESULT 8
TMG3_HUMAN STANDARD; PRT; 231 AA.
AC O9BZD7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxylglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=2111704; PubMed=11171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxylglutamic acid
proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PM: Glu residues are produced after subsequent posttranslational
modifications of glutamic acid by a vitamin K-dependent gamma-
carboxylase.
CC -----
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CC EMBL; AF326350; AAK00955.1; -.
CC HSSP; P00740; 1CFH.
CC InterPro; IPR002383; GLA blood.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00594; gla; 1.
CC PRINTS; PR00001; GLABLOOD.
CC SMART; SM00069; GLA; 1.
CC PROSITE; PS00011; GLU CARBOXYLATION; 1.
CC Gamma-carboxylglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 20 231 PROTEIN 3.
FT TRANSMEM 79 101 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25848 MW; 8A373E4848490D81 CRC64;

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Query Match 55.0%; Score 104; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 1.2e-11;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

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QY 1 ANGFLXXLRGSGSLKRCRXXLCSPXXAEXIFRMXXRTRPFWASY 44
20 ANBEFLERQGTIERECMEICSEYEVKEFKETMEFWKGY 63

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RESULT 9
PRIC_PIG STANDARD; PRT; 459 AA.
AC O9GLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Anticoagrombin IIA) (Anticoagulant protein C) (Blood coagulation
factor XIV).
GN PROC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
RA Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
protein modeling of membrane binding sites and comparative anatomy of
RT domains.";
RL Cell. Mol. Life Sci. 58:148-159(2001).
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
regulates blood coagulation by inactivating factors Va and VIIIa
in the presence of calcium ions and phospholipids.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
into a light chain and a heavy chain held together by a disulfide
bond. The enzyme is then activated by thrombin, which cleaves a
tetradecapeptide from the amino end of the heavy chain; this
reaction, which occurs at the surface of endothelial cells, is
strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PM: The vitamin K-dependent, enzymatic carboxylation of some Glu
residues allows the modified protein to bind calcium.
CC -----

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CC	CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	CC	Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=91271267; PubMed=8972017;	
RA	Idiosgale E., Rosen E.D., Carmeliet P., Collen D., Caetallino F.J.;	
RT	"Nucleotide structure and characterization of the murine blood coagulation factor VII gene."	
RL	Thromb. Haemost. 76:957-964(1996).	
CC	-1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).	
CC	-1- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -ile bond in factor X to form factor Xa.	
CC	-1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).	
CC	-1- TISSUE SPECIFICITY: PLASMA.	
CC	-1- PM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).	
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.	
CC	-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.	
CC	-----	
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CC	-----	
DR	EMBL; U66079; AAC33796.1; -	
DR	HSSP; P08709; 1BF9.	
DR	MEDP; S01.215; -	
DR	MCD; MGI:109325; F7.	
DR	InterPro; IPR000152; Aex_hydroxyl.	
DR	InterPro; IPR001314; Chymotrypsin.	
DR	InterPro; IPR000561; EGF-like.	
DR	InterPro; IPR000742; EGF 2.	
DR	InterPro; IPR001881; EGF CA.	
DR	InterPro; IPR002383; GLA_blood.	
DR	InterPro; IPR001254; Ser_protease_Try.	
DR	InterPro; IPR000294; VitK_dep_GLA.	
DR	Pfam; PF00008; BGF; 2.	
DR	Pfam; PF00089; trypsin; 1.	
DR	Pfam; PF00594; gla; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	PRINTS; PR00001; GLABLOOD.	
DR	SMART; SM00179; EGF_CA; 1.	
DR	SMART; SM00001; EGF_like; 1.	
DR	SMART; SM00069; GLA; 1.	
DR	SMART; SM00020; TRY_PPC; 1.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.	
DR	PROSITE; PS00022; EGF_1; 1.	
DR	PROSITE; PS01186; EGF_2; FALSE_NEG.	
DR	PROSITE; PS01187; EGF_CA; 1.	
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.	
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	
DR	PROSITE; PS00133; TRYPSIN_SER; 1.	
KW	Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;	
KW	Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;	
EC	EC=1.11.1.10	
FT	EC=1.11.1.10	
FT	SIGNAL 1 24 POTENTIAL.	
FT	PROPEP 25 41 POTENTIAL.	
FT	CHAIN 42 193 FACTOR VII LIGHT CHAIN.	
FT	CHAIN 194 446 FACTOR VII HEAVY CHAIN.	
FT	DOMAIN 447 76 GLA-RICH.	

DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLUT CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL; 1
 FT PROPEP; 34 41
 FT CHAIN; 42 196
 FT CHAIN; 199 461
 FT PEPTIDE; 199 212
 FT SITE; 212 213
 FT DOMAIN; 96 131
 FT DOMAIN; 135 175
 FT DOMAIN; 213 461
 FT MOD_RES; 47 47
 FT MOD_RES; 48 48
 FT MOD_RES; 55 55
 FT MOD_RES; 57 57
 FT MOD_RES; 60 60
 FT MOD_RES; 61 61
 FT MOD_RES; 66 66
 FT MOD_RES; 67 67
 FT MOD_RES; 70 70
 FT MOD_RES; 112 112
 FT ACT_SITE; 253 253
 FT ACT_SITE; 299 299
 FT ACT_SITE; 402 402
 FT DISULFID; 58 63
 FT DISULFID; 91 110
 FT DISULFID; 100 105
 FT DISULFID; 104 119
 FT DISULFID; 121 130
 FT DISULFID; 139 150
 FT DISULFID; 146 159
 FT DISULFID; 161 174
 FT DISULFID; 182 319
 FT DISULFID; 238 254
 FT DISULFID; 373 387
 FT DISULFID; 398 426
 FT CARBOHYD; 214 214
 FT CARBOHYD; 290 290
 FT CARBOHYD; 355 355
 FT CARBOHYD; 328 328
 FT CONFLICT; 393 393
 FT CONFLICT; 393 393
 FT SEQUENCE; 461 AA; 51945 MW; 53FA0D5B194D5E CRC64;
 Query Match 57.7%; Score 109; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 2.9e-12;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RC MEDLINE=92329550; PubMed=1627650;
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
 RT "The cdna cloning and mRNA expression of rat protein C";
 RL Biochim. Biophys. Acta 1131:329-332(1992).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIA.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; X64336; CAA45617.1; -;
 DR PIR; S18994; S18994.
 DR PIR; S24312; S24312.
 DR HSP; P04070; IPCU.
 DR MEROPS; S01.218; -;
 DR InterPro; IPR000152; Asx hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF-like.
 DR InterPro; IPR002383; GLA blood.
 DR InterPro; IPR001254; Ser protease Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PR00008; EGF_2.
 DR Pfam; PR00089; trypsin; 1.
 DR Pfam; PF00594; Gla_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA_1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLUT CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCBI_TaxID=9606;
RP [1]
RX MEDLINE=97404347; PubMed=9256434;
RT Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed after subsequent posttranslational
CC -1- PTM: Glu residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
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-----
DR EMBL; AF009242; AAB67070.1; -.
DR HSSP; P00740; 1CFH.
DR DR
DR Genew; HGNC:9469; PRRG1.
DR MIM; 604428; -.
DR DR
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VItK_dep_GLA.
DR Pfam; PF00594; gla_1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROSEP 1 20 POTENTIAL.
FT CHAIN 1 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT FT PROTEIN 1.
FT DOMAIN 21 83 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 84 106 POTENTIAL.
FT DOMAIN 107 218 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 24 61 GLA-RICH.
FT DOMAIN 131 135 POLY-PRO.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

Query Match 58.2%; Score 110; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 8.7e-13;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANGFLXLRGSLRXCRXXLCFXXAEXIFRNXXRTQFWVSY 44
DB 21 ANGFEIRQGNIERCKEFCFEERAEFENNEKTKEFWSY 64

RESULT 5
PRTC MOUSE STANDARD; PRT; 461 AA.
ID P33587; O35498;
AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-UN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Aucoprotein IIa) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
DE PROC.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92316897; PubMed=1618739;
RX Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;

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RT "Isolation and characterization of a mouse protein C cDNA.";
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=98152576; PubMed=9493582;
RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding
RT anticoagulant protein C."
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE OF 274-434 FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=94318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Hara M., Niho Y.;
RT "A comparative study of partial primary structures of the catalytic
RT region of mammalian protein C.";
RL Br. J. Haematol. 86:590-600(1994).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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DR EMBL; D10445; BAA01235.1; -.
DR EMBL; AF034569; AAC33795.1; -.
DR EMBL; D43755; BAA07812.1; -.
DR PIR; JX0210; JX0210.
DR HSSP; P04070; 1PCU.
DR DR
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR001283; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VItK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00059; GLA_1.
DR SMART; SM00020; Tryp_Spec; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.

```

[9]
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=99126538; PubMed=8925787;
RA Zhang E., St Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
inhibited with a BPTI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
RN [10]
RP STRUCTURE BY NMR OF 105-145.
RX MEDLINE=98367502; PubMed=8692950;
RA Muranyi A., Finn B.B., Glibert G.P., Forssen S., Stefflo J.,
RT "Solution structure of the N-terminal EGF-like domain from human
factor VII.";
RL Biochemistry 37:10605-10615(1998).
RN [11]
RP VARIANT GLN-364.
RX MEDLINE=91300047; PubMed=2070047;
RA O'Brien D.P., Galle K.M., Anderson J.S., McVey J.H., Miller G.J.,
RT "Purification and characterization of factor VII 304-Gln: a variant
molecule with reduced activity isolated from a clinically unaffected
male.";
RL Blood 78:132-140(1991).
RN [12]
RP VARIANTS GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=1634227;
RA Marchetti G., Patrachini P., Gemmati D., Derosa V., Pinotti M.,
RA Roderigo G., Caonaro A., Girolami A., Bernardi F.;
RT "Detection of two missense mutations and characterization of a repeat
polymorphism in the factor VII gene (F7).";
RL Hum. Genet. 89:497-502(1992).
RN [13]
RP VARIANT TYR-238.
RX MEDLINE=93372811; PubMed=8364544;
RA Marchetti G., Ferruti M., Patrachini P., Reddelli R., Bernardi F.;
RT "A missense mutation (178Cys->Tyr) and two neutral dimorphisms
(115His and 333Ser) in the human coagulation factor VII gene.";
RL Hum. Mol. Genet. 2:1055-1056(1993).
RN [14]
RP VARIANTS.
RX MEDLINE=94061028; PubMed=8242057;
RA Takamaya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational
polymorphism (SSCP) analysis in five dysfunctional variants of
coagulation factor VII.";
RL Hum. Mol. Genet. 2:1355-1359(1993).
RN [15]
RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE=94264305; PubMed=8204879;
RA Chang S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the
cleavage site for activation and altering binding to tissue factor.";
RL Blood 83:3524-3535(1994).
RN [16]
RP VARIANT VAL-354.
RX MEDLINE=95072589; PubMed=7981691;
RA Bernardi F., Castaman G., Reddelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation
factors VII (294Ala->Val) and X (334Ser->Pro).";
RL Hum. Mol. Genet. 3:1175-1177(1994).
RN [17]
RP VARIANT MIE HIS-307.
RX MEDLINE=95064662; PubMed=7974346;
RA Ohlwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
RA Suzuki K.;
RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by
an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
catalytic domain.";
RT

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RN      Thromb. Haemost. 71:773-777(1994).
RP [18]
RX VARIANT MET-419. Pubmed=8652821;
RA Arbind A.A., Mannucci P.M., Bauer K.A.;
RT "A Thr359met mutation in factor VII of a patient with hereditary
RL Blood 87:5085-5094(1996).
[19]
RN VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
RX MEDLINE=97001216; Pubmed=8844208;
RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
RA Lungi B., Rodeghiero F., Marchetti G.;
RT "Mutation pattern in clinically asymptomatic coagulation factor VII
RL deficiency."?
RM Hum. Mutat. 8:108-115(1996).
[20]
RN VARIANT VAL-304.
RX MEDLINE=97037613; Pubmed=8883260;
RA Tanary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
RA Brenner B., Faz M., Uder A.S., Blau O., Korostishevsky M.,
RA Zatzov R., Seltschik U.;
RT "A1a234Val is a common, probably ancient mutation causing factor VII
RL deficiency in Moroccan and Iranian Jews.";
RM Thromb. Haemost. 76:283-291(1996).
[21]
RN VARIANTS MALTA THR-194 AND VAL-304.
RX MEDLINE=98112461; Pubmed=9452082;
RA Alshinawi C., Secerri C., Galdes R., Aquilina A., Felice A.E.;
RT "Two new missense mutations (P134T and A244V) in the coagulation
RL factor VII gene.";
RM Hum. Mutat. Suppl. 1:S189-S191(1998).
CC -I FUNCTION: CIRCULATES IN THE BLOOD IN A ZWOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIA BY FACTOR XA, FACTOR XIII, FACTOR IXA, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VII THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSIS. FACTOR VII WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -I CATALYTIC ACTIVITY: Hydrolyzes one Arg--|-lle bond in factor x to
CC form factor xa.
CC -I SUBUNIT: HETERO DIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND.
CC CC -I ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; are
CC produced by alternative splicing.
CC CC -I TISSUE SPECIFICITY: PLASMA.
CC CC -I PTM: THE VITAMIN K-DEPENDENT, ENZYMTIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC CC -I DISEASE DEFECTS IN F7 CAN CAUSE CONGULOPLATHY.
CC CC -I PHARMACEUTICAL: Available under the names Niasate or Novoseven
CC (Novo Nordisk). Used for the treatment of bleeding episodes in

```

Query Match

Best Local Similarity:	52.3%	Pred.	No. 7.7e-15;
Matches	23;	Conservative	5; Mismatches 16; Indels 0; Gaps 0,

Oy 1 ANGFLXLRGGSLKRCXXII CSFYXAEIFRNXRTQFWVS 44

||| || | : || : || : || :

Db 61 ANAFLEELRGSGLSRECKECSCFEAREIRFDARTLYLFMSY 104

|||| || || : || : || : || :

RESULT 4

ID	TWG1_HUMAN	STANDARD;	PRT;	218 AA.
AC	TMGI_4668;			
Dt	15-JUN-2002 (Rel. 41, Created)			
Dt	15-JUN-2002 (Rel. 41, Last sequence update)			
Dt	15-JUN-2002 (Rel. 41, Last annotation update)			
Dc	Transmembrane gamma-carboxylglutamic acid protein 1 precursor (Proline-rich Gla protein 1) (Proline-rich gamma-carboxylglutamic acid protein 1).			
Dn	PRPG1 OR TMG1 OR PRGP1.			
Os	Homo sapiens (Human).			

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DR PRINTS; PRO00722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS000240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232
FT ACT_SITE 281
FT ACT_SITE 383
FT BINDING 377
FT DISULFID 56
FT DISULFID 89
FT DISULFID 94
FT DISULFID 111
FT DISULFID 130
FT DISULFID 137
FT DISULFID 151
FT DISULFID 166
FT DISULFID 174
FT DISULFID 198
FT DISULFID 217
FT DISULFID 233
FT DISULFID 349
FT DISULFID 368
FT DISULFID 379
FT MOD_RES 45
FT MOD_RES 46
FT MOD_RES 53
FT MOD_RES 55
FT MOD_RES 58
FT MOD_RES 59
FT MOD_RES 64
FT MOD_RES 65
FT MOD_RES 66
FT MOD_RES 74
FT MOD_RES 102
FT MOD_RES 121
FT CARBOHYD 242
FT CARBOHYD 306
FT CARBOHYD 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;

Query Match 69.3%; Score 131; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.5e-16;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
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RESULT 3
ID_FAT7 HUMAN STANDARD; PRT; 466 AA.
AC P08709; Q14339;
DT 01-JAN-1988 (Rel. 06, Created)
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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Eptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Armet T.Z., Carlington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi O., Nickerson D.A.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Tim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RT Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Tim L., Wiberger F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.";
RT J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
RA Shimomura Y., Iwanga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RT J. Biol. Chem. 264:20320-20325(1989).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RT Adv. Exp. Med. Biol. 281:121-131(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RT Nature 380:41-46(1996).
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DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxylglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
FT CHAIN 153 407 FACTOR VII HEAVY CHAIN.
FT DOMAIN 6 35 GLA-RICH.
FT DOMAIN 87 128 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 153 407 EGF-LIKE 2.
FT SITE 152 153 SERINE PROTEASE.
FT SITE 152 153 CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
FT SITE 152 153 FACTOR IXA, OR THROMBIN).
FT ACT_SITE 193 193 BY SIMILARITY.
FT ACT_SITE 242 242 BY SIMILARITY.
FT ACT_SITE 344 344 BY SIMILARITY.
FT BINDING 338 338 SUBSTRATE (BY SIMILARITY).
FT DISULFID 17 22 BY SIMILARITY.
FT DISULFID 50 61 BY SIMILARITY.
FT DISULFID 55 70 BY SIMILARITY.
FT DISULFID 72 81 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 98 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 135 262 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 178 194 BY SIMILARITY.
FT DISULFID 310 329 BY SIMILARITY.
FT DISULFID 340 368 BY SIMILARITY.
FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 O-LINKED (GLCNAC. . .).
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;
Query Match 76.8%; Score 149; DB 1; Length 407;
Best Local Similarity 68.2%; Pred. No. 1,1e-19;
Matches.. 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 1 ANGFLXXLRBGLXRCXXLGFXXAEXIFRNXXTRQFWISY 44
Db 1 ANGLELLPGSLERCREELCSFEEAHBEIFNEERTQFWISY 44
RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
ID FA7_RABIT P98139; P79224;
AC 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII."
RL Thromb. Res. Suppl. 69:231-238(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSES. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77477; AAB37326.1; -.
DR HSPB; P08709; IFAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10glu28glu_4
Perfect score: 189
Sequence: 1 ANGFLXLRBGLRXRCRX.....XAXEIPNXXRTQRFWSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	78.8	407	FA7_BOVIN	P22457 bos taurus
2	131	69.3	444	FA7_RABIT	P98133 coryctolagus
3	123	65.1	466	FA7_HUMAN	P08709 homo sapien
4	110	58.2	218	TMG1_HUMAN	O14668 homo sapien
5	109	57.7	461	PRTC_MOUSE	P33587 mus musculu
6	108	57.1	461	PRTC_RAT	P31394 rattus norv
7	106	56.1	446	FA7_MOUSE	P70375 mus musculu
8	104	55.0	231	TMG3_HUMAN	O9b2d7 homo sapien
9	102	54.0	459	PRTC_PIG	O9g1p2 sus scrofa
10	97	51.3	456	PRTC_BOVIN	P00745 bos taurus
11	96	50.8	488	FA10_HUMAN	O19045 coryctolagus
12	94	49.7	490	FA10_RABIT	P04070 homo sapien
13	93	49.2	461	PRTC_HUMAN	P00743 bos taurus
14	92	48.7	492	FA10_BOVIN	P00740 homo sapien
15	90	47.6	461	FA9_HUMAN	P00741 bos taurus
16	88	46.6	416	FA9_BOVIN	P00740 homo sapien
17	86	45.5	458	PRTC_RABIT	P25155 gallus gall
18	84	44.4	475	FA10_CHICK	P19540 canis fami
19	83	43.9	452	FA9_MOUSE	P16294 mus musculu
20	83	43.9	459	FA9_MOUSE	P16294 mus musculu
21	78	41.3	622	THRB_HUMAN	P00734 homo sapien
22	75	39.7	617	THRB_RAT	P18292 rattus norv
23	75	39.7	618	THRB_MOUSE	P19221 mus musculu
24	72	38.1	400	PRT2_HUMAN	P22891 homo sapien
25	72	38.1	649	PRTS_MACMU	O28520 macaca mula
26	72	38.1	675	PRTS_BOVIN	P07224 bos taurus
27	72	38.1	676	PRTS_HUMAN	P07225 homo sapien
28	71	37.6	202	TMG2_HUMAN	O14669 homo sapien
29	70	37.0	226	PRTS_RABIT	P98118 coryctolagus
30	69	36.5	376	FA10_TROCA	O9b4d6 homo sapien
31	69	36.5	376	THRB_TROCA	P81428 tropidechis
32	69	36.5	625	PRTS_BOVIN	P00735 bos taurus
33	69	36.5	675	PRTS_RAT	P53813 rattus norv

34	68	36.0	396	1	PRT2_BOVIN	P00744 bos taurus
35	62	32.8	675	1	PRTS_MOUSE	O08761 mus musculu
36	56	29.6	413	1	NCAIP_IHNV	P11691 infectious
37	53	28.0	604	1	VE1_BPV2	P03116 bovine papi
38	53	28.0	605	1	VE1_BPV1	P00772 saccharomyc
39	43	22.8	484	1	SLT2_YEAST	P57612 buchnera ap
40	42	22.2	320	1	GSNB_BUCAI	P77493 escherichia
41	41	21.7	315	1	YDHH_ECOLI	P33697 rhizobium m
42	41	21.7	348	1	EXOO_RHIME	P02678 petromyzon
43	41	21.7	477	1	FIBB_PETIM	O50864 myxococcus
44	41	21.7	1275	1	RFBC_MYXMA	P24280 saccharomyc
45	40	21.2	303	1	SC14_YEAST	

ALIGNMENTS

RESULT 1	FA7_BOVIN	STANDARD;	PRT;	407 AA.
ID	FA7_BOVIN			
AC	P22457;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).			
GN	F7.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
NP	[1]			
RP	SEQUENCE.			
RX	MEDLINE=89008362; PubMed=3049594;			
RA	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,			
RA	Iwanaga S.;			
RT	"Bovine factor VII. Its purification and complete amino acid			
RT	sequence.";			
RL	J. Biol. Chem. 263:14868-14877(1988).			
RN	[2]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.			
RX	MEDLINE=91344709; PubMed=2129367;			
RA	Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;			
RA	"A new trisaccharide sugar chain linked to a serine residue in the			
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";			
RT	Adv. Exp. Med. Biol. 281:121-131(1990).			
CC	-I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS			
CC	CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR			
CC	THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR			
CC	AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA			
CC	BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO			
CC	FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.			
CC	-I- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -Ile bond in factor X to			
CC	form factor Xa.			
CC	-I- SUBUNIT: HETERO DIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED			
CC	BY A DISULFIDE BOND.			
CC	-I- TISSUE SPECIFICITY: PLASMA.			
CC	-I- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME			
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND			
CC	CALCIUM.			
CC	-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	-I- SIMILARITY: CONTRAINS 2 EGF-LIKE DOMAINS.			
DR	PIR; A31979; A31979.			
DR	HSP; P08709; 1BP9.			

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A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic
F:1-28/Domain: signal sequence #status predicted <Sig>
F:29-46/Domain: propeptide #status experimental <P>
F:31-91/Domain: Gla domain homology <Gla> light chain #status experimental <ALC>
F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
F:97-128/Domain: EGF homology <EGF>
F:134-170/Domain: EGF homology <EG2>
F:122-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental
F:226-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental

Query Match 47.6%; Score 90; DB 1; Length 461;
Best Local Similarity 39.5%; Pred. No. 9.4e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Db 2 NGFLXLRGSLXKRCRXXLCSPFXAEXIFRNXXRTROFWVS 44
49 SGKLEEFVQGNLRECKMEKCSFEAREVFENTERTTEFWKQY 91

RESULT 12
KFPB0
coagulation factor IXa (EC 3.4.21.22) precursor - bovine
N:Alternate names: Christmas factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence, revision 03-Aug-1984 #text_change 16-Jul-1999
C:Accession: A14757; B20274; I45891; A00923
R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Th
Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa
A:Reference number: A14757; MUID:80056619; PMID:291916
A:Accession: A14757
A:Molecule type: protein
A:Residues: 1-63, 'T', '65-416 <KAT>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Accession: B20274
A:Molecule type: protein
A:Residues: 59-63, 'X', '65-69 <MCM>
R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
Nature 299, 178-180, 1982
A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
A:Reference number: I45891; MUID:82272386; PMID:6287289
A:Accession: 145891
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 52-139 <CHO>
A:Cross-references: GB:00007; NID:g163053; PIDN:AAA30520.1; PID:g163054
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,
J. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
A:Reference number: A44556; MUID:89213999; PMID:3149637
A:Contents: annotation
A:Note: structure and location of a carbohydrate covalently bound to Ser
C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr
C:Comment: The gamma-carboxylglutamic acid residues arise by posttranslational, vitamin K
C:Function: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with stru
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic
F:1-16/Product: coagulation factor IXa light chain #status experimental <ALC>
F:1-45/Domain: Gla domain homology (fragment) <Gla>
F:51-82/Domain: EGF homology <EG1>
F:148-124/Domain: EGF homology <EG2>
F:147-181/Domain: activation peptide #status experimental <AP>
F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:182-409/Domain: trypsin homology <TRY>
F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxylglutamic acid (Glu) #sta
F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfide
F:53/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 46.6%; Score 88; DB 1; Length 416;
Best Local Similarity 37.2%; Pred. No. 1.9e-07;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Db 2 NGFLXLRGSLXKRCRXXLCSPFXAEXIFRNXXRTROFWVS 44
3 SGKLEEFVQGNLRECKMEKCSFEAREVFENTERTTEFWKQY 45

RESULT 13
EXCH
coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N:Alternate names: virus-activating proteinase
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence, revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: S15838; S20380; S20381
R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na
FEBS Lett. 293, 281-285, 1991
A:Title: Primary structure of the virus activating protease from chick embryo. Its ident
A:Reference number: S15838; MUID:91257322; PMID:2044767
A:Accession: S15838
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-475 <SUZ>
A:Cross-references: DBJ:00044; NID:g222869; PIDN:BA00724.1; PID:g222870
R:Gotoh, B.; Yamuchi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
A:Reference number: S20380; MUID:92164779; PMID:1537403
A:Accession: S20380
A:Molecule type: protein
A:Residues: 41-55 <GOT>
A:Accession: S20381
A:Molecule type: protein
A:Residues: 241-246, 'X', '248-251, 'X', '253-261 <GOT>
A:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic
F:1-20/Domain: signal sequence #status predicted <Sig>
F:21-40/Domain: propeptide #status predicted <P>
F:25-84/Domain: Gla domain homology <Gla>
F:41-185/Product: coagulation factor X light chain #status experimental <LCH>
F:99-121/Domain: EGF homology <EG1>
F:119-167/Domain: EGF homology <EG2>
F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F:186-240/Domain: activation peptide #status predicted <AP>
F:241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F:241-468/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #-
F:57-62,90-101,99-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,41
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:163,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 44.4%; Score 84; DB 1; Length 475;
Best Local Similarity 34.1%; Pred. No. 1.1e-06;

A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-92 <KOZ>
R:McCrarw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
A:Reference number: A22673; MUID:85190593; PMID:3857619
A:Accession: A22673
A:Molecule type: mRNA
A:Residues: 1-193,'T',195-461 <MCG>
A:Cross-references: GB:M1309; NID:G180552; PIDN:AAA52023.1; PID:G180553
A:Note: the authors translated the codon ACA for residue 29 as Tyr
R:Jaye, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Finkel, A.; Tolstoch
Nucleic Acids Res. 11, 2325-2335, 1983
A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-b
A:Reference number: A21337; MUID:83320788; PMID:6687940
A:Accession: A21337
A:Molecule type: mRNA
A:Residues: 1-193,'T',195-461 <JNY>
A:Cross-references: GB:J00137; NID:G182610; PIDN:AAA52763.1; PID:G182611
R:Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A:Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
A:Reference number: A37546; MUID:84300526; PMID:6089357
A:Accession: A37546
A:Molecule type: mRNA
A:Residues: 38-193,'T',195-326 <JAG>
A:Cross-references: GB:M35672
R:Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A:Title: Isolation and characterization of a cDNA coding for human factor IX.
A:Reference number: A30623; MUID:83065193; PMID:6959130
A:Accession: A30623
A:Molecule type: mRNA
A:Residues: 1-12,'S',14-73,'P',75-82,'K',84-203,'P',205-216,'G',218-298,'A',299-356,'R',
A:Cross-references: GB:J00136; NID:G182608; PIDN:AAA98726.1; PID:G182609
A:Experimental source: liver
R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 59, 21-29, 1990
A:Title: Development of an immunoaffinity process for factor IX purification.
A:Reference number: A60486; MUID:90194857; PMID:2316207
A:Accession: A60486
A:Molecule type: protein
A:Residues: 47-52,'XX',55-60,'X',62,'XX',65 <THA>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Accession: A20274
A:Molecule type: protein
A:Residues: 105-109,'X',111-115 <MCN>
R:Ballard, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sal
Eur. J. Biochem. 172, 565-572, 1988
A:Title: Characterisation of two differently processed forms of human recombinant factor
A:Reference number: S02527; MUID:8816735; PMID:3280512
A:Accession: S02527
A:Molecule type: protein
A:Residues: 29-63 <BAL>
A:Note: processed forms expressed in recombinant system
R:Allat, S.; Perraud, F.; Dalemans, W.; Ballard, A.; Dieterle, A.; Faure, T.; Meulien,
EMBO J. 9, 3295-3301, 1990
A:Title: Characterization of recombinant human factor IX expressed in transgenic mice an
A:Reference number: S12058; MUID:91006024; PMID:2209546
A:Accession: S12058
A:Molecule type: mRNA; protein
A:Residues: 1-68 <JAL>
A:Note: processed forms expressed in recombinant system
R:Hanford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
EMBO J. 9, 475-480, 1990
A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
A:Reference number: S12377; MUID:90151623; PMID:2406129
A:Accession: S12377
A:Molecule type: protein

A:Residues: 92-130 <HAN>
A:Note: NMR detection of calcium binding by domain expressed in recombinant system
R:de la Salle, C.; Charmanlier, J.L.; Baab, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
Thromb. Haemost. 70, 370-371, 1993
A:Title: A deletion located in the 3' non translated part of the factor IX gene responsi
A:Reference number: I59612; MUID:94054330; PMID:8236150
A:Accession: I59612
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 444-461 <RES>
A:Cross-references: GB:S66752; NID:G439773; PIDN:AA828588.1; PID:G439774
R:Stotler, E.S.; Koebler, D.D.; Sarkar, G.; Sommer, S.S.
Science 239, 491-494, 1988
A:Title: Genomic amplification with transcript sequencing.
A:Reference number: I59529; MUID:88127096; PMID:3340835
A:Accession: I59529
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 290-359 <RE2>
A:Cross-references: GB:M19063; NID:G182622; PIDN:AAA52456.1; PID:G182623
R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw
Biochemistry 33, 5167-5171, 1994
A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin
A:Reference number: A54255; MUID:94227047; PMID:8172892
A:Accession: A54255
A:Molecule type: protein
A:Residues: 'D',204,'X',206-211,'212','D',214,'X',216-221,'D' <AGA>
A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrat
R:Di Scipio, R.G.; Kurachi, K.; Davie, E.W.
J. Clin. Invest. 61, 1528-1538, 1978
A:Title: Activation of human factor IX (Christmas factor).
A:Reference number: A18483; MUID:78194509; PMID:659613
A:Contents: annotation; activation; active site; carbohydrate binding
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
A:Reference number: A37569
A:Contents: annotation
A:Note: 194-Thr was also found
R:Morita, T.; Isaacs, B.S.; Bemon, C.T.; Johnson, A.E.
J. Biol. Chem. 259, 5698-5704, 1984
A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
A:Reference number: A37543; MUID:84185715; PMID:6425296
A:Contents: annotation; calcium binding
R:Morita, T.; Isaacs, B.S.; Bemon, C.T.; Johnson, A.E.
J. Biol. Chem. 260, 2583, 1985
A:Reference number: A37544
A:Contents: annotation; calcium binding, correction
R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
Cell 45, 343-348, 1986
A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation
A:Reference number: A37545; MUID:86189947; PMID:3009023
A:Contents: annotation; signal sequence cleavage site
R:Suethiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
J. Biol. Chem. 264, 21257-21265, 1989
A:Title: Blood clotting factor IX (BIM) Nagoya: subunit of arginine 180 by tryptophan
A:Reference number: A30622; MUID:90078229; PMID:2592373
A:Contents: annotation; sequence of mutant BIM Nagoya
A:Note: carboxylation, glycosylation, and cleavage sites
R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle
submitted to the Brookhaven Protein Data Bank, November 1991
A:Reference number: A51252; PDB:1IXA
A:Contents: annotation; conformation in yeast
A:Note: recombinant form expressed in yeast
C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with sero
C:Genetics:
A:Gene: GDB:F9
A:Cross-references: GDB:119900; OMIM:306900
A:Map position: Xq27.1-Xq27.2
A:Functions: 30/1, 84/2, 93/1, 131/1, 174/1, 241/3, 280/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

N, Alternate names: Stuart factor
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999
 C/Accession: A22867; A14997; A12030; A34412; S39414; A00925
 R/Pung, M.R.; Campbell, R.M.; Macgillivray, T.A.
 Nucleic Acids Res. 12, 4481-4492, 1984
 A/Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
 A/Reference number: A22867; PMID:84247315; PMID:6330671
 A/Accession: A22867
 A/Molecule type: mRNA
 A/Residues: 1-487 <RUN>
 A/Cross-references: GB:X06673; NID:g192; P1DN:CA25286.1; PID:g193
 R/Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
 Biochemistry 19, 659-667, 1980
 A/Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A/Reference number: A14997; PMID:80130563; PMID:6766735
 A/Accession: A14997
 A/Molecule type: protein
 A/Residues: 41-102, 'N', 104-180 <ENF>
 R/McMullen, B.A.; Fujikawa, K.; Kistiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A/Reference number: A20274; PMID:83308813; PMID:6688526
 A/Contents: annotation; revision to residue 103
 R/Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A/Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
 A/Reference number: A12030; PMID:76053069; PMID:1059093
 A/Accession: A12030
 A/Molecule type: protein
 A/Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKEG', 446-492 <T
 A/Note: carbohydrate binding sites and disulfide bonds were determined
 R/Persson, E.; Selander, M.; Lins, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
 J. Biol. Chem. 264, 16897-16904, 1989
 A/Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
 A/Reference number: A34412; PMID:89380326; PMID:2789221
 A/Accession: A34412
 A/Molecule type: protein
 A/Residues: 85-126 <PER>
 A/Note: beta-hydroxyaspartic acid site
 R/Pine, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A/Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A/Reference number: S39414; PMID:94062825; PMID:8243461
 A/Accession: S39414
 A/Molecule type: protein
 A/Residues: 183-196, 199-209, 216-233 <INO>
 A/Note: carbohydrate binding sites
 R/Titani, K.; Hermodson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
 Biochemistry 11, 4899-4903, 1972
 A/Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali
 A/Reference number: A12453; PMID:73053314; PMID:4264286
 A/Contents: annotation; active site
 R/Fujikawa, K.; Titani, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
 A/Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to
 A/Reference number: A13504; PMID:76053121; PMID:1059122
 A/Contents: annotation; activation
 R/Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
 J. Biol. Chem. 259, 5705-5710, 1984
 A/Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
 A/Reference number: A38024; PMID:84185716; PMID:6546930
 A/Contents: annotation; calcium binding
 R/Morita, T.; Jackson, C.M.
 J. Biol. Chem. 261, 4008-4014, 1986
 A/Reference number: A38025; PMID:86140210; PMID:3949800
 A/Contents: annotation; sulfate binding
 C/Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C/Comment: The two chains are formed from a single-chain precursor by the excision of tw
 C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
 activation.
 C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc
 C/Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C/Genetics:
 A:Gene: F10
 A:Map position: 13q34
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:15-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-180/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:234-492/Product: coagulation factor X heavy chain #status experimental <AHC>
 F:234-461/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status p
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:208,485/Binding site: sulfate (Tyr) (covalent) #status experimental
 F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:233-234/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stat
 F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental
 F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 48.7% Score 92; DB 1; Length 492;
 Best Local Similarity 36.4% Pred. No. 4; Se-08;
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLLKREGSLRXRCXXLCSPXXAEXIFRXRXRTGFWVSY 44
 Db 41 ANGFLEEVKGNLNERGLERAGSLERARVEFVDAEQDTEWVSY 84

RESULT 11
 KFHU
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
 N/Alternate names: antihemophilic factor B; Christmas factor
 C/Species: Homo sapiens (man)
 C/Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 15-Sep-2000
 C/Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20
 R/Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 24, 3736-3750, 1985
 A/Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
 A/Reference number: A00922; PMID:86000558; PMID:2994716
 A/Accession: A00922
 A/Molecule type: DNA
 A/Residues: 1-461 <YOS>
 A/Cross-references: GB:K02402; NID:G182612; P1DN:AAB59620.1; PID:G182613
 R/Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Br
 EMBO J. 3, 1053-1060, 1984
 A/Title: The gene structure of human anti-haemophilic factor IX.
 A/Reference number: A37570; PMID:84236100; PMID:6329734
 A/Accession: A37570
 A/Molecule type: DNA
 A/Residues: 1-461 <ANS>
 A/Cross-references: GB:K02048
 R/Reitma, P.H.; Bettina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
 Blood 72, 1074-1076, 1988
 A/Title: The putative factor IX gene promoter in hemophilia B Leyden.
 A/Reference number: A30511; PMID:88327116; PMID:3416069
 A/Accession: A30511
 A/Molecule type: DNA
 A/Residues: 8-24 <REI>
 A/Cross-references: EMBL:X55008; NID:G311288; P1DN:CA38245.2; PID:G4469253
 R/Koeberl, D.D.; Bottema, C.D.K.; Buerelede, J.M.; Sommer, S.S.
 Am. J. Hum. Genet. 45, 448-457, 1989
 A/Title: Functionally important regions of the factor IX gene have a low rate of polymo
 A/Reference number: A32989; PMID:89371752; PMID:2773937
 A/Accession: A32989

C>Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #ext_change 08-Dec-2000
 C/Accession: S49075; J04670; PS0191; PS0190; 162745
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 N/Note: Res. 80, 63-73, 1995
 A/Title: Evidence for competition between vitamin K-dependent clotting factors for intra-
 A/Reference number: A58498; MUID:96093366; PMID:8578539
 A/Accession: S49075
 A/Molecule type: mRNA
 A/Residues: 1-482 <STA1>
 A/Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
 A/Note: submitted to the EMBL Data Library, June 1994
 A/Note: neither the complete nucleic acid sequence nor the complete translation are shown
 R/Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A/Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A/Reference number: J04670; MUID:96194815; PMID:8647460
 A/Accession: J04670
 A/Molecule type: mRNA
 A/Residues: 1-482 <STA2>
 A/Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
 A/Experimental source: Cos-1 cell
 R/Enyoji, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 890-898, 1991
 A/Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma
 A/Reference number: PS0190; MUID:92041742; PMID:1718949
 A/Accession: PS0191
 A/Molecule type: protein
 A/Residues: 41-58, 'X', 60-65 <ENJ1>
 A/Accession: PS0190
 A/Molecule type: protein
 A/Residues: 183-186, 'X', 188-207 <ENJ2>
 R/Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Nihou, Y.
 Eur. J. Hematol. 52, 162-168, 1994
 A/Title: Analysis of the partial nucleotide sequences and deduced primary structures of
 A/Reference number: 146196; MUID:94222160; PMID:8168596
 A/Accession: 162745
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 295-383, 'G', 385-455 <MUR>
 A/Cross-references: GB:D21215; NID:g415309; PIDN:BA04756.1; PID:g455336
 C/Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 F:123/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-179/Product: coagulation factor X light chain #status predicted <LCH>
 F:90-121/Domain: EGF homology <EGF>
 F:129-164/Domain: EGF homology <EG2>
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:183-231/Domain: activation peptide #status predicted <APT>
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
 F:232-460/Domain: trypsin homology <TRY>
 F:57-63, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402, 411-413/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:187/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:208/Binding site: carboxylate (Thr) (covalent) #status predicted
 F:218/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:231-232/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #status predicted
 F:231-232/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #status predicted

Query Match 50.8%; Score 96; DB 1; Length 482;
 Best Local Similarity 36.4%; Pred. No. 8,76-09;
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRBSGLRXCKXXLCSEFXAXEIRFNXXRTQPMVSY 44
 41 ANSFPEETKGNLREKVEEISCFEAREVFDENKTEFFMVKY 84

RESULT 8

EXHU

coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
 N/Alternate names: Stuart factor

C/Species: Homo sapiens (man)

C/Date: 15-Nov-1984 #sequence revision 02-May-1994 #ext_change 08-Dec-2000

C/Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00

R/Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.

Biochemistry 25, 5098-5102, 1986

A/Title: Gene for human Factor X: a blood coagulation factor whose gene organization is

A/Reference number: A24478; MUID:87026600; PMID:3768336

A/Accession: A24478

A/Molecule type: DNA

A/Residues: 1-488 <LEY>

A/Cross-references: GB:I129433; GB:M14327; NID:g459809; PIDN:AAA52764.1; PID:g182831

A/Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.

Gene 99, 291-294, 1991

A/Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor X

A/Reference number: J00917; MUID:91216473; PMID:1902434

A/Accession: J00917

A/Molecule type: mRNA

A/Residues: 1-488 <MES>

A/Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390

R/Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.

J. Biol. Chem. 267, 7395-7401, 1992

A/Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation factor

A/Reference number: A42485; MUID:92218390; PMID:1313796

A/Accession: A42485

A/Molecule type: DNA

A/Residues: 1-15 <MIA>

A/Experimental source: liver

A/Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:93787)

R/Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.

Gene 41, 311-314, 1986

A/Title: Isolation and characterization of human blood-coagulation factor X cDNA.

A/Reference number: A25853; MUID:86221713; PMID:3011603

A/Accession: A25853

A/Molecule type: mRNA

A/Residues: 19-284, 'E', 289-488 <KAU>

A/Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336

R/Pung, M.R.; Hay, C.W.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A/Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X

A/Reference number: A22208; MUID:85216545; PMID:2582420

A/Accession: A22208

A/Molecule type: mRNA

A/Residues: 13-441, 'S', 443-488 <FUN>

A/Cross-references: GB:K03194; NID:g182840; PIDN:AAA52490.1; PID:g182841

R/Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A/Title: Characterization of a cDNA coding for human factor X.

A/Reference number: A21284; MUID:84222026; PMID:6587384

A/Accession: A21284

A/Molecule type: mRNA

A/Residues: 13-284, 'E', 289-488 <LE2>

A/Cross-references: GB:K01886

R/Momulu, B.A.; Fujikawa, K.; Kistiel, W.; Sasaagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss

Biochemistry 22, 2875-2884, 1983

A/Title: Complete amino acid sequence of the light chain of human blood coagulation factor X

A/Reference number: A20362; MUID:83257207; PMID:6671167

A/Accession: A20362

A/Molecule type: protein

A/Residues: 183-234 <INO>

A/Note: glycosylation sites
 A/Note: identification and characterization of beta-hydroxyaspartic acid
 R/Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanham, K.; Lyman, G.

```
F:217-445/Domain: trypsin homology <TRY>  
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F:121-130,139-150,146-159,161-174,182-319,238-251,373-387,398-426/Disulfide bonds: #statu  
F:214,290,335/Binding site: carbohydrate (Aasn) [covalent] #status predicted  
F:253,299,402/Active site: His, Asp, Ser #status predicted
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```
Query Match      57.7%   Score 109; DB 1; Length 461;  
Best Local Similarity 45.5%; Pred. No. 4,4e-11;  
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
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```
OY    1 ANGFLLXLRREGSLKRXCRXXLCSFYAXEIPFNXXXRTQRFWVS Y 44  
         ||| :||| |::| ::||| ::||| ::||| ::|||  
Db     42 A NSFLEEMRPGSLERECMEIICDFEAQEIFONVEDTLAFWKY R 85
```

```
RESULT 5  
S18994 protein C (activated) (BC 3,4,21,69) precursor - rat  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999  
J.Accession: S18994; S24312  
R.OKafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
submitted to the EMBL Data Library, February 1992  
A.Description: The cDNA cloning and mRNA expression of rat protein C.  
A.Reference number: S18994  
A.Accession: S18994  
A.Status: preliminary  
Molecule type: RNA  
A.Residues: 1-461 <OKA>  
A.Cross-references: EMBL:X64336; NID:S56962; PIDN:CAA45617.1; PID:S56963  
R.Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
Biochim. Biophys. Acta 1131, 329-332, 1992  
A.Title: The cDNA cloning and mRNA expression of rat protein C.  
A.Reference number: S24312; PMID:92329550; PMID:1627650  
A.Accession: S24312  
A>Status: preliminary  
Molecule type: RNA  
A.Residues: 1-461 <OKA2>  
A.Cross-references: EMBL:X64336; NID:S56962; PIDN:CAA45617.1; PID:S56963  
G.Superfamily: coagulation factor X; BGF homology; Gla domain homology;  
C.Keywords: beta-hydroxyaspartic acid, glycoprotein, hydrolase, serine protease  
F:11-33/Domains: signal sequence #status predicted <Sig>  
F:27-85/Domains: Gla domain homology <GLA>  
F:43-62/Domains: propeptide #status predicted <PRO>  
F:91-130/Product: protein C #status predicted <PRC>  
F:91-130/Domains: EGF homology <EG1>  
F:139-174/Domains: EGF homology <EG2>  
F:213-445/Domains: trypsin homology <TRY>  
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F:121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #statu  
F:215,291,335/Binding site: carbohydrate (Aasn) [covalent] #status predicted  
F:254,300,402/Active site: His, Asp, Ser #status predicted
```

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Query Match      57.1%   Score 108; DB 1; Length 461;  
Best Local Similarity 45.5%; Pred. No. 6,6e-11;  
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
```

```
OY    1 ANGFLLXLRREGSLKRXCRXXLCSFYAXEIPFNXXXRTQRFWVS Y 44  
         ||| :||| |::| ::||| ::||| ::||| ::|||  
Db     42 A NSFLEEVRAAGSLERECEIEICDPEAQEIFONVEDTLAFWKY R 85
```

```
KKB0 protein C (activated) (BC 3,4,21,69) precursor - bovine (fragment)  
N.Alternate names: autoproteolytic IIa; plasminogen activator (cattle)  
C.Species: Bos primigenius taurus (cattle)  
C.Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999  
J.Accession: A26250; A18385; A18386; A00928  
P.Liong, G.L.; Balazsgé, R.M.; Macgillivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
```

A>Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A:Reference number: A26250; MUID:85014826; PMID:6031100
A:Accession: A26250
A:Molecule type: mRNA
A:Residues: 1-456 <LON>
R:Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982
A>Title: Amino acid sequence of the light chain of bovine protein C.
A:Reference number: A18385; MUID:83007325; PMID:6696876
A:Accession: A18385
A:Molecule type: protein
A:Residues: 40-194 <FER>
A:Note: 82-Lys was also found
R:Kraakberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A>Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
A:Reference number: A19316; MUID:83169769; PMID:6572939
A:Contents: annotation; revision to residue 110
R:Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A>Title: Amino acid sequence of the heavy chain of bovine protein C.
A:Reference number: A18386; MUID:83007326; PMID:6696877
A:Accession: A18386
A:Molecule type: protein
A:Residues: 197-454, 'PV' <STB>
R:Bomon, N.L.; DeBaule, L.E.; Bomon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A>Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless p
A:Reference number: A37541; MUID:8323513; PMID:6304092
A:Contents: annotation; activation; calcium binding
R:Johnson, A.E.; Bomon, N.L.; Laue, T.M.; Bomon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A>Title: Structural changes required for activation of protein C are induced by Ca2+ bin
A:Reference number: A37542; MUID:8323514; PMID:6406503
A:Contents: annotation; activation; calcium binding
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
B.
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with sero
cognition of the thrombin-thrombomodulin complex.
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
F:24-83/Domain: Gla domain homology <GLA>
F:30-33/Domain: propeptide #status predicted <PRO>
F:40-194/Product: protein C light chain #status experimental <LCH>
F:98-128/Domain: EGF homology <EGF>
F:137-172/Domain: EGF homology <EG2>
F:197-456/Product: protein C heavy chain #status experimental <HCH>
F:197-210/Domain: activation peptide #status experimental <APT>
F:211-440/Domain: trypsin homology <TRY>
F:445,46,53,55,56,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:110/Modified site: Eyrthro-beta-hydroxyaspartic acid (Asp) #status experimental
F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #stat
F:136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:252,299,397/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	51.3%	Score 97	DB 1	Length 456
Best Local Similarity	43.2%	Pred. No. 5,5e-09		
Matches	19	Conservative	4	Mismatches 21; Indels 0; Gaps 0;
QY	1	ANGFLXLRBGLXRXCRXXLCSFFXXAEXIFRXNXXRPRQFWVS	44	
Db	40	ANSFLBRLRGVNERECSEVCEFEARELIFONTEDTMAWFSY	83	

RESULT 7

EXRT

coagulation factor Xa (EC 3.4.21.6) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds
(without alignment)
145.545 Million cell updates/sec

Title: 10GLU28GLU_4

Perfect score: 189

Sequence: 1 ANGFLXKUREGSLKRXCRXX.....XXAEXIFRNXXRTQFWVS Y 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	78.8	407	1 KFB07	coagulation factor
2	131	69.3	443	2 I46932	coagulation factor
3	123	65.1	466	1 KFHU7	coagulation factor
4	109	57.7	461	1 UK0210	protein C (activat
5	108	57.1	461	1 S18994	protein C (activat
6	97	51.3	456	1 KXBO	protein C (activat
7	96	50.8	482	1 EXRT	coagulation factor
8	96	50.8	488	1 EXHU	coagulation factor
9	93	49.2	461	1 EXHU	protein C (activat
10	92	49.7	492	1 EXBO	coagulation factor
11	90	47.6	461	1 KFHU	coagulation factor
12	88	46.6	416	1 KFB0	coagulation factor
13	84	44.4	475	1 EXCH	coagulation factor
14	83	44.9	452	1 A30351	coagulation factor
15	83	43.9	459	2 JU0419	coagulation factor
16	78	41.3	622	1 TBHU	thrombin (EC 3.4.2
17	77	40.7	642	2 S53433	thrombin (EC 3.4.2
18	75	39.7	617	2 S10511	thrombin (EC 3.4.2
19	75	39.7	618	2 A35827	thrombin (EC 3.4.2
20	72	38.1	422	1 KKHU2	plasma protein Z p
21	72	38.1	642	2 S53434	plasma protein Z p
22	72	38.1	675	1 KXBO	plasma protein S p
23	72	38.1	676	1 KXHU	plasma protein S p
24	71	37.6	646	2 S38819	thrombin (EC 3.4.2
25	69	36.5	625	1 TBBO	thrombin (EC 3.4.2
26	69	36.5	625	1 KXRTS	plasma protein S p
27	68	36.0	396	1 KXBOZ	plasma protein Z -
28	62	32.8	675	1 KXMS	plasma protein S p
29	61	32.3	678	2 B48089	growth arrest-spec

30	60	31.7	673	2 A48089	growth arrest-spec
31	58	30.7	674	2 I55476	growth potential
32	56	29.6	413	1 VHNH	nucleoprotein - in
33	53	28.0	605	1 W1WLB	E1 protein - bovin
34	53	28.0	620	1 W1WLB2	E1 protein - bovin
35	49.5	26.2	594	2 D84859	probable MAP kinase
36	49.5	26.2	603	2 C96575	probable MAP kinase
37	48.5	25.7	576	2 G86763	probable MAP kinase
38	45.5	24.1	706	2 D86441	unknown protein (l
39	45	23.8	687	2 T08528	probable DNA topol
40	44	23.3	267	2 JC1527	coat protein - pot
41	43	22.8	219	2 AE2449	hypothetical prote
42	43	22.8	484	2 S47377	protein kinase SUR
43	43	22.8	1101	2 T26919	hypothetical prote
44	43	22.8	1217	2 T21403	hypothetical prote
45	42.5	22.5	907	2 T15792	hypothetical prote

ALIGNMENTS

RESULT 1

KFB07

C:Species: Bos primigenius taurus (cattle) - bovine

C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999

C:Accession: A31979; C20274

J.Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A:Title: Bovine factor VII. Its purification and complete amino acid sequence.

A:Reference number: A31979; PMID:89008362; PMID:3049594

A:Accession: A31979

A:Molecule type: protein

A:Residues: 1-407 <TAK>

R.McMullen, B.A.; Fujikawa, K.; Kistel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; PMID:83308813; PMID:688526

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCW>

A>Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R.Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A44556; PMID:89213999; PMID:3149637

A:Contents: annotation

A>Note: structure and location of covalently bound carbohydrate

C:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

gulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylutam

F:1-152/Product: coagulation factor VIIa light chain #status experimental <MAI>

F:1-44/Domain: Gla domain homology (fragment) <GUA>

F:50-81/Domain: EGF homology <EG1>

F:91-127/Domain: EGF homology <EG2>

F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F:153-387/Domain: trypsin homology <TRY>

F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxylglutamic acid (Glu) #status

F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/

F:52/Binding site: carboxylate (Ser) (covalent) #status experimental

F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experiment

F:145,203/Binding site: carboxylate (Asn) (covalent) #status experimental

F:152-153/Cleavage site: Arg-1le (coagulation factor XIIIa) #status experimental

F:193,244,344/Active site: His, Asp, Ser #status predicted

F:290-291/Cleavage site: Arg-Gly (coagulation factor XIa) #status experimental

Query Match Score 149; DB 1; Length 407;
Best Local Similarity 68.2%; Pred. No. 3.8e-18;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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CC	The invention relates to novel Factor VII (FVII) or Factor VIIIa (FVIIIa)
CC	polypeptide conjugates, comprising at least one non-polypeptide group
CC	covalently attached to a polypeptide, where the amino acid sequence of
CC	polypeptide differs from that of the wildtype FVIIIa (AAM52171) in that at
CC	least one amino acid residue containing an attachment group for the
CC	non-polypeptide group has been introduced or removed. The FVIIIa
CC	conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC	cerebroprotective activity and are useful for treating FVIIIa/FI-related
CC	diseases or disorders such as haemophilia, liver disease, myocardial
CC	infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC	have increased functional in vivo half life and/or increased plasma half
CC	life, increased bioavailability and/or reduced sensitivity to proteolytic
CC	degradation. Consequently medical treatment using the conjugates has a
CC	number of advantages over currently available such as longer duration
CC	between injections.
CC	
SQ	Sequence 406 AA;
Query Match	65.1%; Score 123; DB 22; Length 406;
Best Local Similarity	75.0%; Pred. No. 1.1e-11;
Matches 33; Conservative	5; Mismatches 6; Indels 0; Gaps 0
Oy	1 AANGFLXLLREGSLRXRCRRXXLCSFFXAEXIFRNXXRTRPQWVSV 44
Dd	1 AANFLXXLRPSLXRKCKXKCSPFXARXIKFAAXRTKLFWISY 44
RESULT 15	
ID	AAM52172
AC	AAM52172 standard; Protein; 406 AA.
XX	
AC	AAM52172;
XX	
DT	07-FEB-2002 (first entry)
DE	Mammalian expressed human FVII SEQ ID NO 3.
XX	
KW	Factor Vll; Fvll; Factor Vila; Fvlla; haemostatic; thrombolytic;
KV	cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
XX	myocardial infarction; thrombotic stroke; deep-vein thrombosis.
OS	Homo sapiens.
XX	
FH	Key
FH	Location/Qualifiers
FT	Modified-site 52
FT	/note= "O-glycosylated"
FT	Modified-site 60
FT	/note= "O-glycosylated"
FT	Modified-site 145
FT	/note= "N-glycosylated"
FT	Cleavage-site 152..153
FT	/note= "proteolytic cleavage site converting FVII zymogen
FT	to an activated form, comprising two chains
FT	linked by a single disulphide bridge"
FT	Modified-site 322
FT	/note= "N-glycosylated"
PX	
PN	WO200158935-A2.
XX	
PD	16-AUG-2001.
XX	
PF	12-FEB-2001; 2001WO-DK00094.
XX	
PR	11-FEB-2000; 2000DK-0000218.
PR	18-OCT-2000; 2000DK-0001558.
XX	
PA	(MAXY-) MAXYGEN APS.
XX	
PI	Andersen KV, Pedersen AH, Bornaes C;
XX	
DR	WPI; 2001-581807/65.
XX	
DR	N-PsDB; AA19983.
XX	

	New conjugate, useful for treating Factor VIIa related diseases or
PT	disorders such as haemophilia, liver disease, myocardial infarction and
PR	deep-vein thrombosis, comprises non-polypeptide group covalently
PT	attached to polypeptide group -
xx	
PS	Disclosure; Page 85-86; 89pp; English.
xx	
CC	The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC	polypeptide conjugates, comprising at least one non-polypeptide group
CC	covalently attached to a polypeptide, where the amino acid sequence of
CC	polypeptide differs from that of the wildtype FVIIa (AAM5217) in that at
CC	least one amino acid residue containing an attachment group for the
CC	non-polypeptide group has been introduced or removed. The FVIIa
CC	conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC	cerebroprotective activity and are useful for treating FVIIa/TF-related
CC	diseases or disorders such as haemophilia, liver disease, myocardial
CC	infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC	have increased functional in vivo half life and/or increased plasma half
CC	life, increased bioavailability and/or reduced sensitivity to proteolytic
CC	degradation. Consequently medical treatment using the conjugates has a
CC	number of advantages over currently available such as longer duration
CC	between injections.
xx	
SQ	Sequence 406 AA;
	Query Match 65.1%; Score 123; DB 22; Length 406;
	Best Local Similarity 52.3%; Pred. No. 1.le-11;
	Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0
Gy	1 ANGFLXLRREGSLRXCRXXLCSFXKAEIFNNXXRTROFWMSY 44
DB	1 ANAFLLELRPGSLRECKREEQCSFEAREIRFDARTRKJFWISY 44

Search completed: March 19, 2003, 14:51:13
Job time : 32.4375 secs

CC	The invention relates to novel Factor VII (FVII) or Factor VIII (FVIII)
CC	polypeptide conjugates, comprising at least one non-polypeptide group
CC	covalently attached to a polypeptide, where the amino acid sequence of
CC	polypeptide differs from that of the wildtype FVIII (AAM52171) in that at
CC	least one amino acid residue containing an attachment group for the
CC	non-polypeptide group has been introduced or removed. The FVIII
CC	conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC	cerebroprotective activity and are useful for treating FVIII/FI-related
CC	diseases or disorders such as haemophilia, liver disease, myocardial
CC	infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC	have increased functional in vivo half life and/or increased plasma half
CC	life, increased bioavailability and/or reduced sensitivity to proteolytic
CC	degradation. Consequently medical treatment using the conjugates has a
CC	number of advantages over currently available such as longer duration
CC	between injections.
CC	
SQ	Sequence 406 AA;
Oy	
Db	1 ANGFLXLLREGSLRXRCRRXXLCSFFXAEXIFRNXXRTRPQWVSV 44 1 AAFPLXXLRPSGLRXCKKXCSCSFXAXRKIFKQAXRTKLFWISY 44
RESULT 15	
ID	AAM52172
XX	AAM52172 standard; Protein; 406 AA.
AC	AAM52172;
XX	
DT	07-FEB-2002 (first entry)
DE	Mammalian expressed human FVIII SEQ ID NO 3.
XX	
KW	Factor VII; FVIII; Factor Vlla; FvIIa; haemostatic; thrombolytic;
KV	cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
XX	myocardial infarction; thrombotic stroke; deep-vein thrombosis.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 52
FT	/note= "O-glycosylated"
FT	Modified-site 60
FT	/note= "O-glycosylated"
FT	Modified-site 145
FT	/note= "N-glycosylated"
FT	Cleavage-site 152..153
FT	/note= "proteolytic cleavage site converting FVIII zymogen
FT	to an activated form, comprising two chains
FT	linked by a single disulphide bridge"
FT	Modified-site 322
FT	/note= "N-glycosylated"
PX	
PN	WO200158935-A2.
XX	
PD	16-AUG-2001.
XX	
PF	12-FEB-2001; 2001WO-DK00094.
XX	
PR	11-FEB-2000; 2000DK-0000218.
PR	18-OCT-2000; 2000DK-0001558.
XX	
PA	(MAXY-) MAXYGEN APS.
XX	
PI	Andersen KV, Pedersen AH, Bornaes C;
XX	
DR	WPI; 2001-581807/65.
XX	N-PsDB; AA19983.
XX	

KM		Factor VIIA; human; shock heat treatment; protein stability;
KM		protein manufacture; protein conformation; mutant; mutain.
OS	Homo sapiens.	
XX	Synthetic.	
FT	Key	Location/Qualifiers
FT	Active-site	193
FT	/note= "Member of the factor VIIA catalytic triad"	
FT	Active-site	242
FT	/note= "Member of the factor VIIA catalytic triad"	
FT	Active-site	344
FT	/note= "Member of the factor VIIA catalytic triad"	
FT	Misc-difference	344
FT	/label= Gly, Met, Thr	
FT	/note= "Preferably Ala. wild type Ser"	
XX		
PN	WO200177141-A1.	
XX		
PD	18-OCT-2001.	
XX		
PF	06-APR-2001; 2001WO-DK00234.	
XX		
PR	06-APR-2000; 2000DK-0000573.	
PR	17-APR-2000; 2000US-197650P.	
XX		
PA	(NOVO) NOVO NORDISK AS.	
XX		
PI	Matchlesen F;	
DR	WPI; 2001-657162/75.	
XX		
PT	Stabilisation of a polypeptide e.g. in a pharmaceutical composition	
PT	involves a shock heat treatment -	
XX		
PS	Disclosure; Page -: 22pp; English.	
XX		
CC	The invention describes a method of stabilising a polypeptide involving	
CC	shock heat treatment of the polypeptide. The method is useful in a	
CC	pharmaceutical composition, in the industrial or large scale method of	
CC	manufacturing a polypeptide, also as a unit operation during preparation,	
CC	purification, recovery and/or formulation of polypeptides. The shock heat	
CC	treatment improves the protein stability without substantial loss of	
CC	biological activity. The method can be applied to change polypeptide	
CC	conformation in a very fast and non-invasive manner. The polypeptide	
CC	formed is stable. The method is also useful for decreasing the	
CC	association of the polypeptide. This sequence represents a modified	
CC	human factor VIIA protein, mutated at the catalytic site, described	
CC	in the invention.	
CC	Note: This sequence does not appear in the specification but has	
CC	been obtained using information given in the invention.	
XX		
SQ	Sequence 406 AA:	
	Query Match 65.1%; Score 123; DB 22; Length 406;	
	Best Local Similarity 52.3%; Pred.No. 1.1e-11;	
	Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;	
OY	1 ANGFLXLRREGSLRXCRXXLCSFXXAEIIFNNXXRTROFWMSY 44	
Dd	1 ANAFLEELRPGLERCKEKEQCSFEEDARIEFDXAERTKLFWISY 44	
	RESULT 14	
ID	AAM52171 standard; Protein; 406 AA.	
XX	AAM52171	
AC	AAM52171;	
XX		
DT	07-FEB-2002 (first entry)	
DE	Human FVII SEQ ID NO 1.	
XX		

KM	Factor VII; FVIII, Factor VIIa; FVIIA; haemostatic; thrombolytic;
KW	cardiac; hepatotropic; cerebroprotective; haemophilia; liver disease;
KW	myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 6 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 7 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 14 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 16 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 19 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 20 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 25 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 26 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 29 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 35 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Modified-site 52 /note= "O-glycosylated"
FT	Modified-site 60 /note= "O-glycosylated"
FT	Modified-site 145 /note= "N-glycosylated"
FT	Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
FT	Modified-site 322 /note= "N-glycosylated"
FT	
XX	
PN	WO200158935-A2.
XX	
PD	16-AUG-2001.
XX	
PB	12-FEB-2001; 2001WO-DK00094.
XX	
PR	11-FEB-2000; 2000DK-0000218.
PR	18-OCT-2000; 2000DK-0001558.
XX	
PA	(MAXY-) MAXYGEN APS.
XX	
PI	Andersen KV, Pedersen AH, Bornaes C;
XX	
DR	WPI; 2001-581807/65.
XX	
N-PSDB:	AAI99982.
XX	
PT	New conjugate, useful for treating Factor VIIa related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -
XX	
PS	Claim 1; Page 81-83; 89pp; English.
XX	

RESULT	11
AAW14509	
ID	AAW14509 standard; protein; 406 AA.
XX AC	
XX	AAW14509;
DT	14-MAY-1997 (first entry)
XX	
DE	Modified blood coagulation Factor VII (R290S).
XX	
KM	Blood coagulation; factor 7; mutein; mutation; modification;
RW	thrombocytopenia; von Willebrand's disease; plasma substitute
XX OS	
OS	Homo sapiens.
XX	Synthetic.
FH	
FT	Key
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Disulfide-bond
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Cleavage-site
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Cleavage-site
FT	/note= "proteolytic site"
FT	
FT	Cleavage-site
FT	/note= "proteolytic site"
FT	
FT	Disulfide-bond
FT	Disulfide-bond
FT	Modified-site
FT	
FT	/label= OTHER
FT	/note= "beta-hydroxy-aspartic acid"
FT	
FT	Disulfide-bond
FT	91..102
FT	Disulfide-bond
FT	98..112
FT	Disulfide-bond
FT	114..127
FT	Disulfide-bond
FT	135..162
FT	Cleavage-site
FT	143..144
FT	/note= "proteolytic site"
FT	
FT	Modified-site
FT	145
FT	/note= "glycosylation site"
FT	159..164
FT	Disulfide-bond

FT	Disulfide-bond	178..194	
FT	Active-site	193	
FT	Active-site	242	
FT	Active-site	344	
FT	Cleavage-site	290..291	
FT	Misc-difference	290	
FT	/note=	"proteolytic site in unmodified factor VII"	
FT	/note=	"native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"	
FT	Disulfide-bond	310..329	
FT	Cleavage-site	315..316	
FT	/note=	"proteolytic site"	
FT	Modified-site	322	
FT	/note=	"glycosylation site"	
FT	Disulfide-bond	340..368	
FT	Cleavage-site	341..342	
FT	/note=	"proteolytic site"	
FT	Cleavage-site	392..393	
FT	/note=	"proteolytic site"	
FT	Cleavage-site	396..397	
FT	/note=	"proteolytic site"	
FT	Cleavage-site	402..403	
FT	/note=	"proteolytic site"	
XX	US5580560-A.		
XX	03-DEC-1996.		
XX	13-NOV-1989;	89US-0434149.	
XX	09-AUG-1993;	93US-0104509.	
PR	13-NOV-1989;	89US-0434149.	
PR	12-JUN-1992;	92US-0898248.	
XX	22-AUG-1994;	94US-0293778.	
PA	(NOVO) NOVO-NORDISK AS.		
XX	Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;		
XX	WPI; 1997-033523/03.		
PT	Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability		
PS	Example 3; Page -: 28pp; English.		
CC	Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys88, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys441 by an amino acid that provides a proteolytically more stable peptide bond, provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser. The modified proteins are useful for treating bleeding disorders such as thrombocytopenia and von Willebrand's disease. They are also suitable for addition to plasma substitutes. The present sequence is a specific example of a modified factor VII protein.		
CC	The present sequence is a specific example of a modified factor VII protein.		
CC	Sequence	406 AA;	
CC	Query Match	65.1%;	Score 123; DB 18; Length 406;
CC	Best Local Similarity	52.3%;	Pred. No. 1,1e-11;
CC	Matches	23; Conservative	5; Mismatches 16; Indels 0; Gaps 0.
QY	1	ANGPLXLRREGSLRXRCRXLCSFXXAEXIFPNXXRTRQFWVS	44
DB	1	ANAFLEELRPGLERCKEBOCCSFEDAREIFDARTKLFWSY	44
XX	XX	XX	XX

XX	Sequence	401 AA;
SQ		
Query Match	65.1%; Score 123; DB 22;	Length 401;
Best Local Similarity	52.3%; Pred. No. 1,le-11;	
Matches	23; Conservative	5; Mismatches 16; Indels 0; Gaps 0;
Oy	1 ANGFLXXLREGSLXRXCRXXLCSPFXAEXIFRNXXRTQFWVS	44
Dd	1 ANAFLEELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY	44
RESULT 9		
ID	AAB84871	standard; Protein; 401 AA.
XX	AAB84871;	
AC		
DT	31-JUL-2001	(first entry)
XX		
DE	Mutant blood coagulant factor VII (FVII-39).	
XX		
KM	Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;	
KW	mutant; mutcin.	
XX		
OS	Homo sapiens.	
XX	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 235..239	/note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-Arg-Lys-Thr-Leu"
FT	Misc-difference 311..317	/note= "Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp-Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
FN	JP2001061479-A.	
PD	13-MAR-2001.	
PF	24-AUG-1999;	99JP-0237610.
PR	24-AUG-1999;	99JP-0237610.
PA	(KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.	
DR	WPI; 2001-310677/33.	
XX	N-PSTDB; AAH19464.	
PT	Mutant of blood coagulant factor VII, used for substitution therapy in the treatment of hemophilia -	
PS	Claim 16; Page 23-24; 29pp; Japanese.	
CC	The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is one such mutant FVII-39. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients.	
SQ	Sequence	401 AA;
Query Match	65.1%; Score 123; DB 22;	Length 401;
Best Local Similarity	52.3%; Pred. No. 1,le-11;	
Matches	23; Conservative	5; Mismatches 16; Indels 0; Gaps 0;
Oy	1 ANGFLXXLREGSLXRXCRXXLCSPFXAEXIFRNXXRTQFWVS	44
Dd	1 ANAFLEELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY	44
RESULT 10		
ID	AAR35764	standard; protein; 406 AA.
AA	AAR35764	

XX	AAR35764;
AC	
XX	
DT	24-SEP-1993 (first entry)
XX	
DE	Factor VII (VII).
XX	
KM	PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
KW	Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
XX	exosite; catalytic activity.
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	/note= "Factor VII light chain"
FT	153..406
FT	/note= "Factor VII heavy chain"
FT	374..388
FT	/note= "exosite 1"
FT	290..310
FT	/note= "exosite 2"
FT	290..310
FT	/note= "pref. PC polypeptide; claim 2, page 136"
FT	374..388
FT	/note= "pref. PC polypeptide; claim 2, page 136"
FT	289..304
FT	/note= "pref. PC polypeptide; claim 4, page 137"
FT	290..304
FT	/note= "pref. PC polypeptide; claim 4, page 137"
FT	245..266
FT	/note= "claim 9, page 138-139 describes an antibody that reacts with Factor VII; fragments 289-304, 290-304, 290-310, 374-388 and 400-414 but not with fragment 245-266"
PN	WO9309804-A.
XX	
PD	27-MAY-1993.
XX	
PF	18-NOV-1992; 92MO-US10242.
XX	
PR	18-NOV-1991; 91US-0793989.
XX	
PA	(SCRI) SCRIPPS RES INST.
XX	
PI	Griffin JH, Masters RM;
XX	
DR	WPI; 1993-182244/22.
XX	
PT	Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples
PT	
XX	
PS	Disclosure; Page 133-135; 149pp; English.
XX	
CC	The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood CC common. of 0.1-100 (pref. 0.5-10) microm. CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described CC in the specification but have not yet been added to the SEQUENCE CC listing.
XX	
SQ	Sequence 406 AA:
Query Match	65.1%; Score 123; DB 14; Length 406;
Best Local Similarity	52.3%; Pred. No. 1,1e-11;
Matches 23; Conservative	5; Mismatches 16; Indels 0; Gaps 0;
Y	1 ANGFLXLRBGLRXRCXXILCSFYXAAXIFRNXXRTQFWVS 44
DB	1 ANAFLELRLPGSLRECKEBOGCSFEAREEIFDQARTKLFWSI 44

XX 29-APR-1999.
 XX 20-OCT-1996; 98WO-US22152.
 XX 23-OCT-1997; 97US-0955636.
 XX (MINU) UNIV MINNESOTA.
 XX Nelsestuen GL;
 XX WPI; 1999-288309/24.
 XX
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 XX acid domain, useful for treating clotting disorders
 XX Disclosure; Page 15; 86pp; English.
 XX
 XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
 XX domain. The invention relates to a vitamin K-dependent polypeptide
 XX comprising a modified GLA domain containing an amino acid substitution
 XX which enhances membrane binding of the modified polypeptide as compared
 XX to the native polypeptide. The polypeptide is used to treat a clotting
 XX disorder by decreasing or increasing clot formation. Modification of the
 XX GLA domain results in a protein which has enhanced membrane binding
 XX affinity as compared to the native protein.
 XX
 XX Sequence 44 AA;
 XX
 XX Query Match 65.1%; Score 123; DB 20; Length 44;
 XX Best Local Similarity 75.0%; Pred. No. 1.3e-12;
 XX Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 XX
 XX QY 1 ANGFLXXLRGSLXRCXXLCSPFXAEXIFRNXXRTROFWVS 44
 XX 1 ANAFLLXXLRPGLXRCXXKQCSFXXARXIFKDXRKLFWISY 44
 XX DB
 XX
 XX RESULT 7
 XX AAB36395
 XX ID AAB36395 standard; peptide; 44 AA.
 XX AC AAB36395;
 XX DT 27-FEB-2001 (first entry)
 XX DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 XX gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 XX factor X; prothrombin; enhanced membrane binding affinity;
 XX clot formation; thrombolytic; haemostatic; bleeding disorder;
 XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
 XX liver disease.
 XX OS Homo sapiens.
 XX PN WO200066753-A2.
 XX PD 09-NOV-2000.
 XX PF 28-APR-2000; 2000WO-US11416.
 XX PR 29-APR-1999; 99US-0302239.
 XX PA (MINU) UNIV MINNESOTA.
 XX PI Nelsestuen GL;
 XX WPI; 2001-007226/01.
 XX Novel vitamin K-dependent polypeptide useful for treating clotting
 XX disorders such as thrombosis and hemophilia, comprises modified

PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity -
 XX
 XX PS Disclosure; Page 12; 81pp; English.
 XX
 XX The present invention describes a vitamin K-dependent polypeptide (I)
 XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 XX at least one amino acid substitution, that enhances membrane binding
 XX affinity and the activity of the polypeptide relative to a corresponding
 XX native vitamin K-dependent polypeptide and inhibits clot formation.
 XX (I) can have thrombolytic and haemostatic activities, and can be used
 XX as an inhibitor of clot formation. (I) is useful for decreasing clot
 XX formation in a mammal, a factor VII or factor IX containing a modified
 XX GLA domain is useful for increasing clot formation and for treating a
 XX bleeding disorder, including thrombosis and clotting disorders such as
 XX haemophilia A, haemophilia B and liver disease. The present sequence
 XX represents a wild type human factor VII GLA domain sequence, given in
 XX the exemplification of the present invention.
 XX
 XX Sequence 44 AA;
 XX
 XX Query Match 65.1%; Score 123; DB 22; Length 44;
 XX Best Local Similarity 75.0%; Pred. No. 1.3e-12;
 XX Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 XX
 XX QY 1 ANGFLXXLRGSLXRCXXLCSPFXAEXIFRNXXRTROFWVS 44
 XX 1 ANAFLLXXLRPGLXRCXXKQCSFXXARXIFKDXRKLFWISY 44
 XX DB
 XX
 XX RESULT 8
 XX AAB84870
 XX ID AAB84870 standard; Protein; 401 AA.
 XX AC AAB84870;
 XX DT 31-JUL-2001 (first entry)
 XX DE Mutant blood coagulant factor VII (FVII-31).
 XX KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 XX mutant; mutain.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 311..317
 XX FT /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 XX -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX JP2001061479-A.
 XX PD 13-MAR-2001.
 XX PF 24-AUG-1999; 99JP-0237610.
 XX PR 24-AUG-1999; 99JP-0237610.
 XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX WPI; 2001-310677/33.
 XX N-PSDB; AAH19463.
 XX PT Mutant of blood coagulant factor VII, used for substitution therapy in
 XX the treatment of hemophilia -
 XX Claim 14; Page 20-21; 29pp; Japanese.
 XX The present invention relates to mutants of blood coagulant factor VII
 XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
 XX sequence is one such mutant FVII: VII-31. The mutants can be used as an
 XX agent for the substitution therapy of haemophilia inhibitor patients.

```
Oy 1 ANGFLXXLRGSLRXRCRXXLCSPFXXAEXIFRNXXRTROFWSY 44
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ANAFLXXLRGSLRXRCRXXQCSFPXXARXIFDAXRTKLFWISY 44

RESULT 4
ID AAY18311 standard; peptide; 44 AA.
XX
AC AAY18311;
XX
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KW therapy.
XX
KW Homo sapiens.
XX
OS Synthetic.
OS
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
FT
FT WO9920767-A1.
XX
PN 29-APR-1999.
XX
PD 20-OCT-1998; 98WO-US22152.
XX
PF 23-OCT-1997; 97US-0955636.
XX
PR (MINU ) UNIV MINNESOTA.
XX
PA Nelsestuen GL;
XX
PI WPI; 1999-288309/24.
XX
DR Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
PT
XX
PS Disclosure; Page 80; 86pp; English.
XX
ES This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
SQ Sequence 44 AA;

Query Match 66.7%; Score 126; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 4,3e-13;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRGSLRXRCRXXLCSPFXXAEXIFRNXXRTROFWSY 44
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ANAFLXXLRDGSIXRCRXXQCSFPXXARXIFDAXRTKLFWISY 44

RESULT 5
ID AAY18302 standard; peptide; 44 AA.
XX
AC AAY18302;
XX
DT 17-AUG-1999 (first entry)
XX
```

```
DE Modified GLA domain of vitamin K-dependent protein.
XX
KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KW therapy.
XX
KW Homo sapiens.
XX
OS Synthetic.
OS
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
FT
FT WO9920767-A1.
XX
PN 29-APR-1999.
XX
PD 20-OCT-1998; 98WO-US22152.
XX
PF 23-OCT-1997; 97US-0955636.
XX
PR (MINU ) UNIV MINNESOTA.
XX
PA Nelsestuen GL;
XX
PI WPI; 1999-288309/24.
XX
DR Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
PT
XX
PS Claim 11; Page 81; 86pp; English.
XX
ES This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
SQ Sequence 44 AA;

Query Match 65.6%; Score 124; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 9,1e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRGSLRXRCRXXLCSPFXXAEXIFRNXXRTROFWSY 44
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ANAFLXXLRGSLRXRCRXXQCSFPXXARXIFDAXRTKLFWISY 44

RESULT 6
ID AAY18305 standard; peptide; 44 AA.
XX
AC AAY18305;
XX
DT 17-AUG-1999 (first entry)
XX
DE Human factor VII GLA domain.
XX
KW GLA domain; vitamin K-dependent protein; clotting disorder;
KW therapy.
XX
KW Homo sapiens.
XX
OS
OS
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
FT
FT WO9920767-A1.
XX
PN
```

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure, Page 15; 86pp; English.
 XX
 CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA;
 XX
 Query Match 82.5%; Score 156; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 6.1e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ANGFLXXLRGSLRXRCRXLCSPFXAEXIFRNXXRTRQFWVS 44
 DB 1 ANGFLXXLRGSLRXRCRXLCSPFXAHXIFRNXXRTRQFWVS 44
 RESULT 2
 AAB36396
 ID AAB36396 standard; peptide; 44 AA.
 AC AAB36396;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.
 XX
 XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KM factor X; prothrombin; enhanced membrane binding affinity;
 KM clot formation; thrombolytic; haemostatic; bleeding disorder;
 KM thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KM liver disease.
 XX
 OS Bos taurus.
 XX
 PN WO200066753-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US11416.
 XX
 PR 29-APR-1999; 99US-0302239.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsstuen GL;
 XX
 PS WPI; 2001-007226/01.
 DR
 XX
 PT Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprises modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity
 XX
 PS Disclosure, Page 12; 81pp; English.
 XX
 CC The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified
 CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type bovine factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 44 AA;
 XX
 Query Match 82.5%; Score 156; DB 22; Length 44;
 Best Local Similarity 95.5%; Pred. No. 6.1e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ANGFLXXLRGSLRXRCRXLCSPFXAEXIFRNXXRTRQFWVS 44
 DB 1 ANGFLXXLRGSLRXRCRXLCSPFXAHXIFRNXXRTRQFWVS 44
 RESULT 3
 AAY18310
 ID AAY18310 standard; peptide; 44 AA.
 AC AAY18310;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KM therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note="Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 PN MO9920767-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsstuen GL;
 XX
 PS WPI; 1999-288309/24.
 DR
 XX
 PT vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure, Page 80; 86pp; English.
 XX
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA;
 XX
 Query Match 68.3%; Score 129; DB 20; Length 44;
 Best Local Similarity 77.3%; Pred. No. 1.4e-13;
 Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-312

Query Match          35.3%; Score 67; DB 9; Length 209;
Best Local Similarity 38.2%; Pred. No. 0.00039;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLRXRCRXXLCSFXXAFXIFRNXXRTQFWVS 44
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 46 GNLERECNEELCNVEAREIFVDEDKTIAFWQEV 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kiser, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-759-130B-310

Query Match          35.3%; Score 67; DB 9; Length 226;
Best Local Similarity 38.2%; Pred. No. 0.00042;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLRXRCRXXLCSFXXAFXIFRNXXRTQFWVS 44
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 63 GNLERECNEELCNVEAREIFVDEDKTIAFWQEV 96

Search completed: March 20, 2003, 13:30:19
Job time : 9.375 secs
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;; CURRENT APPLICATION NUMBER: US/10/132,829
;; CURRENT FILING DATE: 2002-04-25
;; PRIOR APPLICATION NUMBER: 60/286,314
;; PRIOR FILING DATE: 2001-04-25
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 5
;; LENGTH: 461
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match 45.8%; Score 87; DB 9; Length 461;
Best Local Similarity 39.5%; Pred. No. 2.8e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRBEGSLKRXCKXLLCSFXKXAFIFRNXXRTQFWSY 44
DB 49 SGKLEFVQGNLERECMEKCSFEAREVFENTERTEFEWQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homosapien
US-09-884-901-3

Query Match 45.8%; Score 87; DB 10; Length 461;
Best Local Similarity 39.5%; Pred. No. 2.8e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRBEGSLKRXCKXLLCSFXKXAFIFRNXXRTQFWSY 44
DB 49 SGKLEFVQGNLERECMEKCSFEAREVFENTERTEFEWQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B

;; CURRENT FILING DATE: 2002-09-16
;; PRIOR APPLICATION NUMBER: US 09/479,249
;; PRIOR FILING DATE: 2000-01-07
;; PRIOR APPLICATION NUMBER: US 09/559,497
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: US 09/578,063
;; PRIOR FILING DATE: 2000-05-24
;; PRIOR APPLICATION NUMBER: US 09/333,159
;; PRIOR FILING DATE: 1999-06-14
;; PRIOR APPLICATION NUMBER: US 09/596,194
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 09/342,364
;; PRIOR FILING DATE: 1999-06-29
;; PRIOR APPLICATION NUMBER: US 09/608,452
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/393,996
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: US 09/602,871
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: US 09/420,707
;; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match 35.3%; Score 67; DB 9; Length 96;
Best Local Similarity 38.2%; Pred. No. 0.00018;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLKRXCKXLLCSFXKXAFIFRNXXRTQFWSY 44
DB 46 GNLERECNEBLCNVERAREIFVDEKTIATFQWQY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29


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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          47.9%; Score 91; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 5e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLKRXCRXXLCSPFXAXFIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECTIEICDPEEAKEIFEDVDTLAFW 41

RESULT 3
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLKRXCRXXLCSPFXAXFIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECTIEICDPEEAKEIFQNVDDTLAFW 41

RESULT 4
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLKRXCRXXLCSPFXAXFIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECTIEICDPEEAKEIFEDVDTLAFW 41

RESULT 5
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLKRXCRXXLCSPFXAXFIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECTIEICDPEEAKEIFEDVDTLAFW 41

RESULT 6
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10glu28phe_4
Perfect score: 190
Sequence: 1 ANGFLXXLRREGSLRXCRXX.....XXAFXIFRNXXRTQFWVS 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues
Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	63.2	406	US-10-109-498-1	Sequence 1, Appl1
2	91	47.9	419	US-10-182-263-6	Sequence 6, Appl1
3	89	46.8	419	US-10-182-263-1	Sequence 3, Appl1
4	89	46.8	419	US-10-182-263-3	Sequence 4, Appl1
5	89	46.8	419	US-10-182-263-4	Sequence 5, Appl1
6	89	46.8	419	US-10-182-263-5	Sequence 2, Appl1
7	89	46.8	419	US-09-978-917A-4	Sequence 2, Appl1
8	89	46.8	461	US-10-182-263-2	Sequence 2, Appl1
9	89	46.8	461	US-09-978-917A-2	Sequence 2, Appl1
10	87	45.8	415	US-09-118-748-2	Sequence 2, Appl1
11	87	45.8	461	US-10-132-829-5	Sequence 5, Appl1
12	87	45.8	461	US-09-884-901-3	Sequence 3, Appl1
13	67	35.3	96	US-09-759-130B-312	Sequence 312, App
14	67	35.3	209	US-09-759-130B-312	Sequence 312, App
15	67	35.3	226	US-09-759-130B-310	Sequence 310, App
16	50	26.3	95	US-09-759-130B-356	Sequence 356, App
17	50	26.3	208	US-09-759-130B-355	Sequence 355, App
18	50	26.3	225	US-09-759-130B-353	Sequence 353, App
19	44	23.2	1438	US-10-006-091-1	Sequence 1, Appl1

20	44	23.2	1438	12	US-10-047-257-1	Sequence 1, Appl1
21	44	23.2	1471	12	US-10-095-718-2	Sequence 2, Appl1
22	44	23.2	2332	9	US-09-957-641-2	Sequence 2, Appl1
23	44	23.2	2351	9	US-10-132-829-4	Sequence 4, Appl1
24	42	22.1	233	10	US-09-867-550-1024	Sequence 1024, Ap
25	41	21.6	1431	12	US-10-095-718-4	Sequence 4, Appl1
26	40	21.1	1484	10	US-09-801-368-314	Sequence 314, App
27	39	20.5	197	9	US-10-076-622-516	Sequence 516, App
28	39	20.5	197	12	US-10-007-805-516	Sequence 516, App
29	39	20.5	232	9	US-10-076-622-517	Sequence 517, App
30	39	20.5	232	12	US-10-007-805-517	Sequence 517, App
31	39	20.5	243	9	US-09-938-418-7	Sequence 7, Appl1
32	39	20.5	243	9	US-10-045-992-4	Sequence 4, Appl1
33	39	20.5	243	9	US-10-063-547-122	Sequence 122, App
34	39	20.5	243	9	US-10-174-590-366	Sequence 366, App
35	39	20.5	243	9	US-10-176-758-366	Sequence 366, App
36	39	20.5	243	9	US-10-063-616-122	Sequence 122, App
37	39	20.5	243	9	US-10-175-737-366	Sequence 366, App
38	39	20.5	243	9	US-10-063-502-122	Sequence 122, App
39	39	20.5	243	9	US-10-076-622-514	Sequence 514, App
40	39	20.5	243	9	US-10-173-706-366	Sequence 366, App
41	39	20.5	243	9	US-10-175-738-366	Sequence 366, App
42	39	20.5	243	9	US-10-175-752-366	Sequence 366, App
43	39	20.5	243	9	US-10-176-482-366	Sequence 366, App
44	39	20.5	243	9	US-10-176-757-366	Sequence 366, App
45	39	20.5	243	9	US-10-176-913-366	Sequence 366, App

ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match          63.2%; Score 120; DB 9; Length 406;
Best Local Similarity 75.0%; Pred. No. 4.3e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      1  ANGFLXXLRREGSLRXCRXXLCSEFXAXFXIFRNXXRTQFWVS 44
Db      1  ANAFLLXLRREGSLRXCRXXQCSFXAXRXLFDAXRTKLFWSY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E

```

Query Match 63.2%; Score 120; DB 2; Length 444;
 Best Local Similarity 52.3%; Pred. No. 3.5e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRREGSLKRCXKXLCSPFXAFXIFRNXXRTROFWVS 44
 DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14
 US-08-537-807-2
 ; Sequence 2, Application US/08537807
 ; Patent No. 5861374
 ; GENERAL INFORMATION:

APPLICANT:
 TITLE OF INVENTION: Modified Factor VII
 NUMBER OF SEQUENCES: 4
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/537,807
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05779
 FILING DATE: 23-MAY-1994
 APPLICATION NUMBER: US 08/065,725
 FILING DATE: 21-MAY-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/662,920
 FILING DATE: 28-FEB-1991
 ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 13952-8-1PC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-467-9600
 TELEFAX: 415-543-5043
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-537-807-2

Query Match 63.2%; Score 120; DB 2; Length 444;
 Best Local Similarity 52.3%; Pred. No. 3.5e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRREGSLKRCXKXLCSPFXAFXIFRNXXRTROFWVS 44
 DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15
 US-08-871-003-2
 ; Sequence 2, Application US/08871003
 ; Patent No. 5997864
 ; GENERAL INFORMATION:

APPLICANT: Hart, Charles E.
 APPLICANT: Petersen, Lars C.
 APPLICANT: Hedner, Ulla
 APPLICANT: Rasmussen, Mirella E.
 TITLE OF INVENTION: Modified Factor VII
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESS: Zymogenetics, Inc.
 STREET: 1201 Eastlake Avenue East
 CITY: Seattle

STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/871,003
 FILING DATE:

CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:

NAME: Sawisjak, Deborah A
 REGISTRATION NUMBER: 37,438
 REFERENCE/DOCKET NUMBER: 90-0707
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-871-003-2

Query Match 63.2%; Score 120; DB 2; Length 444;
 Best Local Similarity 52.3%; Pred. No. 3.5e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRREGSLKRCXKXLCSPFXAFXIFRNXXRTROFWVS 44
 DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

Search completed: March 19, 2003, 15:16:20
 Job time: 10.75 secs

FILING DATE: 21-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-845-2

Query Match 63.2%; Score 120; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 3.5e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLXRCXKXLCSPFXAFIFRNXXRTROFWY 44
DB 39 ANAFLELRPGSLERCKEQCSFEARLIFKDAERTKLFWISY 82

RESULT 12
US-08-327-690-2
Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match 63.2%; Score 120; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 3.5e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLXRCXKXLCSPFXAFIFRNXXRTROFWY 44
DB 39 ANAFLELRPGSLERCKEQCSFEARLIFKDAERTKLFWISY 82

RESULT 13
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,289
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TR1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 63.2%; Score 120; DB 2; Length 406;
Best Local Similarity 52.3%; Pred. No. 3.2e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXXLCSPFXAFIFRNXXRTROFVWSY 44
DB 1 ANAFLELRPGSLERCKEQCSFEAREIRKDAERTKLFWISY 44

RESULT 10
PCT-US92-10242-5
Sequence 5, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242

FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match 63.2%; Score 120; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 3.2e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCXXLCSPFXAFIFRNXXRTROFVWSY 44
DB 1 ANAFLELRPGSLERCKEQCSFEAREIRKDAERTKLFWISY 44

RESULT 11
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5788965

GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725

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GENERAL INFORMATION:
APPLICANT: Nicolaesen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: No. 55805600 No. 55805600 of No. 55805600h America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agrib, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129,224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24

Query Match 63.2%; Score 120; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 3.2e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRGSLRXRCXXLCSPFXAFIFRNXXRTROFWVS 44
Db 1 ANAFLYLRLPGSLRYCKYQCSFYARIFKDAYRTKLFWISY 44

RESULT 8
US-08-295-411-5
Sequence 5, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Filling, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSP1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-295-411-5

Query Match 63.2%; Score 120; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 3.2e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRGSLRXRCXXLCSPFXAFIFRNXXRTROFWVS 44
Db 1 ANAFLELRPGSLRCKEKGCSFEARIFKDAYRTKLFWISY 44

RESULT 9
US-08-955-471-5
Sequence 5, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
```



```

; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid
US-08-955-636-28

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Query Match	67.9%	Score 129;	DB 3;	Length 44;
Best Local Similarity	77.3%;	Pred. No. 8.2e-16;		
Matches 34;	Conservative 5;	Mismatches 5;	Indels 0;	Gaps 0;

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Db      1  ANAFLXXLRPGSLRXCKKXQCSFXXAFXIFKDAKRTKLFWISY 44

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RESULT 3
US-08-955-636-26
; Sequence 26, Application US/08955636A

US-08-955-636-26

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RESULT 4
US-08-955-636-27
Sequence 27, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelasestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

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Best Local Similarity	75.0%	Pred. No. 9.3e-15;		
Matches 33; Conservative	6;	Mismatches 5;	Indels 0;	Gaps 0;

[illegible]

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RESULT 5
US-08-955-636-30
; Sequence 30, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30

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Query Match	63.7%	Score 121;	DB 3;	Length 44;
Best local Similarity	75.0%	Pred. No. 2.1e-14;		
Matches 33;	Conservative 5;	Mismatches 6;	Indels 0;	Gaps 0;

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Qy 1 ANGFLXXLRGSLRXCRXXLCSFXXAFXIFRNXXRTRQFWISY 44
    |||||:|||||:||||| |||: |||: |||
Db 1 ANAFLXXLRQSLRXCKXQXCSFXXARXIFEDAXRTRKLFWISY 44
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RESULT 6
US-08-955-636--3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ. ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636--3

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Query Match	63.2%	Score 120;	DB 3;	Length 44;
Best Local Similarity	75.0%	Pred. No. 3.1e-14;		
Matches 33; Conservative	5;	Mismatches 6;	Indels 0;	Gaps 0;

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Oy      1  ANGFLXLIREGSLRXCPXXLCSFYXAFXI FRNXXRTROFWVSY 44
        || ||||| : ||||| ||| : ||| : |||
Db      1  ANAFLLXLRPGSLRXCKXQCSFYXARXIFKDAKRTKLFWISY 44

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RESULT 7
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using SW model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10glu28phe_4
Perfect score: 190
Sequence: 1 ANGFLXXLRGSLRXCRXX.....XAXFIIFRNXXTRQFWVS 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	155	81.6	44	3	US-08-955-636-4
2	129	67.9	44	3	US-08-955-636-28
3	126	66.3	44	3	US-08-955-636-26
4	123	64.7	44	3	US-08-955-636-27
5	121	63.7	44	3	US-08-955-636-30
6	120	63.2	44	3	US-08-955-636-3
7	120	63.2	406	1	US-08-293-778-24
8	120	63.2	406	1	US-08-295-411-5
9	120	63.2	406	2	US-08-955-471-5
10	120	63.2	406	5	PCT-US92-10242-5
11	120	63.2	444	1	US-08-475-845-2
12	120	63.2	444	2	US-08-327-690-2
13	120	63.2	444	2	US-08-660-289-2
14	120	63.2	444	2	US-08-537-807-2
15	120	63.2	444	2	US-08-871-003-2
16	120	63.2	444	3	US-08-464-233-2
17	120	63.2	444	4	US-09-189-607-2
18	120	63.2	444	4	US-09-378-907-2
19	120	63.2	444	5	PCT-US94-05779-2
20	120	63.2	466	1	US-07-882-202A-4
21	120	63.2	466	1	US-08-021-615A-4
22	120	63.2	466	1	US-08-321-777-4
23	120	63.2	466	4	US-09-009-217-14
24	120	63.2	466	4	US-09-009-656-14
25	120	63.2	466	5	PCT-US93-04493-4
26	116	61.1	44	3	US-08-955-636-29
27	106	55.8	41	1	US-08-229-280-4

28	98	51.6	139	1	US-08-330-978-2	Sequence 2, Appl1
29	98	51.6	139	1	US-08-474-042-2	Sequence 2, Appl1
30	98	51.6	139	1	US-08-484-558-2	Sequence 2, Appl1
31	98	51.6	139	1	US-08-774-592-2	Sequence 2, Appl1
32	98	51.6	437	1	US-08-487-037-2	Sequence 2, Appl1
33	98	51.6	437	1	US-08-487-037-3	Sequence 1, Appl1
34	98	51.6	488	1	US-08-487-037-1	Sequence 1, Appl1
35	95	50.0	44	3	US-08-955-636-23	Sequence 23, Appl1
36	94	49.5	44	3	US-08-955-636-35	Sequence 35, Appl1
37	94	49.5	44	3	US-08-955-636-35	Sequence 35, Appl1
38	93	48.9	448	1	US-08-295-411-3	Sequence 3, Appl1
39	93	48.9	448	2	US-08-955-471-3	Sequence 3, Appl1
40	93	48.9	448	5	PCT-US92-10068-1	Sequence 1, Appl1
41	93	48.9	448	5	PCT-US92-10242-3	Sequence 3, Appl1
42	92	48.4	44	3	US-08-955-636-25	Sequence 25, Appl1
43	92	48.4	44	3	US-08-955-636-33	Sequence 33, Appl1
44	91	47.9	44	3	US-08-955-636-24	Sequence 24, Appl1
45	89	46.8	41	1	US-08-229-280-5	Sequence 5, Appl1

ALIGNMENTS

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RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      81.6%; Score 155; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 2.2e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 ANGFLXXLRGSLRXCRXXLCGFXAXFIIFRNXXTRQFWVS 44
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Db      1 ANGFLXXLRGSLRXCRXXLCGFXAXFIIFRNXXTRQFWVS 44

RESULT 2
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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Thu Mar 20 14:52:19 2003

10glu28phe_4.rspt

Page 8

Search completed: March 19, 2003, 15:13:40
Job time : 46.3125 secs

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DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR PROSITE; PS00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
DR Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match
Best Local Similarity 45.8%; Score 87; DB 6; Length 461;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
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RESULT 14

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ID O9PTW7;
AC O9PTW7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Prothrombin.
GN OSPT.
OS Struthio camelus (Ostrich).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
OC Struthio.
OX NCBI_TaxID=8801;
RN [1]
RP TISSUE=LIVER;
RC MEDLINE=20579470; PubMed=1137455;
RA Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.;
RT "Purification and characterization of ostrich prothrombin.";
RL Int. J. Biochem. Cell Biol. 32:1151-1159(2000).
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AB028871; BA89046.1; -.
DR HSSP; P00734; IUVS.
DR MEROPS; S01.217; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00051; kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS50240; KRINGLE_2; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease.
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SQ SEQUENCE 608 AA; 69392 MW; 11B974B9A5E54E82 CRC64;
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Query Match
Best Local Similarity 45.8%; Score 87; DB 13; Length 608;
Matches 15; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
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OY 3 GFLXLRREGSLKRCXKXLCSPFXAFLIRNXXRTROFWVSY 44
DB 47 GFLXLRREGSLKRCXKXLCSPFXAFLIRNXXRTROFWVSY 88
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RESULT 15

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O9GMD9 PRELIMINARY; PRT; 469 AA.
ID O9GMD9;
AC O9GMD9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Coagulation factor X.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015017; PubMed=1132153;
RA Poorafshar M., Aveskogh M., Munday B., Hellman L.;
RT "Identification and structural analysis of four serine proteases in a
monotreme, the platypus, Ornithorhynchus anatinus.";
RL Immunogenetics 52:19-28(2000).
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF275654; AAG00453.1; -.
DR HSSP; P00742; IXXB.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease.
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match
Best Local Similarity 45.3%; Score 86; DB 6; Length 469;
Matches 15; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
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OY 1 ANGFLXLRREGSLKRCXKXLCSPFXAFLIRNXXRTROFWVSY 44
DB 41 ANGFLXLRREGSLKRCXKXLCSPFXAFLIRNXXRTROFWVSY 84
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Reitema P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Briel E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033463; CA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSP; P00740; ICFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00101; EGFBLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
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DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 45.8%; Score 87; DB 4; Length 456;
Best Local Similarity 39.5%; Pred. No. 1e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRREGSLRXCRXXLCSPXAFXIRNXXRTQFWVSY 44
Db 44 SGKLEEFVQGNLRECEMEKCSFEAREVFENTERTTEFWKQY 86

RESULT 12
Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Gene Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 45.8%; Score 87; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 1e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRREGSLRXCRXXLCSPXAFXIRNXXRTQFWVSY 44
Db 49 SGKLEEFVQGNLRECEMEKCSFEAREVFENTERTTEFWKQY 91

RESULT 13
Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Gene Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; -.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.

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DR PROSITE; PS01187; EGF_CA. 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease; Signal.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 47.4%; Score 90; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 2.9e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXRCRXLLCSFXXAFXIFRNXXRTQFWVS 44
Db 41 ANSFEEFKKGNLERECMEICSYEEVREIFEDDEKTKKEYWTXY 84

RESULT 9
ID 088947; PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; Pubmed=9684791;
RA Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,
RA Caselliino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X."
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129S3;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene."
RL Thromb. Haemost. 0:0-0(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC36345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

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DR PROSITE; PS01187; EGF_CA. 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease; Signal.
FT SIGNAL 1
FT CHAIN 41
SQ SEQUENCE 481 AA; 54018 MW; 8AC09DE5F9D271E CRC64;

Query Match 47.4%; Score 90; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 2.9e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXRCRXLLCSFXXAFXIFRNXXRTQFWVS 44
Db 41 ANSFEEFKKGNLERECMEICSYEEVREIFEDDEKTKKEYWTXY 84

RESULT 10
ID 015253; PRELIMINARY; PRT; 100 AA.
AC 015253;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Thrombin precursor (Fragment).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; Pubmed=3471151;
RA Macgillivray R.T., Irwin D.M., Guinco E.R., Stone J.C.;
RT "Recombinant genetic approaches to functional mapping of thrombin."
RL Ann. N. Y. Acad. Sci. 485:73-79(1986).
DR EMBL; M33031; AAA60220.1; -.
DR HSSP; P00735; 2PFI.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00594; GLA; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KM Signal.
FT SIGNAL 1
FT CHAIN 44
FT NON TER 100
SQ SEQUENCE 100 AA; 11302 MW; FDB5D0174E1F6FE CRC64;

Query Match 45.8%; Score 87; DB 4; Length 100;
Best Local Similarity 38.6%; Pred. No. 2.3e-08;
Matches 17; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXRCRXLLCSFXXAFXIFRNXXRTQFWVS 44
Db 44 ANTFLEVRKGNLERECVETCSYBEAFALSSSTATDVFWAKY 87

RESULT 11
ID 014316; PRELIMINARY; PRT; 456 AA.
AC 014316;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-AUG-1999 (TReMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas
DE disease, HAEMOPHILIA B) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).

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DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; GLA_1.
 DR Pfam: PF00889; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA_1.
 DR SMART: SM00001; EGF_Like_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; Tryp_Spc_1.
 DR PROSITE: PS00020; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS50240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPsin_SER_1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
 KM Hydroxylation; Repeat; Serine protease
 SQ SEQUENCE 482 AA; 54265 MW; 02846783954A698 CRC64;

Query Match 48.9%; Score 93; DB 11; Length 482;
 Best Local Similarity 36.4%; Pred. No. 8e-09;
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLXRCRXKLCSPFXAFLFRNXXRTROFVSY 44
 DB 41 ANSFEEIKKGNLERECVEECISFEAREVFEDEKTEFWNKY 84

RESULT 7
 ID 054740 PRELIMINARY; PRT; 481 AA.

AC 054740;
 DT 01-JUN-1998 (Tremblrel_06, Created)
 DT 01-JUN-1998 (Tremblrel_06, Last sequence update)
 DT 01-JUN-2002 (Tremblrel_21, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6).
 GN F10 OR FA10.
 OS Mus musculus (Mouse).
 OC Plasmid DBLuescript.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RC MEDLINE=98454993; PubMed=9783672;
 RA Heidemann H.H., Kontermann R.B.;
 RT "Cloning and recombinant expression of mouse coagulation factor X.";
 RT Thromb. Res. 92:33-41(1998).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: AJ222677; CAAL0933.1; -
 DR HSP; P00742; IYKA.
 DR MEROPS; S01.216; -.
 DR MGD; MGI:103107; F10.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-Like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; GLA_1.
 DR Pfam; PF00889; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA_1.
 DR SMART: SM00001; EGF_Like_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; Tryp_Spc_1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS50240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPsin_SER_1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
 KM Repeat; Serine protease; Signal.
 FT SIGNAL 1 40 POTENTIAL.
 FT CHAIN 41 481 COAGULATION FACTOR X.
 SQ SEQUENCE 481 AA; 53986 MW; CF702D5EF9D97AE CRC64;

Query Match 47.4%; Score 90; DB 11; Length 481;
 Best Local Similarity 31.8%; Pred. No. 2.9e-08;
 Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLXRCRXKLCSPFXAFLFRNXXRTROFVSY 44
 DB 41 ANSFEEIKKGNLERECVEECISFEAREVFEDEKTEFWNKY 84

RESULT 8
 ID 099132 PRELIMINARY; PRT; 481 AA.

AC 099132;
 DT 01-JUN-2001 (Tremblrel_17, Created)
 DT 01-JUN-2001 (Tremblrel_17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel_21, Last annotation update)
 DE Coagulation factor X.
 GN F10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: BC003877; AAH03877.1; -
 DR HSP; P00742; IYKA.
 DR MEROPS; S01.216; -.
 DR MGD; MGI:103107; F10.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-Like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR001438; EGF_I1.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; GLA_1.
 DR Pfam; PF00889; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00001; EGF_Like_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; Tryp_Spc_1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.

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RT "Complete sequence of UC72A01."
CC Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: AF318182; AAK07918.1; -.
DR HSSP: P04070; 1PCU.
DR MEROPS: S01.218; -.
DR MGD: MGI:97771; PROC.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; GLA; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00001; EGF_like; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

Query Match 51.6%; Score 98; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 8.9e-10;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCRXLLCSFYXAFXIFRNXXRTQPFWSY 44
Db 42 ANSFLEBRPGSLERECMEICDFEEAKEIFQVNDTLAWMYKY 85

RESULT 5
Q9TR0 PRELIMINARY; PRT; 456 AA.
AC Q9TR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Protein C precursor.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene.";
RL Mamm. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=9371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms.";
RL Anim. Genet. 30:237-238(1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
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DR EMBL: AJ001979; CAA05126.1; -.
DR HSSP: P04070; 1PCU.
DR MEROPS: S01.218; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; GLA; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL 1 42 POTENTIAL.
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
FT CHAIN 193 194 PROTEIN C HEAVY CHAIN.
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59F CRC64;

Query Match 50.5%; Score 96; DB 6; Length 456;
Best Local Similarity 43.2%; Pred. No. 2.1e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCRXLLCSFYXAFXIFRNXXRTQPFWSY 44
Db 43 ANSFLEBRPGSLERECMEICDFEEAKEIFQVNDTLAWMYKY 86

RESULT 6
Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: X79807; CAA56202.1; -.
DR HSSP: P00742; 1XKA.
DR MEROPS: S01.216; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
```


DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KM Hydroxylase; Serine protease.
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 63.2%; Score 120; DB 4; Length 701;
 Best Local Similarity 52.3%; Pred. No. 1e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLKRXCRXXLCSPXAXFIFRNXXRTROFWVS 44
 DB 61 ANAPLEELRPGSLERECNEQCSFEAREIFKDAERTKLFWIST 104

RESULT 2

O91WN8 PRELIMINARY; PRT; 460 AA.
 AC Q91WN8;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Similar to protein C.
 DE PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013896; AAH13896.1; -.
 DR MGD; MGI:97771; Proc.
 DR InterPro; IPR00152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KM Hydroxylase; Serine protease.
 SQ SEQUENCE 460 AA; 51818 MW; 0117F26E8FCC274 CRC64;

Query Match 54.7%; Score 104; DB 11; Length 460;
 Best Local Similarity 45.5%; Pred. No. 6.7e-11;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLKRXCRXXLCSPXAXFIFRNXXRTROFWVS 44
 DB 42 ANSFLERMPGSLERECNEQCSFEAREIFQNVEDTLAFWIKY 85

RESULT 3

O61109 PRELIMINARY; PRT; 446 AA.
 AC Q61109;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Coagulation factor VII.
 DE F7 OR FVII.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Characterization of a cDNA encoding murine coagulation factor VII.",
 RT Thromb. Haemost. 75:481-487(1996).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC EMBL; U44795; AAC52570.1; -.
 DR HSSP; P08709; IFAK.
 DR MEROPS; S01.215; -.
 DR MGD; MGI:109325; F7.
 DR InterPro; IPR002066; Aldehyde dehydr.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylase; Repeat;
 KM Serine protease.
 SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 54.2%; Score 103; DB 11; Length 446;
 Best Local Similarity 47.7%; Pred. No. 1e-10; Indels 0; Gaps 0;
 Matches 21; Conservative 4; Mismatches 19;

OY 1 ANGFLXXLRGSLKRXCRXXLCSPXAXFIFRNXXRTROFWVS 44
 DB 42 ANSLLEELMPGSLERECNEQCSFEAREIFKSPERTKQFIWY 85

RESULT 4

O99PC6 PRELIMINARY; PRT; 460 AA.
 AC O99PC6;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Anticoagulant protein C.
 DE PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Korf I.;

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10glu28phe_4
Perfect score: 190
Sequence: 1 ANGFLXXLRSGSLKRXCRXX.....XXAFXIFRNXXRTQFWVS Y 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertibrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriapi.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	63.2	701	4 Q96P08	Q96P08 homo sapien
2	104	54.7	460	11 Q91M08	Q91M08 mus musculu
3	103	54.2	446	11 Q61109	Q61109 mus musculu
4	98	51.6	460	11 Q99PC6	Q99PC6 mus musculu
5	96	50.5	456	6 Q91P00	Q91P00 canis faml
6	93	48.9	482	11 Q63207	Q63207 rattus norv
7	90	47.4	481	11 Q54740	Q54740 mus musculu
8	90	47.4	481	11 Q99L32	Q99L32 mus musculu
9	90	47.4	481	11 Q88947	Q88947 mus musculu
10	87	45.8	100	4 Q15253	Q15253 homo sapien
11	87	45.8	456	4 Q14316	Q14316 homo sapien
12	87	45.8	461	6 Q95ND7	Q95ND7 pan troglod
13	87	45.8	461	6 Q95ND6	Q95ND6 pan troglod
14	87	45.8	608	13 Q9PTW7	Q9PTW7 struthio ca
15	86	45.3	469	6 Q95MD9	Q95MD9 ornithorhyn
16	85	44.7	49	6 Q95ME8	Q95ME8 bos taurus

17	78	41.1	138	6 Q28994	Q28994 sus scrofa
18	77	40.5	433	13 Q90YK1	Q90YK1 brachydanio
19	75	39.5	607	13 Q91001	Q91001 gallus gall
20	74	38.9	648	6 Q29094	Q29094 sus scrofa
21	73	38.4	399	11 Q9COW3	Q9COW3 mus musculu
22	70.5	37.1	542	5 Q8TF13	Q8TF13 halocynthia
23	69	36.3	650	4 Q9NSD0	Q9NSD0 homo sapien
24	69	36.3	650	4 Q16519	Q16519 homo sapien
25	68	35.8	179	4 Q8TAS3	Q8TAS3 homo sapien
26	68	35.8	198	11 Q8R182	Q8R182 mus musculu
27	58	30.5	25	11 Q9QVH6	Q9QVH6 rattus sp.
28	58	30.5	678	4 Q14393	Q14393 homo sapien
29	57	30.0	673	11 Q61592	Q61592 mus musculu
30	57	30.0	674	11 Q99K57	Q99K57 mus musculu
31	55	28.9	674	11 Q63772	Q63772 rattus sp.
32	54	28.4	98	13 P82807	P82807 notechis sc
33	51	26.8	130	12 Q9DUB8	Q9DUB8 bt virus.
34	50	26.3	184	10 Q91VFL	Q91VFL arabidopsis
35	47.5	25.0	575	10 Q94E17	Q94E17 oryza sativ
36	47.5	25.0	608	10 Q9XF36	Q9XF36 medicago sa
37	46.5	24.5	196	10 Q8W4U2	Q8W4U2 selaginella
38	46.5	24.5	567	10 Q8W4U2	Q8W4U2 arabidopsis
39	46.5	24.5	603	10 Q91PG7	Q91PG7 arabidopsis
40	46.5	24.5	606	10 Q9S1G9	Q9S1G9 arabidopsis
41	46.5	24.5	651	10 Q8S218	Q8S218 oryza sativ
42	46	24.2	174	2 Q93FY1	Q93FY1 bruceella ab
43	45.5	23.9	249	5 Q9VYS0	Q9VYS0 drosophila
44	45.5	23.9	431	10 Q94EY5	Q94EY5 arabidopsis
45	45.5	23.9	492	10 Q9SMU7	Q9SMU7 cicer arlet

ALIGNMENTS

RESULT 1

Q96P08 ID Q96P08 PRELIMINARY; PRT; 701 AA.
AC Q96P08;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunocjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.",
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AKS58686.1; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF 2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vlk_dep_gla.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla_1.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00181; EGF_2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.

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RN [16]
RP STRUCTURE OF CARBOHYDRATE ON SER-107.
RX MEDLINE=9238094; PubMed=1517205;
RA Nishimura H., Takao T., Hase S., Shimoniishi Y., Iwanaga S.;
RT "Human factor IX has a tetrasaccharide O-glycosidically linked to
RT serine 61 through the fucose residue";
RL J. Biol. Chem. 267:17520-17525(1992).
RN [17]
RP PHOSPHORYLATION OF SER-114.
RA Harris R.J., Papac D.I., Truong L., Smith K.J.;
RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX";
RL (in) Abstracts of Xth International conference on methods in protein
structure analysis, pp.50-50, Annecy (1996).
RN [18]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=20575397; PubMed=1133752;
RA Arruda V.R., Hagestrom J.N., Delich J., Heiman-Patterson T.,
RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,
RA Larson P.J., High K.A.;
RT "Posttranslational modifications of recombinant myotube-synthesized
RT human factor IX";
RL Blood 97:130-138(2001).
RN [19]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=95229607; PubMed=7713897;
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane
RT binding region of factor IX by two-dimensional NMR spectroscopy";
RL J. Biol. Chem. 270:7980-7987(1995).
RN [20]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=96032604; PubMed=7547952;
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich
RT domain of factor IX";
RL Biochemistry 34:12126-12137(1995).
RN [21]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=96279169; PubMed=8663165;
RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,
RA Furie B.;
RT "Identification of the phospholipid binding site in the vitamin K-
RT dependent blood coagulation protein factor IX";
RL J. Biol. Chem. 271:16227-16236(1996).
RN [22]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=97199336; PubMed=9047312;
RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,
RA Smith H., Hisey R.G., Pedersen L.G.;
RT "Refinement of the NMR solution structure of the
RT gamma-carboxyglutamic acid domain of coagulation factor IX using
RT molecular dynamics simulation with initial Ca2+ positions determined
RT by a genetic algorithm";
RL Biochemistry 36:2132-2138(1997).
RN [23]
RP STRUCTURE BY NMR OF 91-133.
RX MEDLINE=91308127; PubMed=1854745;
RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;
RT "Sequence-specific 1H NMR assignments, secondary structure, and
RT location of the calcium binding site in the first epidermal growth
RT factor like domain of blood coagulation factor IX";
RL Biochemistry 30:7402-7409(1991).
RN [24]
RP STRUCTURE BY NMR OF 92-130.
RX MEDLINE=93284090; PubMed=1304885;
RA Baron M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,
RA Tse A.G.D., Brownlee G.G., Campbell I.D.C.;
RT "The three-dimensional structure of the first EGF-like module of
RT human factor IX: comparison with EGF and TGF-alpha";
RL Protein Sci. 1:81-90(1992).
RN [25]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.
RX MEDLINE=95330802; PubMed=7606779;

RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;
RT "The structure of a Ca(2+)-binding epidermal growth factor-like
RT domain: its role in protein-protein interactions";
RL Cell 82:131-141(1995).
RN [26]
RP MOLECULAR PATHOLOGY OF HEMOPHILIA B.

Query Match 45.8%; Score 87; DB 1; Length 461;
Best Local Similarity 39.5%; Pred. No. 5,4e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
QY 2 NGFLXXLRGGSLKRXCRXXLCSPFXAFXJPRNXXRRPFWVS 44
DB 49 SGKLEPFVQGNLERBCEMKCKSPFEAREVFPENTERITTFWKQY 91

Search completed: March 19, 2003, 14:52:58
Job time : 6.625 secs

FT DOMAIN 125 165 EGF-LIKE 2.
 FT DOMAIN 234 492 SERINE PROTEASE.
 FT ACT_SITE 275 275 CHARGE RELAY SYSTEM.
 FT ACT_SITE 321 321 CHARGE RELAY SYSTEM.
 FT ACT_SITE 418 418 CHARGE RELAY SYSTEM.
 FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

Query Match 46.8%; Score 89; DB 1; Length 492;
 Best Local Similarity 36.4%; Pred. No. 2.5e-08;
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLXRCRXXLCSPFXAFLFRNXXRTQRFVSY 44
 Db 41 ANSFLERKQGNLRECELEACSLSEAREVEDAQTDEFWSKY 84

RESULT 15
 ID FA9 HUMAN STANDARD; PRT; 461 AA.
 AC P00740;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
 GN F9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86000558; PubMed=2994716;
 RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;
 RT "Nucleotide sequence of the gene for human factor IX (antihemophilic
 factor B).";
 RL Biochemistry 24:3736-3750(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85190593; PubMed=3857619;
 RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
 RA Graham J.B., Stafford D.W.;
 RT "Evidence for a prevalent dimorphism in the activation peptide of
 human coagulation factor IX.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84236100; PubMed=6329734;
 RA Anson D.S., Choo K.H., Rees D.J.G., Gianneli F., Gould K.G.,
 RA Huddleston J.A., Brownlee G.G.;
 RT "The gene structure of human anti-haemophilic factor IX.";
 RL EMBO J. 3:1053-1060(1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83220788; PubMed=6687940;
 RA Jaye M., de la Salle H., Schamber F., Ballard A., Kohli V.,
 RA Fidelelli A., Tolstoshev P., Lecocq J.P.;
 RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a
 unique 52-base synthetic oligonucleotide probe deduced from the amino
 acid sequence of bovine factor IX.";
 RL Nucleic Acids Res. 11:2325-2335(1983).
 RN [5]
 RP SEQUENCE OF 36-326 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=84300526; PubMed=6089357;
 RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;
 RT "Isolation and characterization of human factor IX cDNA;

RT identification of Tag I polymorphism and regional assignment.";
 RL Somat. Cell Mol. Genet. 10:465-473(1984).
 RN [6]
 RP SEQUENCE OF 290-359 FROM N.A.
 RX MEDLINE=88127096; PubMed=3340835;
 RA Stoflet B.S., Koebert D.D., Sarkar G., Sommer S.S.;
 RT "Genomic amplification with transcript sequencing.";
 RL Science 239:491-494(1988).
 RN [7]
 RP SEQUENCE OF 444-461 FROM N.A.
 RX MEDLINE=94054330; PubMed=8236150;
 RA de la Salle C., Charmanier J.L., Baas M.J., Schwartz A.,
 RA Wiesel M.L., Grunbaum L., Cazenave J.-P.;
 RT "A deletion located in the 3' non translated part of the factor IX
 gene responsible for mild haemophilia B.";
 RL Thromb. Haemost. 70:370-371(1993).
 RN [8]
 RP SEQUENCE OF 47-461 (VARIANT NAGOYA).
 RX MEDLINE=90078229; PubMed=2592373;
 RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
 RA Ogata K., Kamiya T., Saito H., Niho Y., Iwanaga S.;
 RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by
 tryptophan and its activation by alpha-chymotrypsin and rat mast cell
 chymase.";
 RL J. Biol. Chem. 264:21257-21265(1989).
 RN [9]
 RP HYDROXYLATION OF ASP-110.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kisiel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 K-dependent blood coagulation zymogens.";
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [10]
 RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=78194509; PubMed=659613;
 RA di Scipio R.G., Kurachi K., Davie E.W.;
 RT "Activation of human factor IX (Christmas factor).";
 RL J. Clin. Invest. 61:1528-1538(1978).
 RN [11]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185715; PubMed=6425296;
 RA Morita T., Isaacs B.S., Esmen C.T., Johnson A.E.;
 RT "Derivatives of blood coagulation factor IX contain a high affinity
 Ca²⁺-binding site that lacks gamma-carboxyglutamic acid.";
 RL J. Biol. Chem. 259:5698-5704(1984).
 RN [12]
 RP ERRATUM.
 RA Morita T., Isaacs B.S., Esmen C.T., Johnson A.E.;
 RL J. Biol. Chem. 260:2583-2583(1985).
 RN [13]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=86189947; PubMed=3009023;
 RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;
 RT "Defective propeptide processing of blood clotting factor IX caused
 by mutation of arginine to glutamine at position -4.";
 RL Cell 45:343-348(1986).
 RN [14]
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.
 RX MEDLINE=90062160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimomitsu Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 epidermal growth factor-like domain of human factors VII and IX and
 protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [15]
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).

RL Blood 78:890-894(1991).
 RN [14]
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
 RX MEDLINE=92190481; PubMed=1347706;
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
 RA Rainville I.R., Long G.L.;
 RT "Protein Cvermont: symptomatic type II protein C deficiency
 RT associated with two GLA domain mutations.";
 RL Blood 79:1456-1465(1992).
 RN [15]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Sugahara Y., Mura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RT a missense mutation.";
 RL Blood 80:126-133(1992).
 RN [16]
 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RT causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [17]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schulman S., Tenhoben L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RT gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [18]
 RP VARIANT GLN-220.
 RX MEDLINE=93250852; PubMed=1301959;
 RA Gandrille S., Vdauud M., Alach M., Alhenc-Gelas M., Fischer A.M.,
 RA Gonaud-Hellman M., Toulon P., Fiesinger J.N., Goossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
 RT deficiency: characterization by denaturing gradient gel
 RT electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [19]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yamamoto K., Matsushita T., Sugiura I., Takamatsu J., Iwasaki E.,
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 RT mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
 RN [20]
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE=93313192; PubMed=8324221;
 RA Gandrille S., Alhenc-Gelas M., Gaussem P., Aillaud M.-F., Dupuy E.,
 RA Uhan-Vague I., Alach M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RT gene in patients presenting with defective protein C anticoagulant
 RT activity.";
 RL Blood 82:159-166(1993).
 RN [21]
 RP VARIANTS G-14; Q-21; Y-244; Q-253; L-321; C-328; I-385; T-388 AND
 RP V-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poort S.R., Fabinger-Fasching I., Mannhalter C., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RT with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [22]
 RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A GLA domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 RT causing type 2 protein C deficiency and recurrent venous

RT thrombosis.";
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [23]
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
 RX MEDLINE=94122329; PubMed=8292730;
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
 RA Koerber M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with
 RT symptomatic type I protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).
 RN [24]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Patraccini P., Gemmati D., Caetaman G., Rodeghiero F.,
 RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RL Br. J. Haematol. 84:285-289(1993).
 RN [25]
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
 QY 1 ANGFLXRLREGSLKRCXKXLCSEFXAFKIFRNXXRTQW 41
 Db 43 ANSFLELRHSSLERECIEICDFEAKEIFQWVDTLAFW 83
 Query Match 46.8%; Score 89; DB 1; Length 461;
 Best Local Similarity 46.3%; Pred. No. 2,3e-08;
 Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;
 RESULT 14
 ID FA10_BOVIN STANDARD; PRT; 492 AA.
 AC P00743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-487 FROM N.A.
 RX MEDLINE=84247315; PubMed=6330671;
 RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
 RT containing a prepro leader sequence.";
 RL Nucleic Acids Res. 12:4481-4492(1984).
 RN [2]
 RP SEQUENCE OF 41-180.
 RX MEDLINE=80130563; PubMed=6766735;
 RA Entfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
 RA Tiliari K.;
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
 RT factor).";
 RL Biochemistry 19:659-667(1980).
 RN [3]
 RP REVISION TO 103.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kistel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens.";
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [4]
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Tiliari K., Fujikawa K., Entfield D.L., Ericsson L.H., Walsh K.A.,
 RA Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 RT chain.";

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FT DOMAIN 125 165 EGF-LIKE 2.
FT MOD_RES 235 488 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .).
FT CARBOHYD 231 231 /FTID=CAR_000013.
FT ACT_SITE 276 276 CHARGE RELAY SYSTEM.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110
FT DISULFID 112 121
FT DISULFID 129 140

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Query Match 48.9%; Score 93; DB 1; Length 488;
Best Local Similarity 36.4%; Pred. No. 4,7e-09;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

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Oy 1 ANGFLXXLRGSLRXCRXXLCSPFXAFXIERNXXRTQRFVWSY 44
Db 41 ANGFLEEMKXGLERECMEETCSYEAREVFEEDSDKTNERNWXY 84

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RESULT 13
PRIC_HUMAN STANDARD; PRT; 461 AA.
AC P04070; Q16001; Q15190; Q15189;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=85270390; PubMed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RT "The nucleotide sequence of the gene for human protein C.";
RT Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85269639; PubMed=2991859;
RA Beckmann R.J., Schmidt R.J., Sautter R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs.";
RT Nucleic Acids Res. 13:5233-5247(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120978; PubMed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RT "Evolution and organization of the human protein C gene.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).

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RN [4]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Peol C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=84272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RT Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN [6]
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Mielich J.P., Broze G.J., Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN [7]
RP HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN [8]
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Machner T., Oganesyan V., Hof F., Huber R., Foundling S., Eamon C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Glu-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN [10]
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitema P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN [11]
RP VARIANT CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Hassan H.J., Straampfl S., Roncuzzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN [12]
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=90098906; PubMed=2602169;
RA Grundy C.B., Chitollie A., Talbot S., Bevan D., Kakkay V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN [13]
RP VARIANT CYS-272.
RX MEDLINE=91329836; PubMed=1868249;
RA Reitema P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";

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RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;
 RT "characterization of an almost full-length cDNA coding for human
 RL blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RL cDNA.";
 RL Gene 41:311-314(1986).
 [5]
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kistiel W., Sasagawa T., Howald W.N.,
 RA Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884(1983).
 [6]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Laytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 [7]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 [8]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RL encoding human factor X.";
 RL Gene 84:517-519(1989).
 [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tullinsky A., Park C.H., Bode W.,
 RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966(1993).
 [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kanata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 [11]
 RP FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE

CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: K03194; AAA52490.1; -;
 CC EMBL: M57285; AAA52421.1; -;
 CC EMBL: L29433; AAA52764.1; -;
 CC EMBL: L00390; AAA52764.1; JOINED.
 CC EMBL: L00391; AAA52764.1; JOINED.
 CC EMBL: L00392; AAA52764.1; JOINED.
 CC EMBL: L00393; AAA52764.1; JOINED.
 CC EMBL: L00394; AAA52764.1; JOINED.
 CC EMBL: L00395; AAA52764.1; JOINED.
 CC EMBL: L00396; AAA52764.1; JOINED.
 CC EMBL: M22613; AAA51984.1; -;
 CC EMBL: K01886; AAA52486.1; -;
 CC EMBL: M31297; AAA52636.1; -;
 CC PIR: A00924; EXHU.
 CC PIR: A25853; A25853.
 CC PIR: A24478; A24478.
 CC PDB: 1HCG; 08-MAY-95.
 CC PDB: 1FXI; 29-OCT-97.
 CC PDB: 1FXI; 17-JUN-98.
 CC PDB: 1XXA; 23-MAR-99.
 CC PDB: 1XXB; 23-MAR-99.
 CC MEROPS: S01.216; -;
 CC GlycoStatedB: P00742; -;
 CC Genew: HGNC:3528; P10.
 CC MIM: 134530; -;
 CC MIM: 227600; -;
 CC InterPro: IPR000152; Asx_hydroxyl.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR000742; EGF_2.
 CC InterPro: IPR001881; EGF_Ca.
 CC InterPro: IPR002383; GLA_blood.
 CC InterPro: IPR001254; Ser_protease_Try.
 CC InterPro: IPR000294; VitK_dep_GLA.
 CC Pfam: PF00089; EGF_2.
 CC Pfam: PF00089; trypsin; 1.
 CC Pfam: PF00594; Gla_1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00001; GLABLOOD.
 CC SMART: SM00179; EGF_CA; 1.
 CC SMART: SM00001; EGF_like; 1.
 CC SMART: SM00069; GLA_1.
 CC SMART: SM00020; TRY_Spc; 1.
 CC PROSITE: PS00010; ASX_HYDROXYL; 1.
 CC PROSITE: PS00022; EGF_1; 1.
 CC PROSITE: PS01186; EGF_2; 2.
 CC PROSITE: PS01187; EGF_CA; 1.
 CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC GlycoProfile: Hydrolase; Serine protease; Plasma; Blood coagulation;
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 CC SIGNAL: 1 31
 CC PROPEP 32 40
 CC CHAIN 41 179 FACTOR X LIGHT CHAIN.
 CC CHAIN 183 488 FACTOR X HEAVY CHAIN.
 CC PROPEP 183 234 ACTIVATION PEPTIDE.
 CC CHAIN 235 486 ACTIVATED FACTOR XA, HEAVY CHAIN.
 CC DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

RL J. Biol. Chem. 258:5548-5553(1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmen N.L., Lane T.M., Esmen C.T.;
RT "Structural changes required for activation of protein C are induced
by Ca2+ binding to a high affinity site that does not contain gamma-
carboxyglutamic acid.";
RL J. Biol. Chem. 258:5554-5560(1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
SITE IS NECESSARY FOR THE RECOGNITION OF THE
THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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CC EMBL: K02435; AAA30685.1; -.
DR PIR: A00928; KKB0.
DR HSP: P04070; LPCU.
DR MEROPS: S01.218; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR SMART: SMO0181; EGF; 2.
DR SMART: SMO0069; GLA; 1.
DR SMART: SMO0020; TRYD_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_Ca; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00014; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT NON_TER 1
FT SIGNAL 1
FT PROPEP 29
FT CHAIN 30 39
FT CHAIN 40 194
FT CHAIN 197 456
FT PEPTIDE 197 210
FT DOMAIN 94 129
FT DOMAIN 133 173
FT DOMAIN 211 456
SERINE PROTEASE.

FT MOD_RES 45 45 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 53 53 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 62 62 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 68 68 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 74 74 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 110 110 HYDROXYLATION.
FT ACT_SITE 252 252 CHARGE RELAY SYSTEM.
FT ACT_SITE 298 298 CHARGE RELAY SYSTEM.
FT ACT_SITE 397 397 CHARGE RELAY SYSTEM.
FT DISULFID 56 61 BY SIMILARITY.
FT DISULFID 89 108 BY SIMILARITY.
FT DISULFID 98 103 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 119 128 BY SIMILARITY.
FT DISULFID 137 148 BY SIMILARITY.
FT DISULFID 144 157 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 180 318 INTERCHAIN.
FT DISULFID 227 253
FT DISULFID 368 382
FT DISULFID 393 421
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .).
FT VARIANT 82 82 F -> K.
FT CONFLICT 455 456 VP -> PV (IN REF. 4).
SQ SEQUENCE 456 AA; 51407 MW; CAAFE633F894C209 CRC64;

Query Match 49.5%; Score 94; DB 1; Length 456;
Best Local Similarity 43.2%; Pred. No. 2.9e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXCRXLCSPFXAFPIFNXXXTROQFWYSY 44
DB 40 ANSFLRPRGNVERECSEVCEFEARREI FQVTEDTMAFWSTY 83

RESULT 12
FA10 HUMAN STANDARD; PRT; 488 AA.
AC P00742; Q14340;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91216473; PubMed=1902434;
RA Messier T.V., Pittman D.D., Long G.L., Kaufman R.U., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RT human coagulation factor X.";
RL Gene 99:291-294(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87026600; PubMed=3768336;
RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
RT organization is essentially identical with that of factor IX and
RT protein C.";
RL Biochemistry 25:5098-5102(1986).
RN [3]

CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the GLA domain. This GLA-independent binding
CC site is necessary for the recognition of the
CC chrombin-chromomodulin complex.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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CC or send an email to license@isb-sib.ch).

CC EMBL: AF191307; AAC28380.1; -.
CC HSSP: P04070; 1PCU.
CC MEROPS: S01.218; -.
DR InterPro: IPR000152; Axx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00001; EGF-like; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS02040; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KM Blood coagulation; Glycoprotein; Serine protease;
KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL 1 18
FT PROPEP 19 41
FT CHAIN 42 459
FT CHAIN 42 196
FT CHAIN 199 459
FT PEPTIDE 199 213
FT SITE 213 214
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 214 459
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67

FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 255 255
FT ACT_SITE 301 301
FT ACT_SITE 400 400
FT DISULFID 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 321
FT DISULFID 240 256
FT DISULFID 371 385
FT DISULFID 396 424
FT CARBOHYD 138 138
FT CARBOHYD 292 292
FT CARBOHYD 353 353
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

Query Match 52.1%; Score 99; DB 1; Length 459;
Best Local Similarity 45.5%; Pred. No. 3.7e-10;
Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCRXXLGFXXAFIPFRXXTRQFWWSY 44
DB 42 ANSFLERLPSLSLRCKERTCDPEAREIFONTENTMAFWSKY 85

RESULT 10
FA10_RABBIT STANDARD; PRT; 490 AA.
AC 019045;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97256311; PubMed=9101642;
RA Pendurthi U.R.; Anderson K.D.; James H.L.;
RT "Characterization of a full-length cDNA for rabbit factor X.";
RL Thromb. Res. 85:503-514(1997).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
CC (BY SIMILARITY).
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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DT	01-NOV-1997	Rel. 35, Created)
DR	PROSITE; PS01186; EGF_2; 2.	
DR	PROSITE; PS01187; EGF_CA; 1.	
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.	
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	
KM	Blood coagulation; Glycoprotein; Serine protease;	
KM	Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;	
KM	EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.	
FT	SIGNAL	1 33
FT	PROPEP	34 41
FT	CHAIN	42 196
FT	CHAIN	199 461
FT	PEPTIDE	199 212
FT	SITE	212 213
FT	DOMAIN	96 131
FT	DOMAIN	135 175
FT	DOMAIN	213 461
FT	MOD_RES	47 47
FT	MOD_RES	48 48
FT	MOD_RES	55 55
FT	MOD_RES	57 57
FT	MOD_RES	60 60
FT	MOD_RES	61 61
FT	MOD_RES	66 66
FT	MOD_RES	67 67
FT	MOD_RES	70 70
FT	MOD_RES	112 112
FT	ACT_SITE	253 253
FT	ACT_SITE	299 299
FT	ACT_SITE	402 402
FT	DISULFID	58 63
FT	DISULFID	91 110
FT	DISULFID	100 105
FT	DISULFID	104 119
FT	DISULFID	121 130
FT	DISULFID	139 150
FT	DISULFID	146 159
FT	DISULFID	161 174
FT	DISULFID	182 319
FT	DISULFID	238 254
FT	DISULFID	373 387
FT	DISULFID	398 426
FT	CARBOHYD	214 214
FT	CARBOHYD	230 290
FT	CARBOHYD	355 355
FT	CARBOHYD	328 328
FT	CONFLICT	393 393
FT	CONFLICT	461 461
FT	SEQUENCE	461 AA; 53PAAD0858194D6E CXC64;
Qy	1 ANGFLXLRREGSLXRXCRXXLCSFXKAFYIFRNXXTRQFWMSY 44	
Db	42 ANSFLEBNRPGSLERECMEICDFEAEQELFQWEVTLAFLWIKY 85	
RESULT 6		
AC	FA7 MOUSE	STANDARD; PRT; 446 AA.
DT	01-NOV-1997	Rel. 35, Created)

01-NOV-1997 (Ref. 35, last sequence update)
DT 15-JUN-2002 (Ref. 41, last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
DE F7 OR C7.
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91127167; Pubmed=8972017;
RA Iadugog E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
RT "Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene".
RL Thromb. Haemost. 76:957-964(1996).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; U66079; AAC33796.1; -.
CC DR HSSP; P08709; 1BP9.
CC DR MEROPS; S01.215; -.
CC MGD; MGI:109325; F7.
CC InterPro; IPR000152; Aex_hydroxy1.
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR000742; EGF 2.
CC InterPro; IPR001881; EGF Ca.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR001254; Ser_protease_Try.
CC InterPro; IPR000294; Vitk_dep_GLA.
CC Pfam; PF00089; EGF; 2.
CC Pfam; PF00594; gla; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00001; GLABLOOD.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00001; EGF_Like; 1.
CC SMART; SM00069; GLA; 1.
CC SMART; SMO0020; Tryp_Spc; 1.
CC PROSITE; PS00020; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00011; GLU CARBOXYLATION; 1.
CC PROSITE; PS02040; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;

[9] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=99126538; PubMed=9925787; A.;
RA Zhang B., St Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
inhibited with a BPTI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
RN [10]
RP STRUCTURE BY NMR OF 105-115.
RX MEDLINE=96367502; PubMed=9629950; A.;
RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stefflo J.,
RT Drakenberg T.;
RL "Solution structure of the N-terminal EGF-like domain from human
factor VII.";
RL Biochemistry 37:10605-10615(1998).
RN [11]
RP VARIANT GLN-364.
RX MEDLINE=91300046; PubMed=2070047; A.;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RA Meade T.W., Tuddenham E.G.D.;
RT "Purification and characterization of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
male.";
RL Blood 78:132-140(1991).
RN [12]
RP VARIANTS GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=1634227; A.;
RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,
RA Rodorigo F., Casonato A., Girolami A., Bernardi F.;
RT "Detection of two missense mutations and characterization of a repeat
RT polymorphism in the factor VII gene (F7).";
RL Hum. Genet. 89:497-502(1992).
RN [13]
RP VARIANT TYR-238.
RX MEDLINE=93372811; PubMed=8364544; A.;
RA Marchetti G., Ferrati M., Patrascchini P., Reddelli R., Bernardi F.;
RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
RT (115His and 333Ser) in the human coagulation factor VII gene.";
RL Hum. Mol. Genet. 2:1055-1056(1993).
RN [14]
RP VARIANTS.
RX MEDLINE=94061028; PubMed=8242057; A.;
RA Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,
RA von Felten A., Meili E., Hahn T., Prangnell D.R., Lumley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational
RT polymorphism (SSCP) analysis in five dysfunctional variants of
RT coagulation factor VII.";
RL Hum. Mol. Genet. 2:1355-1359(1993).
RN [15]
RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE=94264305; PubMed=8204879; A.;
RA Chang S., Clarke B., Sridhara S., Chu K., Friedman P., Vandenusen W.,
RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the
RT cleavage site for activation and altering binding to tissue factor.";
RL Blood 83:3524-3535(1994).
RN [16]
RP VARIANT VAL-354.
RX MEDLINE=95072589; PubMed=7981691; A.;
RA Bernardi F., Castaman G., Reddelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation
RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
RL Hum. Mol. Genet. 3:1175-1177(1994).
RN [17]
RP VARIANT MET HIS-307.
RX MEDLINE=95064662; PubMed=7974346; A.;
RA Ohwa M., Hayashi T., Wada H., Minamikawa K., Shitakawa S.,
RA Suzuki K.;
RT "Factor VII Met: homozygous asymptomatic type I deficiency caused by
RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
RT catalytic domain.";

RL Thromb. Haemost. 71:773-777(1994).
[18]
RP VARIANT MET-419.
RX MEDLINE=96247510; PubMed=8652821;
RA Aibini A.A., Mannucci P.M., Bauer K.A.;
RT "A Thr359Met mutation in factor VII of a patient with a hereditary
RT deficiency causes defective secretion of the molecule.";
RL Blood 87:5085-5094(1996).
RN [19]
RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
RX MEDLINE=97001216; PubMed=8844208;
RA Bernardi F., Gaetman G., Pinotti M., Ferraresi P., di Iasio M.G.,
RA Lunghi B., Rodeghiero F., Marchetti G.;
RT "Mutation pattern in clinically asymptomatic coagulation factor VII
RT deficiency.";
RL Hum. Mutat. 8:108-115(1996).
RN [20]
RP VARIANT VAL-304.
RX MEDLINE=97037613; PubMed=8883260;
RA Tanerly H., Fromovich Y., Shalom L., Reich Z., Dym O., Lanir N.,
RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
RA Zaizov R., Seligson U.;
RT "Ala24Val is a common, probably ancient mutation causing factor VII
RT deficiency in Moroccan and Iranian Jews.";
RL Thromb. Haemost. 76:283-291(1996).
RN [21]
RP VARIANTS MALTA THR-194 AND VAL-304.
RX MEDLINE=98112461; PubMed=9452082;
RA Alshinawi C., Scerrit C., Galides R., Aquilina A., Felice A.E.;
RT "Two new missense mutations (P134T and A244V) in the coagulation
RT factor VII gene.";
RL Hum. Mutat. Suppl. 1:S189-S191(1998).
CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg--Ile bond in factor X to
CC form factor Xa.
CC -I- SUBUNIT: HETERO DIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND.
CC -I- ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; are
CC produced by alternative splicing.
CC -I- TISSUE SPECIFICITY: PLASMA.
CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMOLOGICAL CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
CC -I- PHARMACEUTICAL: Available under the names Niasse or Novoseven
CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match 63.2%; Score 120; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 6e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGELXLIRSGSLXRCXRXCSPFXKXFFIKFNXXRTRTFQFWSY 44
||| ||| ||| ||| ||| ||| :||: ||: ||| |||
Db 61 ANAFLEELRPGSLRECKEEOCSFEDEAREIFXDERTKLWFISY 104

RESULT 4
TMG1_HUMAN
ID TMG1_HUMAN STANDARD; PRT; 218 AA.

AC 014668;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxylglutamic acid protein 1 precursor (Proline-rich Gla protein 1) (Proline-rich gamma-carboxylglutamic acid protein 1)
DE PRKG1 OR TMG1 OR PRGP1.
OS Homo sapiens (Human).

DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00001; EGF-like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASK_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPE 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT BINDING 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 203
FT DISULFID 198 233
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SO SEQUENCE 444 AA; 49011 MW; 0481ABCFFE5427F8 CRC64;

Query Match 67.4%; Score 128; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 2; 1e-15;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLXRXCRXXLCGFXAFXIFRNXXRTROFMVY 44
DB 40 ANSFLEBLRPGSLRBECKELCSFEERARVFOSTERTKQFWITY 83

RESULT 3
FAT_HUMAN STANDARD; PRT; 466 AA.
ID P08709; Q14339;
AC P08709; Q14339;
DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (BC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C., Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K., Davie E.W.;
RA "Characterization of a cDNA coding for human factor VII."
RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RL [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y., Hagen F.S., Murray M.J.;
RA "Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein participating in blood coagulation."
RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RL [3]
RN SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L., Boel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RA Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RL [4]
RN SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjoern S., Christensen M., Nicolaissen E.M., Lund-Hansen T., Pedersen A.H., Hedner U.;
RA "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells."
RT Biochemistry 27:7785-7793(1988).
RL [5]
RN CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M., Komiyama Y., Pedersen A.H., Kistiel W.;
RA "Human plasma and recombinant factor VII. Characterization of O-glycosylations at serine residues 52 and 60 and effects of site-directed mutagenesis of serine 52 to alanine."
RT J. Biol. Chem. 266:11051-11057(1991).
RL [6]
RN STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T., Shimonihi Y., Iwanaga S.;
RA "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl2-Glc) O-glycosidically linked to a serine residue in the epidermal growth factor-like domain of human factors VII and IX and protein Z and bovine protein Z."
RT J. Biol. Chem. 264:20320-20325(1989).
RL [7]
RN STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=9144709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RA "A new trisaccharide sugar chain linked to a serine residue in the first BGF-like domain of clotting factors VII and IX and protein Z."
RT Adv. Exp. Med. Biol. 281:121-131(1990).
RL [8]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Gunu A., Konigsberg W.H., Newreson Y., Kirchhofer D.;
RA "The crystal structure of the complex of blood coagulation factor VIIa with soluble tissue factor."
RT Nature 380:41-46(1996).

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DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR001438; EGF-11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
FT ACT_SITE 242 242 FACTOR VII HEAVY CHAIN.
FT ACT_SITE 344 344 GLA-RICH.
FT BINDING 338 338 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DISULFID 17 22 EGF-LIKE 2.
FT DISULFID 50 61 SERINE PROTEASE.
FT DISULFID 55 70 CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
FT DISULFID 72 81 FACTOR IXA, OR THROMBIN).
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 98 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 135 262 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 178 194 BY SIMILARITY.
FT DISULFID 310 329 BY SIMILARITY.
FT DISULFID 340 368 BY SIMILARITY.
FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 32 35 O-LINKED (GLC. . .).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
SO SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;
Query Match 77.9%; Score 148; DB 1; Length 407;
Best Local Similarity 68.2%; Pred. No. 4.6e-19;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 1 ANGFLXXLRGSLXRYCRXXLCSFXXAFIERNXXRTQFWSY 44
Db 1 ANGFLLELLPGSLERCRELCSPFEAHEIFRNEERTROFWSY 44
RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=liver;
RX MEDLINE=93190306; PubMed=8383355;
RA Brothers A.B., Clarke B.O., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII."
RL Thromb. Res. Suppl. 69:231-238 (1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=liver;
RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RL Blajchman M.A., Clarke B.O., Sheffield W.P., Brothers A.B.,
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIa BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77477; AAB37326.1; -.
DR HSP; P08709; IPAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR001438; EGF-11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds

(without alignments)
328.082 Million cell updates/sec

Title: 10G1U28PHE_4

Perfect score: 190

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	77.9	407	1	FA7_BOVIN
2	128	67.4	444	1	FA7_RABIT
3	120	63.2	466	1	FA7_HUMAN
4	107	56.3	218	1	TMG1_HUMAN
5	104	54.7	461	1	PRTC_MOUSE
6	103	54.2	446	1	FA7_MOUSE
7	103	54.2	461	1	PRTC_RAT
8	100	52.6	231	1	TMG3_HUMAN
9	99	52.1	459	1	PRTC_PIG
10	97	51.1	490	1	FA10_RABIT
11	94	49.5	456	1	PRTC_BOVIN
12	93	48.9	488	1	FA10_HUMAN
13	89	46.8	461	1	PRTC_HUMAN
14	89	46.8	492	1	FA10_BOVIN
15	87	45.8	461	1	FA9_HUMAN
16	87	45.8	622	1	THRB_HUMAN
17	85	44.7	416	1	FA9_BOVIN
18	84	44.2	617	1	THRB_RAT
19	84	44.2	618	1	THRB_MOUSE
20	82	43.2	475	1	PRTC_RABIT
21	81	42.6	458	1	FA10_CHICK
22	80	42.1	452	1	FA9_CANFA
23	80	42.1	459	1	FA9_MOUSE
24	78	41.1	625	1	THRB_BOVIN
25	69	36.3	400	1	PRTC_HUMAN
26	69	36.3	649	1	PRTC_MACMU
27	69	36.3	675	1	PRTC_BOVIN
28	69	36.3	676	1	PRTC_HUMAN
29	68	35.8	202	1	TMG2_HUMAN
30	68	35.8	646	1	PRTC_RABIT
31	67	35.3	226	1	TMG4_HUMAN
32	66	34.7	376	1	FA10_TROCA
33	66	34.7	675	1	PRTC_RAT

34	65	34.2	396	1	PRTC_BOVIN	P00744 bos taurus
35	59	31.1	675	1	PRTC_MOUSE	Q08761 mus musculus
36	52	27.4	604	1	VE1_BPV2	P11298 bovine papl
37	52	27.4	605	1	VE1_BPV1	P03116 bovine papl
38	48.5	25.5	2133	1	FA8_PIG	P12263 sus scrofa
39	48	25.3	413	1	NCAP_PIG	P16691 infectio
40	44	23.2	2351	1	FA8_HUMAN	P00451 homo sapien
41	42.5	22.4	105	1	UL03_HCMVA	P16775 human cytom
42	42	22.1	320	1	GSHB_BUCAI	P57612 buchneera ap
43	41	21.6	97	1	YCRB_MYCCA	P45619 mycoplasma
44	41	21.6	315	1	YDJH_ECOLI	P77493 escherichia
45	41	21.6	348	1	EXOO_RHIME	P33697 rhizobium m

ALIGNMENTS

RESULT 1	FA7_BOVIN	STANDARD;	PRT;	407 AA.
ID	FA7_BOVIN			
AC	P22457;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-UTN-2002 (Rel. 41, Last annotation update)			
DE	Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).			
GN	F7.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RP	[1]			
RP	SEQUENCE.			
RX	MEDLINE=89008362; PubMed=3049594;			
RA	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,			
RA	Iwanaga S.;			
RT	"Bovine factor VII. Its purification and complete amino acid			
RT	sequence.";			
RL	J. Biol. Chem. 263:14868-14877(1988).			
RN	[2]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.			
RX	MEDLINE=91344709; PubMed=2129367;			
RA	Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;			
RA	Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.;			
RA	Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;			
RT	"A new trisaccharide sugar chain linked to a serine residue in bovine			
RT	blood coagulation factors VII and IX.";			
RL	J. Biochem. 104:867-868(1988).			
RN	[3]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.			
RX	MEDLINE=91344709; PubMed=2129367;			
RA	Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;			
RT	"A new trisaccharide sugar chain linked to a serine residue in the			
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";			
RL	Adv. Exp. Med. Biol. 281:121-131(1990).			
CC	- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS			
CC	CONVERTED TO FACTOR VIIa BY FACTOR Xa, FACTOR XIIa, FACTOR IXa, OR			
CC	THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR			
CC	AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa			
CC	BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO			
CC	FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.			
CC	- CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor X to			
CC	form factor Xa.			
CC	- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED			
CC	BY A DISULFIDE BOND.			
CC	- TISSUE SPECIFICITY: PLASMA.			
CC	- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME			
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND			
CC	CALCIUM.			
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.			
DR	PIR; A31979; A31979.			
DR	HSSP; P08709; 1BF9.			

Thu Mar 20 14:52:17 2003

10g1u28phe_4.rpr

Page 10

Search completed: March 19, 2003, 15:01:00
Job time : 30.125 secs

A:Residues: 59-63, X', 65-69 <MCM>
R:Choo, K.H.; Gould, K.G.; Reese, D.J.G.; Brownlee, G.G.
Nature 289, 178-180, 1982
A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
A:Reference number: I45891, MUID:82272386; PMID:6287289
A:Accession: I45891
A:Status: translated from GB/EMBL/DDBB
A:Molecule type: mRNA
A:Residues: 52-139 <CHO>
A:Cross-references: GB:J00007; NID:g163053; PIDN:AAA30520.1; PID:g163054
J.Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,
U. Biochim. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
A:Reference number: A44566; MUID:99213999; PMID:3149637
A:Contents: annotation
A:Note: structure and location of a carboxylate covalently bound to Ser
C:Comment: Factor IX is activated by factor XIIa, which excises the activation peptide pr
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypan homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F:1-46/Product: coagulation factor IXa light chain #status experimental <ALIC>
F:1-45/Domains: Gla domain homology (fragment) <GLA>
F:51-82/Domains: EGF homology <EGF>
F:88-124/Domains: EGF homology <EG2>
F:147-181/Domains: activation peptide #status experimental <APT>
F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:182-409/Domains: trypan homology <TRY>
F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #sta
F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfid
F:53/Binding site: carbonylate (Ser) (covalent) #status experimental
F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:158,168,173,261/Binding site: carbonylate (Asn) (covalent) #status experimental
F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 44.7%; Score 85; DB 1; Length 416;
Best Local Similarity 37.2%; Pred. No. 3.8e-07;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXXLRBGSLLRXCRXLCSFYXAFIRNNXXRTQFWWSY 44
Db 3 SCGLEEFVRGNLRECKEKSCSFEEAREVFENXTETFEWKY 45

RESULT 14
S10511
chrombin (EC 3.4.21.5) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1993 #sequence revision 07-May-1993 #text_change 03-May-2002
C:Accession: S10511, Acc0576; B42636
D:Dmanich, M.; Monard, D.
Nucleic Acids Res. 18, 4251, 1990
A:Title: cDNA sequence of rat prothrombin.
A:Reference number: S10511, MUID:90332426; PMID:2377469
A:Accession: S10511
A:Molecule type: mRNA
A:Residues: 1-617 <DIH>
A:Cross-references: EMBL:X52835; NID:g56969; PIDN:CAA37017.1; PID:g56970
R.Henrikson, K.P.; Jazin, B.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
A:Reference number: A60576; MUID:90091942; PMID:2293980
A:Accession: A60576
A:Molecule type: protein
A:Residues: 44-58 <HEN>
A:Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat uter
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq

A:Accession: B42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 383-617, 'E' <BAN>
A:Cross-references: GB:M81397
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hydr
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-617/Product: prothrombin #status experimental <PMAT>
F:109-187/Domain: kringle homology <KR1>
F:215-292/Domain: kringle homology <KR2>
F:360-605/Domain: trypsin homology <TRY>
F:50, 51, 58, 60, 63, 64, 69, 70, 73, 76/Modified site: gamma-carboxylglutamic acid (Glu) #status
F:61-66, 91-104, 109-187, 130-170, 158-182, 215-292, 236-276, 264-287, 332-478, 387-403, 532-546, 5
F:402, 458, 564/Active site: His, Asp, Ser #status predicted

Query Match 44.2%; Score 84; DB 2; Length 617;
Best Local Similarity 39.5%; Pred. No. 8.3e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXXLRGSLXRCRXXLCSPFXAFPIFRNXXRTQFWWSY 44
DB 46 SGFLBELRKGNLERECVEQCSTYEAFALESPODTVPWAKY 88

RESULT 15
A35827
thrombin (EC 3.4.21.5) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence, revision 14-Dec-1990 #text_change 03-May-2002
C:Accession: A35827; A42696; S12081
R:Degeen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pal, J.A
DNA Cell Biol. 9, 487-498, 1990
A>Title: Characterization of the cDNA coding for mouse prothrombin and localization of t
A:Reference number: A35827; MUID:9102551; PMID:2222810
A:Accession: A35827
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-618 <DEG>
A:Cross-references: GB:X52308, NID:953813, PID:CAA36548.1; PID:953814
A:Experimental source: strain C57BL/6
A>Note: the data were obtained from females resulting from the cross of M. domesticus an
R:Banfield, D.K.; Macgillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A>Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Accession: A42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 384-618, 'E' <BAN>
A:Cross-references: GB:M81394
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hydr
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-618/Product: prothrombin B #status predicted <MAT>
F:109-187/Domain: kringle homology <KR1>
F:215-293/Domain: kringle homology <KR2>
F:361-610/Domain: trypsin homology <TRY>
F:50, 51, 58, 60, 63, 64, 69, 70, 73, 76/Modified site: gamma-carboxylglutamic acid (Glu) #status
F:61-66, 91-104, 109-187, 130-170, 158-182, 215-293, 236-276, 264-288, 333-479, 388-404, 533-547, 5
F:403, 459, 565/Active site: His, Asp, Ser #status predicted

Query Match 44.2%; Score 84; DB 2; Length 618;
Best Local Similarity 39.5%; Pred. No. 8.3e-07;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXXLRGSLXRCRXXLCSPFXAFPIFRNXXRTQFWWSY 44
DB 46 SGFLBELRKGNLERECVEQCSTYEAFALESPODTVPWAKY 88

A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic
 F:1-26/Domain: signal sequence #status experimental <PPT>
 F:29-46/Domain: propeptide #status experimental <ACT>
 F:31-91/Domain: Gla domain homology <GLA>
 F:47-91/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:97-128/Domain: EGF homology <EGG>
 F:134-170/Domain: EGF homology <EG2>
 F:227-226/Domain: activation peptide #status experimental <ACT>
 F:227-61/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F:227-454/Domain: trypsin homology <TRY>
 F:237-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxylglutamic acid (Glu) #
 F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D
 F:99/Binding site: carboxylate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:191-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental
 F:203,213/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:205,215/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

Query Match 45.8%; Score 87; DB 1; Length 461;
 Best Local Similarity 39.5%; Pred. No. 1.8e-07;
 Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXLRBGSILKRXCRXXLCSPXXAFIFRNXXRTROFWVS 44
 49 SGLKEFVQGNLERECMEKESFEEAREVFENTERTTEFWQY 91

RESULT 12

Thrombin (EC 3.4.21.5) precursor [validated] - human

N:Alternate names: coagulation factor II

N:Contains: prothrombin

C:Species: Homo sapiens (man)

C:Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000

C:Accession: A29351; A00914; B00914; A37549; A37550; I51952

R:Degem, S.J.F.; Davie, E.W.

Biochemistry 26, 6165-6177, 1987

A:Title: Nucleotide sequence of the gene for human prothrombin.

A:Reference number: A29351; MUID:88077877; PMID:12825773

A:Accession: A29351

A:Molecule type: DNA

A:Residues: 1-622 <DEG>

A:Cross-references: GB:M17262; GB:M33691; NID:G558069; PIDN:AAC63054.1; PID:G339641

R:Degem, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.

Biochemistry 22, 2087-2097, 1983

A:Title: Characterization of the complementary deoxyribonucleic acid and gene coding for

A:Reference number: A00914; MUID:83231469; PMID:6305407

A:Accession: A00914

A:Molecule type: mRNA

A:Residues: 8-163, 'N', 165-622 <DE2>

A:Cross-references: GB:V00595; GB:U00307; NID:G37128; PIDN:CAA23842.1; PID:G1335344

A:Accession: B00914

A:Molecule type: DNA

A:Residues: 188-311 <DE3>

R:Malz, D.A.; Hewett-Ewmett, D.; Seegers, W.H.

Proc. Natl. Acad. Sci. U.S.A. 74, 1968-1972, 1977

A:Reference number: A37549; MUID:77193964; PMID:266717

A:Accession: A37549

A:Molecule type: Protein

A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'W', 196-308,

R:Butkowski, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.

J. Biol. Chem. 252, 4942-4957, 1977

A:Title: Primary structure of human prothrombin 2 and alpha-thrombin.

A:Reference number: A37550; MUID:77207112; PMID:873923

A:Accession: A37550

A:Molecule type: Protein

A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-

J. Biol. Chem. 261, 13210-13215, 1986

A:Reference number: A37551; MUID:87008532; PMID:3759958

A:Contents: annotation; activation cleavages

R:MacGillivray, R.T.; Irwin, D.M.; Guinno, E.R.; Stone, J.C.

Ann. N.Y. Acad. Sci. 485, 73-79, 1986

A:Title: Recombinant genetic approaches to functional mapping of thrombin.

A:Reference number: I51952; MUID:87182874; PMID:3471151

A:Accession: I51952

A:Molecule type: mRNA

A:Residues: 1-2, 'R', 5-100 <RES>

A:Cross-references: GB:M33031; NID:G190723; PIDN:AAA60220.1; PID:G190724

C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin

C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds

ter 314-Arg, are released in natural blood clotting.

C:Comment: The gamma-carboxylglutamate residues bind calcium ions, result from the carboxy

ent interaction with the negatively charged phospholipid membrane surface.

C:Comment: The prothrombin precursor is synthesized in the liver.

C:Genetics:

A:Gene: GDB:F2

A:Cross-references: GDB:119894; OMIM:176930

A:Map position: 11p11-11q12

A:Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 555/

C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology

C:Keywords: acute phase; blood coagulation; calcium binding; carboxylglutamic acid; dupl

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-43/Domain: propeptide #status predicted <PRO>

F:28-87/Domain: Gla domain homology <GLA>

F:44-622/Product: prothrombin #status experimental <MNT>

F:108-186/Domain: kringle homology <KR1>

F:213-291/Domain: kringle homology <KR2>

F:328-363/Product: thrombin light chain #status experimental <LCH>

F:364-622/Product: thrombin heavy chain #status experimental <HCH>

F:364-613/Domain: trypsin homology <TRY>

F:49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxylglutamic acid (Glu) #status

F:60-65,90-103,108-186,129-165,151-181,213-291,234-274,282-286/Disulfide bonds: #status

F:121,143/Binding site: carboxylate (Asn) (covalent) #status predicted

F:316-482,536-550,564-594/Disulfide bonds: #status predicted

F:391-407/Disulfide bonds: #status experimental

F:406-462/Active site: His, Asp #status predicted

F:416/Binding site: carboxylate (Asn) (covalent) #status experimental

F:568/Active site: Ser #status experimental

Query Match 45.8%; Score 87; DB 1; Length 622;
 Best Local Similarity 38.6%; Pred. No. 2.4e-07;

Matches 17; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANGFLXLRBGSILKRXCRXXLCSPXXAFIFRNXXRTROFWVS 44
 44 ANFLKEVRKGNLERECVEETCSYEEAFEALESSTATDVWAKY 87

RESULT 13

KFBO coagulation factor IXa (EC 3.4.21.22) precursor - bovine

N:Alternate names: Christmas factor

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text change 16-Jul-1999

C:Accession: A14757; B20274; I55891; A00923

R:Katsuyama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; T

Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979

A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas f

A:Reference number: A14757; MUID:8005619; PMID:291916

A:Accession: A14757

A:Molecule type: Protein

A:Residues: 1-63, 'T', 65-416 <KAT>

R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood c

A:Reference number: A20274; MUID:83308813; PMID:668526

A:Accession: B20274

A:Molecule type: Protein

A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 30-92 <KOB>
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
 A>Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
 A:Reference number: A22673; PMID:85190593; PMID:3857619
 A:Accession: A22673
 A:Molecule type: mRNA
 A:Residues: 1-193, 'T', 195-461 <MCG>
 A:Cross-references: GB:M11309; NID:G180552; PIDN:AAA52763.1; PID:G180553
 A>Note: the authors translated the codon ACG for residue 29 as Tyr
 R:Uye, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Finkel, A.; Tolstosh
 Nucleic Acids Res. 11, 2325-2335, 1983
 A>Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
 A:Reference number: A21337; PMID:83220788; PMID:6687940
 A:Accession: A21337
 A:Molecule type: mRNA
 A:Residues: 1-193, 'T', 195-461 <JAY>
 A:Cross-references: GB:J00137; NID:G182610; PIDN:AAA52763.1; PID:G182611
 R:Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
 Somat. Cell Mol. Genet. 10, 465-473, 1984
 A>Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
 A:Reference number: A37546; PMID:84300526; PMID:6089357
 A:Accession: A37546
 A:Molecule type: mRNA
 A:Residues: 38-193, 'T', 195-326 <JAG>
 A:Cross-references: GB:M35672
 R:Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
 A>Title: Isolation and characterization of a cDNA coding for human factor IX.
 A:Reference number: A30623; PMID:83065193; PMID:6595130
 A:Accession: A30623
 A:Molecule type: mRNA
 A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',
 A:Cross-references: GB:J00136; NID:G182608; PIDN:AAA58726.1; PID:G182609
 A:Experimental source: liver
 R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
 Vox Sang. 58, 21-29, 1990
 A>Title: Development of an immunofluorescent process for factor IX purification.
 A:Reference number: A60486; PMID:90194857; PMID:2216207
 A:Accession: A60486
 A:Molecule type: protein
 A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
 R:McMullen, B.A.; Fujikawa, K.; Kiesel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; PMID:83308813; PMID:6688526
 A:Accession: A20274
 A:Molecule type: protein
 A:Residues: 105-109, 'X', 111-115 <MCM>
 R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall
 Eur. J. Biochem. 172, 565-572, 1988
 A>Title: Characterisation of two differently processed forms of human recombinant factor
 A:Reference number: S02527; PMID:8816735; PMID:3380312
 A:Accession: S02527
 A:Molecule type: protein
 A:Residues: 29-63 <BAU>
 A>Note: processed forms expressed in recombinant system
 R:Jallat, S.; Perraud, F.; Dalemans, W.; Ballard, A.; Dieterle, A.; Faure, T.; Meulien,
 EMBO J. 9, 3295-3301, 1990
 A>Title: Characterization of recombinant human Factor IX expressed in transgenic mice an
 A:Reference number: S12058; PMID:91006024; PMID:2209546
 A:Accession: S12058
 A:Molecule type: mRNA
 A:Residues: 1-68 <JAL>
 A>Note: processed forms expressed in recombinant system
 R:Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
 EMBO J. 9, 475-480, 1990
 A>Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
 A:Reference number: S12377; PMID:90151623; PMID:2406129
 A:Accession: S12377
 A:Molecule type: protein

A:Residues: 92-130 <HAN>
 A>Note: NMR detection of calcium binding by domain expressed in recombinant system
 Ride la Salle, C.; Charmanlier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
 Thromb. Haemost. 70, 370-371, 1993
 A>Title: A deletion located in the 3' non translated part of the factor IX gene responsi
 A:Reference number: I59612; PMID:94054330; PMID:8236150
 A:Accession: I59612
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 444-461 <RES>
 A:Cross-references: GB:S66752; NID:G439773; PIDN:AA82858.1; PID:G439774
 R:Stoflet, E.S.; Koebel, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A>Title: Genomic amplification with transcript sequencing.
 A:Reference number: I59529; PMID:88127096; PMID:3340835
 A:Accession: I59529
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 290-359 <RES>
 A:Cross-references: GB:M19063; NID:G182622; PIDN:AAA52456.1; PID:G182623
 R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimomishi, Y.; Nishimura, H.; Iw
 Biochemistry 33, 5167-5171, 1994
 A>Title: Activation peptide of human factor IX has oligosaccharide O-glycosidically lin
 A:Reference number: A54255; PMID:94227047; PMID:8172892
 A:Accession: A54255
 A:Molecule type: protein
 A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>
 A>Note: the residues designated 'X' were determined to be threonine bound to carbohydrat
 R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A>Title: Activation of human factor IX (Christmas factor).
 A:Reference number: A18483; PMID:78194509; PMID:659613
 A:Contents: annotation; activation; active site; carboxydrate binding
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64(suppl.1), 262a, 1984
 A:Reference number: A37563
 A:Contents: annotation
 A>Note: 194-Thr was also found
 R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5698-5704, 1984
 A>Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
 A:Reference number: A37543; PMID:84185715; PMID:6425296
 A:Contents: annotation; calcium binding
 R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A:Reference number: A37544
 A:Contents: annotation; calcium binding; correction
 R:Benley, A.K.; Rees, D.O.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A>Title: Defective propeptide processing of blood clotting factor IX caused by mutation
 A:Reference number: A37545; PMID:86189947; PMID:3009023
 A:Contents: annotation; signal sequence cleavage site
 R:Suñeiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
 J. Biol. Chem. 264, 21257-21265, 1989
 A>Title: Blood clotting factor IX (BIM) Nagoya: substitution of arginine 180 by cryptoph
 A:Reference number: A30622; PMID:90078229; PMID:2592373
 A:Contents: annotation; sequence of mutant BIM
 A>Note: carboxylation, glycosylation, and cleavage sites
 R:Baron, M.; Notman, D.G.; Harvey, T.S.; Handford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle
 submitted to the Brookhaven Protein Data Bank, November 1991
 A:Reference number: A51252; PDB:1IXA
 A:Contents: annotation; conformation in yeast
 A>Note: recombinant form expressed in yeast
 C:Comment: Factor IX is activated by factor Xa, which excises the activation peptide pr
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with sero
 C:Genetics:
 A:Gene: GDB:P9
 A:Cross-references: GDB:119900; OMIM:306900
 A:Map position: Xq27.1-Xq27.2
 A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

N: Alternate names: Stuart factor
 C: Species: Bos primigenius taurus (cattle)
 C: Date: 24-Apr-1984 #sequence, revision 17-Mar-1987 #text change 16-Jul-1999
 C: Accession: A22867, #sequence, revision 17-Mar-1987 #text change 16-Jul-1999
 R: Funf, M.R.; Campbell, R.M.; MacGillivray, T.A.
 A: Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
 A: Reference number: A22867, MUID:84247315; PMID:6330671
 A: Accession: A22867
 A: Molecule type: mRNA
 A: Residues: 1-487 <RNA>
 A: Cross-references: GB:X0673; NID:9192; PIDN:CA35286.1; PID:9193
 R: Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
 Biochemistry, 19, 659-667, 1980
 A: Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A: Reference number: A14997, MUID:80130563; PMID:6766735
 A: Accession: A14997
 A: Molecule type: protein
 A: Residues: 41-102, 'N', 104-180 <ENF>
 R: McMullen, B.A.; Fujikawa, K.; Kistiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A: Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor X.
 A: Reference number: A20274, MUID:83308813; PMID:6688526
 A: Contents: annotation; revision to residue 103
 R: Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A: Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
 A: Reference number: A12030, MUID:76053069; PMID:1059093
 A: Accession: A12030
 A: Molecule type: protein
 A: Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GREG', 446-492 <T>
 R: Persson, E.; Slander, M.; Lins, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
 J. Biol. Chem. 264, 16897-16904, 1989
 A: Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
 A: Reference number: A34412, MUID:89380326; PMID:2789221
 A: Accession: A34412
 A: Molecule type: protein
 A: Residues: 85-126 <PER>
 A: Note: beta-hydroxyaspartic acid site
 R: Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A: Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A: Reference number: S39414, MUID:94062825; PMID:8243461
 A: Accession: S39414
 A: Molecule type: protein
 A: Residues: 183-196, 199-209, 216-223 <INO>
 A: Note: carboxylate binding sites
 R: Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
 Biochemistry 11, 4899-4903, 1972
 A: Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammalian
 A: Reference number: A12453, MUID:73053314; PMID:4264266
 A: Contents: annotation; active site
 R: Fujikawa, K.; Titani, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
 A: Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to
 A: Reference number: A13504, MUID:76053121; PMID:1059122
 A: Contents: annotation; activation
 R: Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
 J. Biol. Chem. 259, 5705-5710, 1984
 A: Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
 A: Reference number: A38024, MUID:84185716; PMID:6546930
 A: Contents: annotation; calcium binding
 R: Morita, T.; Jackson, C.M.
 J. Biol. Chem. 261, 4008-4014, 1986
 A: Reference number: A38025, MUID:86140210; PMID:3949800
 A: Contents: annotation; sulfate binding
 C: Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C: Comment: The two chains are formed from a single-chain precursor by the excision of two
 C: Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), and
 C: Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strong
 C: Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C: Genetics:
 A: Gene: F10
 A: Map position: 13q34
 C: Function:
 A: Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V.
 C: Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C: Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic
 F: 1-15/Domain: signal sequence #status predicted <SIG>
 F: 16-40/Domain: propeptide #status predicted <PRO>
 F: 25-84/Domain: Gla domain homology <Gla>
 F: 41-180/Product: coagulation factor X light chain #status experimental <LCH>
 F: 90-121/Domain: EGF homology <EGF>
 F: 129-164/Domain: EGF homology <EG2>
 F: 183-492/Product: coagulation factor X heavy chain #status experimental <RCH>
 F: 233-233/Domain: activation peptide #status experimental <APT>
 F: 234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
 F: 234-461/Domain: trypsin homology <TRY>
 F: 46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F: 57-62,90-101,112-121,123-140,136-149,151-164,172-341/disulfide bonds: #status p
 F: 103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F: 200/Binding site: sulfate (Tyr) (covalent) #status experimental
 F: 208/Binding site: carboxylate (Thr) (covalent) #status experimental
 F: 218/Binding site: carboxylate (Asn) (covalent) #status experimental
 F: 233-234/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stat
 F: 240-245,260-276,389-403,414-442/disulfide bonds: #status experimental
 F: 275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 46.8% Score 89; DB 1; Length 492;
 Best Local Similarity 36.4% Pred. No. 8; 6e-08;
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXRCXXLCSEFXAFLFRXXRTQFWVSY 44
 Db 41 ANSLFEVXQGNRECLERACSLERARVEFEDAEQDFWMSKY 84

RESULT 11
 KFHU
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
 N: Alternate names: antihemophilic factor B; Christmas factor
 C: Species: Homo sapiens (man)
 C: Date: 17-Dec-1982 #sequence, revision 30-Jun-1987 #text change 15-Sep-2000
 C: Accession: A00922, A37570, A30511, A32989, A22673, A21337, A37546, A30623, A60486, A20
 R: Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 24, 3736-3750, 1985
 A: Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
 A: Reference number: A00922, MUID:8600558; PMID:2994716
 A: Accession: A00922
 A: Molecule type: DNA
 A: Residues: 1-461 <YOS>
 A: Cross-references: GB:K02402; NID:9182612; PIDN:AAB59620.1; PID:9182613
 R: Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Glanville, F.; Gould, K.; Huddleston, J.A.; Brc
 EMBO J. 3, 1053-1060, 1984
 A: Title: The gene structure of human anti-haemophilic factor IX.
 A: Reference number: A37570, MUID:84236100; PMID:6329734
 A: Accession: A37570
 A: Molecule type: DNA
 A: Residues: 1-461 <ANS>
 A: Cross-references: GB:K02048
 R: Raitema, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
 Blood 72, 1074-1076, 1988
 A: Title: The putative factor IX gene promoter in hemophilia B Leyden.
 A: Reference number: A30511, MUID:88327116; PMID:3416069
 A: Accession: A30511
 A: Molecule type: DNA
 A: Residues: 8-24 <RBI>
 A: Cross-references: EMBL:X55008; NID:9311288; PIDN:CA38245.2; PID:94469253
 R: Koebel, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
 Am. J. Hum. Genet. 45, 448-457, 1989
 A: Title: Functionally important regions of the factor IX gene have a low rate of polymor
 A: Reference number: A32989, MUID:89371752; PMID:2773937
 A: Accession: A32989

Gene 84, 517-519, 1989

Article: Cloning and characterization of the 5' end (exon 1) of the gene encoding human

A:Reference number: 154051; MUID:90128299; PMID:2612918

A:Accession: 154051

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-23 <RES>

A:Cross-references: GB:M33297; NID:g1813860; PIDN:AAA52636.1; PID:g553330

R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Blazyn, J.; Mol. Biol. 232, 947-966, 1993

A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.

A:Reference number: A49458; MUID:93360277; PMID:8355279

A:Contents: annotation; X-ray crystallography, 2.2 angstroms

C:Comment: The two chains held together by one disulfide bond are formed from a single-c-c-c

C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or

C:Genetics:

A:Gene: GDB:F10

A:Cross-references: GDB:119890; OMIM:227600

A:Map position: 13q34-13q34

A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1

A:Note: deficiency of this factor causes Stuart disease

C:Function:

A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V

A:Pathway: blood coagulation

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-40/Domain: propeptide #status predicted <PRO>

F:25-84/Domain: Gla domain homology <GLA>

F:41-179/Product: coagulation factor X light chain #status experimental <LCH>

F:90-121/Domain: EGF homology <EG1>

F:129-164/Domain: EGF homology <EG2>

F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>

F:183-234/Domain: activation peptide #status experimental <APT>

F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>

F:235-462/Domain: trypsin homology <TRY>

F:457-62/Dsulfide bonds: #status predicted

F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/Disulfide site: gamma-carboxyglutamic acid (Glu) #status experimental

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:199-211/Binding site: carboxylate (Thr) (covalent) #status experimental

F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental

F:234,235/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #status experimental

F:276,322/Active site: His, Asp, Ser #status experimental

Query Match 48.9%; Score 93; DB 1; Length 488;

Best Local Similarity 36.4%; Pred. No. 1.6e-08;

Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXCRXXLCSPFXAXFIFRNXXKRTQFWVS 44

DB 41 ANSFLXEMKKGHLEKRECMETCSYEAREVPEFSDSKTNFPMKY 84

RESULT 9

KXHU

protein C (activated) (BC 3.4.21.69) precursor - human

N:Alternate names: autoprothrombin IIA; plasma protein C

C:Species: Homo sapiens (man)

C:Date: 17-Mar-1987 #sequence, revision 17-Mar-1987 #text_change 16-Jul-1999

C:Accession: A22331; A25426; A21781; A23789; A00927

R:Forster, D.C.; Yoshitake, S.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985

A:Title: The nucleotide sequence of the gene for human protein C.

A:Reference number: A22331; MUID:85270390; PMID:2991887

A:Accession: A22331

A:Molecule type: DNA

A:Residues: 1-461 <FOS1>

A:Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334

R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986

A:Title: Evolution and organization of the human protein C gene.

A:Reference number: A25426; MUID:86120978; PMID:3511471

A.Accession: A25426
A.Molecule type: DNA
A.Residues: 1-445, 'L', 446-461 <PU>
A.Cross-references: GB:M1712; NID:g190330; PIDN:AAA60165.1; PID:g190332
R.Foster, D.; Davie, E.W.
Proc Natl Acad Sci U.S.A. 81, 4766-4770, 1984
A.Title: Characterization of a cDNA coding for human protein C.
A.Reference number: A21781; NID:84227214; PMID:6589623
A.Accession: A21781
A.Molecule type: mRNA
A.Residues: 'Q', 107-461 <POS2>
A.Cross-references: GB:K02059; NID:g190322; PIDN:AAA60164.1; PID:g190323
R.Beckmann, R.U.; Schmidt, R.U.; Sauter, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
Nucleic Acids Res. 13, 5233-5247, 1985
A.Title: The structure and evolution of a 461 amino acid human protein C precursor and
A.Reference number: A23789; NID:85269639; PMID:2991859
A.Accession: A23789
A.Molecule type: mRNA
A.Residues: 1-461 <BEC>
A.Cross-references: GB:X02750; NID:g35689; PIDN:CMA26528.1; PID:g763120
R.Milletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 265, 11397-11404, 1990
A.Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m
A.Reference number: A44605; NID:90283094; PMID:1694119
A.Contents: annotation, carbohydrate binding sites, activation peptide
A.Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
R.Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A.Title: O-linked fucose is present in the first epidermal growth factor domain of facto
A.Reference number: A44606; NID:92184750; PMID:1544894
A.Contents: annotation, beta-hydroxyaspartic acid
C.Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
vation of factor Va is strongly enhanced by complexing with protein S. Protein C also f
C.Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
C.Genetics:
A.Gene: GDB:PROC
A.Cross-references: GDB:120317; OMIM:176860
A.Map position: 2q13-2q21
A.Introns: 24/1, 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
C.Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C.Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F.1-32/Domain: signal sequence #status predicted <SIG>
F.27-86/Domain: Gla domain homology <GLA>
F.33-42/Domain: propeptide #status predicted <PRO>
F.43-197/Product: protein C light chain #status predicted <LCH>
F.92-131/Domain: EGF homology <EGF>
F.140-175/Domain: EGF homology <EG2>
F.200-211/Product: protein C heavy chain #status predicted <HCH>
F.200-211/Domain: activation peptide #status experimental <APT>
F.212-445/Domain: trypsin homology <TRY>
F.48, 49, 56, 58, 61, 62, 67, 68, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
F.106-111/Dsulfide bonds: #status predicted
F.110/Binding site: carbohydrate (Rn) (covalent) #status absent
F.113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F.139-299,355/Binding site: carbohydrate (Asn) (covalent) #status experimental
F.221-212/Cleavage site: Arg-Leu (thrombin) #status experimental
F.253,299,402/Active site: His, Asp, Ser #status predicted
F.371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

C/Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #ext_change 08-Dec-2000
 C/Accession: S49075; Jc4670; PS0191; PS0190; 162745
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A/Title: Evidence for competition between vitamin K-dependent clotting factors for intra
 A/Reference number: A58498; MUID:96093366; PMID:8578539
 A/Accession: S49075
 A/Molecule type: mRNA
 A/Residues: 1-482 <STAL>
 A/Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A/Note: submitted to the EMBL Data Library, June 1994
 A/Note: neither the complete nucleic acid sequence nor the complete translation are shown
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A/Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A/Reference number: Jc4670; MUID:96194815; PMID:8647460
 A/Accession: Jc4670
 A/Molecule type: mRNA
 A/Residues: 1-482 <STAL>
 A/Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A/Experimental source: Cos-1 cell
 R/Enjolji, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 890-898, 1991
 A/Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla
 A/Reference number: PS0190; MUID:92041742; PMID:1718949
 A/Accession: PS0191
 A/Molecule type: protein
 A/Residues: 41-58 'X', 60-65 <ENJ1>
 A/Accession: PS0190
 A/Molecule type: protein
 A/Residues: 183-186, 'X', 188-207 <ENJ2>
 R/Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
 Eur. J. Haematol. 52, 162-168, 1994
 A/Title: Analysis of the partial nucleotide sequences and deduced primary structures of
 A/Reference number: 146196; MUID:94222160; PMID:8168596
 A/Accession: 162745
 A/Molecule type: DNA
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Residues: 295-383, 'G', 385-455 <MUR>
 A/Cross-references: GB:D21215; NID:9415309; PIDN:BAA04756.1; PID:9455396
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A/Pathway: blood coagulation
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-119/Product: coagulation factor X light chain #status predicted <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:183-331/Domain: activation peptide #status predicted <APT>
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
 F:232-460/Domain: trypsin homology <TRY>
 F:46,47,54,55,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:187/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:208/Binding site: carboxylate (Thr) (covalent) #status predicted
 F:218/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 48.9%; Score 93; DB 1; Length 482;
 Best Local Similarity 36.4%; Pred. No. 1.6e-08;
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

1 ANGFLXLDREGSLKRXCRXXLCSFFXAFIFRNXXRTQFWWSY 44
 41 ANSPFEETIKGNLRECEVETICSFEAEAEVPEDNKTEIFNNKY 84

RESULT 8

EXDU
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
 N/Alternate names: Stuart factor
 C/Species: Homo sapiens (man)
 C/Date: 15-Nov-1984 #sequence_revision 02-May-1994 #ext_change 08-Dec-2000
 C/Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00
 R/Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
 Biochemistry 25, 5098-5102, 1986
 A/Title: Gene for human factor X: a blood coagulation factor whose gene organization is
 A/Reference number: A24478; MUID:87026600; PMID:3768336
 A/Accession: A24478
 A/Molecule type: DNA
 A/Residues: 1-488 <LEY>
 A/Cross-references: GB:L29433; GB:M14327; NID:9459809; PIDN:AAA52764.1; PID:9182831
 R/Messler, T.L.; Plittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
 Gene 99, 291-294, 1991
 A/Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coa
 A/Reference number: J00917; MUID:91216473; PMID:1902434
 A/Accession: J00917
 A/Molecule type: mRNA
 A/Residues: 1-488 <MES>
 A/Cross-references: GB:M57285; NID:9182389; PIDN:AAA52421.1; PID:9182390
 R/Mao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
 J. Biol. Chem. 267, 7395-7401, 1992
 A/Title: Liver-specific expression of the gene coding for human factor X, a blood coagul
 A/Reference number: A42485; MUID:92218390; PMID:1313796
 A/Accession: A42485
 A/Molecule type: DNA
 A/Residues: 1-15 <MA>
 A/Experimental source: liver
 A/Note: sequence extracted from NCBI backbone (NCBI:93780, NCBI:93787)
 R/Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
 Gene 41, 311-314, 1986
 A/Title: Isolation and characterization of human blood-coagulation factor X cDNA.
 A/Reference number: A25853; MUID:86221713; PMID:3011603
 A/Accession: A25853
 A/Molecule type: mRNA
 A/Residues: 19-284, 'E', 289-488 <KAU>
 A/Cross-references: GB:M22613; NID:9180335; PIDN:AAA51984.1; PID:9180336
 R/Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
 A/Title: Characterization of an almost full-length cDNA coding for human blood coagulati
 A/Reference number: A22208; MUID:85216545; PMID:2582420
 A/Accession: A22208
 A/Molecule type: mRNA
 A/Residues: 13-441, 'S', 443-488 <FUN>
 A/Cross-references: GB:K03194; NID:9182840; PIDN:AAA52490.1; PID:9182841
 R/Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
 A/Title: Characterization of a cDNA coding for human factor X.
 A/Reference number: A21284; MUID:84222026; PMID:6587384
 A/Accession: A21284
 A/Molecule type: mRNA
 A/Residues: 13-284, 'E', 289-488 <LE2>
 A/Cross-references: GB:K01886
 R/McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Sasaegawa, T.; Howald, W.N.; Kwa, E.Y.; Wein
 Biochemistry 22, 2875-2884, 1983
 A/Title: Complete amino acid sequence of the light chain of human blood coagulation fac
 A/Reference number: A20362; MUID:83257207; PMID:6671167
 A/Accession: A20362
 A/Molecule type: protein
 A/Residues: 41-179 <MCM>
 R/Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A/Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A/Reference number: S39414; MUID:94062825; PMID:8243461
 A/Accession: S39415
 A/Molecule type: protein
 A/Residues: 183-234 <INO>
 A/Note: glycosylation sites
 A/Note: identification and characterization of beta-hydroxyaspartic acid
 R/Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hameshushanham, K.; Lyman, G.

F:212-445/Domain: trypsin homology <TRY>
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat
 F:214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 54.7%; Score 104; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 1,7e-10;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLRXRCRXLLCSFXXAFXIFRXXXRTROFWVS 44
 DB 42 ANSFLEBRPGLSRERECMERICDFEEAOEIFQVEDTLAFWIKY 85

RESULT 5
 S18994
 protein C (activated) (EC 3.4.21.69) precursor - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 29-Oct-1999
 C:Accession: S18994; S24312
 R:Okajui, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
 submitted to the EMBL Data Library, February 1992
 A:Description: The cDNA cloning and mRNA expression of rat protein C.
 A:Reference number: S18994

A:Accession: S18994
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <OKA>

A:Cross-references: EMBL:X64336; NID:G56962; PIDN:CA45617.1; PID:G56963
 R:Okajui, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
 Biochim. Biophys. Acta 1131, 329-332, 1992

A:Title: The cDNA cloning and mRNA expression of rat protein C.
 A:Reference number: S24312; MUID:92329550; PMID:1627650

A:Accession: S24312

A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-461 <OKA>

A:Cross-references: EMBL:X64336; NID:G56962; PIDN:CA45617.1; PID:G56963

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
 F:1-32/Domain: signal sequence #status predicted <SIG>

F:127-85/Domain: Gla domain homology <GLA>

F:33-42/Domain: propeptide #status predicted <PRO>

F:43-461/Product: protein C #status predicted <PRO>

F:91-130/Domain: EGF homology <EG1>

F:139-174/Domain: EGF homology <EG2>

F:213-445/Domain: trypsin homology <TRY>

F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:121-130,139-150,146-159,161-174,182-319,238-255,373-387,398-426/Disulfide bonds: #stat

F:215,299,355/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 54.2%; Score 103; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 2,6e-10;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLRXRCRXLLCSFXXAFXIFRXXXRTROFWVS 44
 DB 42 ANSFLEBRPGLSRERECMERICDFEEAOEIFQVEDTLAFWIKY 85

RESULT 6
 KXBO
 protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)

N:Alternate names: autoproteolysin IIA; plasma protein C
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #ext_change 16-Jul-1999
 C:Accession: A26250; A18385; A18386; A00928
 R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984

A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.

A:Reference number: A26250; MUID:85014826; PMID:6091100

A:Accession: A26250

A:Molecule type: mRNA

A:Residues: 1-456 <LON>

R:Fernlund, P.; Stenflo, J.

U. Biol. Chem. 257, 12170-12179, 1982

A:Title: Amino acid sequence of the light chain of bovine protein C.

A:Reference number: A18385; MUID:83007325; PMID:6896876

A:Accession: A18385

A:Molecule type: protein

A:Residues: 40-194 <FER>

A>Note: 82-Lys was also found

R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.

Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983

A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.

A:Reference number: A19316; MUID:83169769; PMID:6572339

A:Contents: annotation; revision to residue 110

R:Stenflo, J.; Fernlund, P.

J. Biol. Chem. 257, 12180-12190, 1982

A:Title: Amino acid sequence of the heavy chain of bovine protein C.

A:Reference number: A18386; MUID:83007326; PMID:6896877

A:Accession: A18386

A:Molecule type: protein

A:Residues: 197-454, 'PV' <STE>

R:Esmon, N.L.; DeBault, L.E.; Esmon, C.T.

J. Biol. Chem. 258, 5548-5553, 1983

A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-d-domainless p

A:Reference number: A37541; MUID:8313513; PMID:6304092

A:Contents: annotation; activation; calcium binding

R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.

J. Biol. Chem. 258, 5554-5560, 1983

A:Title: Structural changes required for activation of protein C are induced by Ca2+ bin

A:Reference number: A37542; MUID:8313514; PMID:6406503

A:Contents: annotation; activation; calcium binding

C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re

s.

C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c

bin, which cleaves a tetrapeptide from the amino end of the heavy chain; this reacti

C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro

cognition of the thrombin-thrombomodulin complex.

C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding

F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>

F:24-83/Domain: Gla domain homology <GLA>

F:30-39/Domain: propeptide #status predicted <PRO>

F:40-194/Product: protein C light chain #status experimental <LCH>

F:98-128/Domain: EGF homology <EG1>

F:137-172/Domain: EGF homology <EG2>

F:197-456/Product: protein C heavy chain #status experimental <HCH>

F:197-210/Domain: activation peptide #status experimental <APT>

F:211-440/Domain: trypsin homology <TRY>

F:45,46,53,55,56,57,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #stat

F:252,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:252,298,397/Active site: His, Asp, Ser #status predicted

F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.5%; Score 94; DB 1; Length 456;
 Best Local Similarity 43.2%; Pred. No. 1e-08;
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLRXRCRXLLCSFXXAFXIFRXXXRTROFWVS 44
 DB 40 ANSFLEBRPGLSRERECSEVCEFEAREIFONTEDTMAFWFSFY 83

RESULT 7
 EXRT
 coagulation factor Xa (EC 3.4.21.6) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using SW model

Run on: March 19, 2003, 14:42:31 / Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10GLU28PHE_4

Perfect score: 190

Sequence: 1 ANGFLXLLREGSLKRXCRXX.....XXAFXIFRNXXKTRQFWWSY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	77.9	407	1 KFB07	coagulation factor
2	128	67.4	443	2 I46932	coagulation factor
3	120	63.2	466	1 KFH07	coagulation factor
4	104	54.7	461	1 UX0210	protein C (activat
5	103	54.2	461	1 S18994	protein C (activat
6	94	49.5	456	1 KXB0	coagulation factor
7	93	48.9	482	1 EXRT	coagulation factor
8	93	48.9	488	1 EXHU	coagulation factor
9	89	46.8	461	1 KXHU	protein C (activat
10	89	46.8	492	1 EXBO	coagulation factor
11	87	45.8	461	1 KFHU	coagulation factor
12	87	45.8	622	1 TBHU	thrombin (EC 3.4.2
13	85	44.7	416	1 KFB0	coagulation factor
14	84	44.2	617	2 S10511	thrombin (EC 3.4.2
15	84	44.2	618	2 A35827	thrombin (EC 3.4.2
16	81	42.6	475	1 EXCH	coagulation factor
17	80	42.1	452	1 A30351	coagulation factor
18	80	42.1	459	2 JU0419	coagulation factor
19	78	41.1	625	1 TBBO	thrombin (EC 3.4.2
20	74	38.9	642	2 S53433	plasma protein S p
21	69	36.3	422	1 KXHUZ	plasma protein S p
22	69	36.3	642	2 S53434	plasma protein S p
23	69	36.3	675	1 KXBOS	plasma protein S p
24	69	36.3	675	1 KXHUS	plasma protein S p
25	68	35.8	646	2 S18819	plasma protein S -
26	68	34.7	675	1 KXRS	plasma protein S p
27	65	34.2	396	1 KXBOZ	plasma protein Z -
28	59	31.1	675	1 KXMS	plasma protein S p
29	58	30.5	678	2 B48089	growth arrest-spec

30	57	30.0	673	2 A48089	growth arrest-spec
31	55	28.9	674	2 I55476	growth potentialin
32	52	27.4	605	1 MWLEB	E1 protein - bovin
33	52	27.4	620	1 MWLB2	E1 protein - bovin
34	48.5	25.5	2133	2 T42763	coagulation factor
35	48	25.3	413	1 VHYNH	nucleoprotein - in
36	46.5	24.5	594	2 D84859	probable MAP kinase
37	46.5	24.5	603	2 C96575	probable MAP kinase
38	45.5	23.9	576	2 G96763	probable MAP kinase
39	45	23.7	448	2 T18710	hypothetical prote
40	45	23.7	687	2 T08528	probable DNA topoi
41	44.5	23.4	304	2 AP2942	5-dehydro-4-deoxy
42	44.5	23.4	304	2 D96340	5-dehydro-4-deoxy
43	44	23.2	2351	1 EZHU	coagulation factor
44	43	22.6	536	1 E70066	hypothetical prote
45	43	22.6	1171	2 T31635	hypothetical prote

ALIGNMENTS

RESULT 1

KFB07

coagulation factor VIIa (EC 3.4.21.21) - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-May-1990 #sequence__revision 23-Mar-1995 #text_change 16-Jul-1999

C:Accession: A31979; C20274

R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14668-14677, 1988

A:Title: Bovine factor VII. Its purification and complete amino acid sequence.

A:Reference number: A31979; MUID:89008362; PMID:3049594

A:Accession: A31979

A:Molecule type: protein

A:Residues: 1-407 <TAK>

R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; MUID:83308813; PMID:6688526

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCW>

A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new triasaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A44556; MUID:89213999; PMID:3149637

A:Contents: annotation

A:Note: structure and location of covalently bound carbohydrate

C:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

gulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>

F:1-44/Domain: Gla domain homology (fragment) <GDA>

F:50-81/Domain: EGF homology <EG1>

F:91-127/Domain: EGF homology <EG2>

F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F:153-387/Domain: trypsin homology <TRY>

F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/

F:152/Binding site: carbohydrate (Ser) (covalent) #status experimental

F:53/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experiment

F:145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:152-153/Cleavage site: Arg-1le (coagulation factor XIIIa) #status experimental

F:193,242,344/Active site: His, Asp, Ser #status predicted

F:290-291/Cleavage site: Arg-Gly (coagulation factor XIa) #status experimental

Query Match 77.9%; Score 148; DB 1; Length 407;
Best Local Similarity 68.2%; Pred. No. 2,1e-18;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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FT	Misc-difference	14	/label= Glu, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"		
FT	Misc-difference	16	/label= Glu, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"		
FT	Misc-difference	19	/label= Glu, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"		
FT	Misc-difference	20	/label= Glu, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"		
FT	Misc-difference	25	/label= Glu, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"		
FT	Misc-difference	26	/label= Glu, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"		
FT	Misc-difference	29	/label= Glu, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"		
FT	Misc-difference	35	/label= Glu, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"		
FT	Modified-site	52	/note= "OTHER = gamma carboxyglutamic acid"	
FT		/note= "O-glycosylated"		
FT	Modified-site	60	/note= "O-glycosylated"	
FT		/note= "O-glycosylated"		
FT	Modified-site	145	/note= "N-glycosylated"	
FT		/note= "N-glycosylated"		
FT	Cleavage-site	152..153	/note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"	
FT	Modified-site	322	/note= "N-glycosylated"	
FT				
PN	WO200158935-A2.			
PD	16-AUG-2001.			
PF	12-FEB-2001; 2001WO-DK00094.			
PR	11-FEB-2000; 2000DK-0000218.			
PR	18-OCT-2000; 2000DK-0001558.			
PA	(MAXY-) MAXYGEN APS.			
P1	Andersen KV, Pedersen AH, Bornaae C;			
DR	WPI; 2001-581807/65.			
XX	N-PSDB; AAI99982.			
XX				
XX	New conjugate, useful for treating Factor VIIa related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -			
XX				
PS	Claim 1; Page 81-83; 89pp; English.			
CC	The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa) polypeptide conjugates, comprising at least one non-polypeptide group covalently attached to a polypeptide, where the amino acid sequence of polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at least one amino acid residue containing an attachment group for the non-polypeptide group has been introduced or removed. The FVIIa conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and cerebroprotective activity and are useful for treating FVIIa/TF-related diseases or disorders such as haemophilia, liver disease, myocardial infarction, thrombotic stroke and deep-vein thrombosis. The conjugates have increased functional in vivo half life and/or increased plasma half life, increased bioavailability and or reduced sensitivity to proteolytic degradation. Consequently medical treatment using the conjugates has a			

CC	number of advantages over currently available such as longer duration between injections.
CC	
XX	
SQ	Sequence 406 AA;
	Query Match 63.2%; Score 120; DB 22; Length 406;
	Best Local Similarity 75.0%; Pred. No. 1, 1e-11;
	Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
OY	1 ANGFLXLRBGSILRXRCRXYLCSTFYXAFTIRNXXRTROFVSY 44 : : :
bdb	1 ANAFLLXRPGSILRXRCCKXCCTFSYYARXIFKDXMRTLPMISY 44 : : :

Search completed: March 19, 2003, 14:51:15
Job time : 31.4375 secs

FT	Modified-site	322	/note= "glycosylation site"
FT	Disulfide-bond	340..368	
FT	Cleavage-site	341..342	/note= "proteolytic site"
FT	Cleavage-site	392..393	/note= "proteolytic site"
FT	Cleavage-site	396..397	/note= "proteolytic site"
FT	Cleavage-site	402..403	/note= "proteolytic site"
XX			
PN	US5580560-A.		
XX			
PD	03-DEC-1996.		
XX			
PF	13-NOV-1969;	89US-0434149.	
XX			
PR	09-AUG-1993;	93US-0104509.	
PR	13-NOV-1989;	89US-0434149.	
PR	12-JUN-1992;	92US-0898248.	
PR	22-AUG-1994;	94US-0293778.	
XX			
PA	(NOVO) NOVO-NORDISK AS.		
XX			
P1	Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;		
XX			
DR	WPI, 1997-033523/03.		
XX			
PT	Mutated human factor VII or VIIa proteins - with amino acid		
FT	substitutions to improve proteolytic stability		
XX			
PS	Example 3; Page -; 28pp; English.		
XX			
CC	Modified human factor VII or VIIa proteins are stabilised against		
CC	proteolytic cleavage by substitution of one of the residues Lys82,		
CC	Lys88, Ile42, Tyr44, Phe278, Arg290, Arg315, Tyr332 and		
CC	Lys441 by an amino acid that provides a proteolytically more stable		
CC	peptide bond, provided that Lys32 is replaced by Gln, Glu, His,		
CC	Gly, Thr, Ala or Ser. The modified proteins are useful for treating		
CC	bleeding disorders such as thrombocytopenia and von Willebrand's		
CC	disease. They are also suitable for addition to plasma substitutes.		
CC	The present sequence is a specific example of a modified factor VII		
CC	protein.		
XX			
XX			
SQ	Sequence 406 AA:		
Query Match	63.2%;	Score 120;	DB 18;
Best Local Similarity	52.3%;	Pred. No. 1.1e-11;	Length 406;
Matches 23;	Conservative 5;	Mismatches 16;	Indels 0;
Gaps 0;			
QY	1 ANGFLXLLREGSLRXCRXXLCSFXXAFIFPNXXRTROFWISY 44		
DB	1 ANAFLELRPGSLERCKEQQCSFEFARERFDXERTKLFWISY 44		
RESULT 13			
AAW14510			
ID	AAW14510 standard; protein; 406 AA.		
XX			
AC	AAW14510;		
XX			
DT	14-MAY-1997 (first entry)		
XX			
DE	Modified blood coagulation Factor VII (R315S).		
XX			
KW	Blood coagulation; factor 7; mutein; mutation; modification;		
KW	thrombocytopenia; von Willebrand's disease; plasma substitute.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	

FT	Modified-site	6	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	7	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	14	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	16	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	19	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	20	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Disulfide-bond	17..22	/label= OTHER
FT	Modified-site	25	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	26	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	29	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Cleavage-site	32..33	/note= "proteolytic site"
FT	Modified-site	35	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Cleavage-site	38..39	/note= "proteolytic site"
FT	Cleavage-site	42..43	/note= "proteolytic site"
FT	Cleavage-site	44..45	/note= "proteolytic site"
FT	Disulfide-bond	50..61	/label= OTHER
FT	Disulfide-bond	55..70	/label= OTHER
FT	Modified-site	63	/label= OTHER
FT		/note= "beta-hydroxy-aspartic acid"	
FT	Disulfide-bond	72..81	/label= OTHER
FT	Disulfide-bond	91..102	/label= OTHER
FT	Disulfide-bond	98..112	/label= OTHER
FT	Disulfide-bond	114..127	/label= OTHER
FT	Disulfide-bond	135..162	/label= OTHER
FT	Cleavage-site	143..144	/label= OTHER
FT	Modified-site	145	/label= OTHER
FT		/note= "glycosylation site"	
FT	Disulfide-bond	159..164	/label= OTHER
FT	Disulfide-bond	178..194	/label= OTHER
FT	Active-site	193	/label= OTHER
FT	Active-site	242	/label= OTHER
FT	Active-site	344	/label= OTHER
FT	Cleavage-site	290..291	/label= OTHER
FT		/note= "proteolytic site"	
FT	Disulfide-bond	310..329	/label= OTHER
FT	Cleavage-site	315..316	/label= OTHER
FT	Misc-difference	315	/label= OTHER
FT		/note= "native Arg315 has been substituted by Ser to provide a proteolytically more stable peptidic bond"	
FT	Modified-site	322	/label= OTHER
FT		/note= "glycosylation site"	
FT	Disulfide-bond	340..368	/label= OTHER
FT	Cleavage-site	341..342	/label= OTHER
FT		/note= "proteolytic site"	
FT	Cleavage-site	393..393	/label= OTHER

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FH Key Location/Qualifiers
FT Region 1..152
FT /note= "Factor VII light chain"
FT 153..406
FT Region /note= "Factor VII heavy chain"
FT Peptide 374..388
FT /note= "exosite 1"
FT 290..310
FT /note= "exosite 2"
FT 290..310
FT Peptide /note= "pref. PC polypeptide; claim 2, page 136"
FT 374..388
FT Peptide /note= "pref. PC polypeptide; claim 2, page 136"
FT 289..304
FT Peptide /note= "pref. PC polypeptide; claim 4, page 137"
FT 290..304
FT /note= "pref. PC polypeptide; claim 4, page 137"
FT 245..266
FT /note= "claim 9, page 138-139 describes an antibody
that reacts with Factor VII; fragments
289-304, 290-304, 290-310, 374-388 and
400-414 but not with fragment 245-266"
FT Peptide
FT WO9309804-A.
PN 27-MAY-1993.
PD 18-NOV-1992; 92MO-US10242.
XX 18-NOV-1991; 91US-0793989.
PR (SCRI ) SCRIpps RES INST.
XX (SCRI ) SCRIpps RES INST.
PI Griffin JH, Mesters RM;
XX WPI; 1993-182244/22.
XX DR
XX Serine protease derived-polypeptide(s) and anti-peptide
PT antibodies - for inhibiting coagulation and assaying for the
PT presence of serine protease in fluid samples
XX
XX PS Disclosure; Page 133-135; 149pp; English.
XX CC The PC polypeptides indicated in the Features Table inhibit
CC coagulation (they prevent binding of serine protease to natural
CC substrates), esp. when admin. to give an intravascular blood
CC concn. of 0.1-100 (pref. 0.5-10) microm.
CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
CC in the specification but have not yet been added to the SEQUENCE
CC LISTING.
XX
XX SQ Sequence 406 AA;
Query Match 63.2%; Score 120; DB 14; Length 406;
Best Local Similarity 52.3%; Pred. No. 1,1e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
QY 1 ANGFLXLRREGSLKRCXKXLCSPFXAXFRNXXRTQFWVS 44
DQ 1 ANAFLELRPGSLERCKECCSFPEARLTFKDAERTLFWISY 44

```

```

KW Thrombocytopenia; von Willebrand's disease; plasma substitute.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6
FT /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT 7
FT Modified-site /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT 14
FT Modified-site /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT 16
FT Modified-site /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT 19
FT Modified-site /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT 20
FT Modified-site /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT 17..22
FT Disulfide-bond /note= "gamma-carboxylutamic acid"
FT 25
FT Modified-site /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT 26
FT Modified-site /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT 29
FT Modified-site /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT 32..33
FT /note= "gamma-carboxylutamic acid"
FT 35
FT Modified-site /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT 38..39
FT Cleavage-site /note= "proteolytic site"
FT 42..43
FT Cleavage-site /note= "proteolytic site"
FT 44..45
FT Cleavage-site /note= "proteolytic site"
FT 50..61
FT Disulfide-bond /note= "proteolytic site"
FT 63
FT Modified-site /label= OTHER
FT /note= "beta-hydroxy-aspartic acid"
FT 72..81
FT Disulfide-bond /label= "glycosylation site"
FT 91..102
FT Disulfide-bond 158..164
FT 114..127
FT Disulfide-bond 135..162
FT Disulfide-bond 143..144
FT Cleavage-site /note= "proteolytic site"
FT 145
FT Modified-site /note= "glycosylation site"
FT 158..164
FT Disulfide-bond 178..194
FT Active-site 193
FT Active-site 242
FT Active-site 344
FT Cleavage-site 290..291
FT /note= "proteolytic site in unmodified factor VII"
FT 290
FT /note= "native Arg290 has been substituted by Ser to
provide a proteolytically more stable peptide
bond"
FT Disulfide-bond 310..329
FT Cleavage-site 315..316
FT /note= "proteolytic site"

```

CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.

XX Sequence 44 AA;

Query Match 63.2%; Score 120; DB 22; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.4e-12;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCRXKLCSPFXAFKIFRNXXRTROPWVS 44
DB 1 ANAFLEELRPGSLERCKEKGCSFEEREIFXDAERTKLFWISY 44

RESULT 9

ID AAB84870 standard; Protein; 401 AA.

AC AAB84870;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-31).

XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;

KM mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 31..317

FT /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp

FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

PN JP2001061479-A.

PD 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

XX PR 24-AUG-1999; 99JP-0237610.

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI; 2001-310677/33.

XX N-PSDB; AAH19463.

XX Claim 14; Page 20-21; 29pp; Japanese.

XX The present invention relates to mutants of blood coagulant factor VII

XX (FVII) or activated blood coagulant factor VII (FVIIa). The present

XX sequence is one such mutant FVII: VII-31. The mutants can be used as an

XX agent for the substitution therapy of haemophilia inhibitor patients.

XX SQ Sequence 401 AA;

Query Match 63.2%; Score 120; DB 22; Length 401;
Best Local Similarity 52.3%; Pred. No. 1.1e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCRXKLCSPFXAFKIFRNXXRTROPWVS 44
DB 1 ANAFLEELRPGSLERCKEKGCSFEEREIFXDAERTKLFWISY 44

RESULT 10

AAB84871
ID AAB84871 standard; Protein; 401 AA.

AC AAB84871;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-39).

XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;

KM mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 235..239

FT /note="Wild-type Val-Pro-Gly-Thr-Thr substituted by

FT Asp-Arg-Lys-Thr-Leu"

FT Misc-difference 311..317

FT /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp

FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

PN JP2001061479-A.

PD 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

XX PR 24-AUG-1999; 99JP-0237610.

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI; 2001-310677/33.

XX N-PSDB; AAH19464.

XX Claim 16; Page 23-24; 29pp; Japanese.

XX The present invention relates to mutants of blood coagulant factor VII

XX (FVII) or activated blood coagulant factor VII (FVIIa). The present

XX sequence is one such mutant FVII: VII-39. The mutants can be used as an

XX agent for the substitution therapy of haemophilia inhibitor patients.

XX SQ Sequence 401 AA;

Query Match 63.2%; Score 120; DB 22; Length 401;
Best Local Similarity 52.3%; Pred. No. 1.1e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRCRXKLCSPFXAFKIFRNXXRTROPWVS 44
DB 1 ANAFLEELRPGSLERCKEKGCSFEEREIFXDAERTKLFWISY 44

RESULT 11
ID AAR35764 standard; protein; 406 AA.

AC AAR35764;

DT 24-SEP-1993 (first entry)

DE Factor VII (VII).

XX PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;

XX Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;

XX exosite; catalytic activity.

XX OS Homo sapiens.


```

QY 1 ANGFLXXLRGSLXRXCRXXLCSFXXAFXIFRNXXRTROFWWSY 44
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 ANAFLLXXLRGSLXRXCKXXQCSFXXAFXIFKDAKRTKLFWISY 44

RESULT 4
ID AAY18310 standard; peptide; 44 AA.
XX
AC AAY18310;
XX
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KM therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
XX
XX WO9920767-A1.
XX
XX PD 29-APR-1999.
XX
XX PF 20-OCT-1998; 98WO-US22152.
XX
XX PR 23-OCT-1997; 97US-0955636.
XX
XX PA (MINU ) UNIV MINNESOTA.
XX
XX PI Nelsestuen GL;
XX
XX DR WPI; 1999-288309/24.
XX
XX PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX PS Disclosure; Page 80; 86pp; English.
XX
XX CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX SQ Sequence 44 AA;

Query Match 66.3%; Score 126; DB 20; Length 44;
Best Local Similarity 77.3%; Pred. No. 1.4e-13;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRXCRXXLCSFXXAFXIFRNXXRTROFWWSY 44
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 ANAFLLXXLRGSLXRXCKXXQCSFXXARXIFKDAKRTKLFWISY 44

RESULT 5
ID AAY18311 standard; peptide; 44 AA.
XX
AC AAY18311;
XX
DT 17-AUG-1999 (first entry)
XX

```

```

DE Modified GLA domain of vitamin K-dependent protein.
XX
XX KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..44
XX FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
XX acid"
XX
XX
XX WO9920767-A1.
XX
XX PD 29-APR-1999.
XX
XX PF 20-OCT-1998; 98WO-US22152.
XX
XX PR 23-OCT-1997; 97US-0955636.
XX
XX PA (MINU ) UNIV MINNESOTA.
XX
XX PI Nelsestuen GL;
XX
XX DR WPI; 1999-288309/24.
XX
XX PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX PS Disclosure; Page 80; 86pp; English.
XX
XX CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX SQ Sequence 44 AA;

Query Match 64.7%; Score 123; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 4.4e-13;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRXCRXXLCSFXXAFXIFRNXXRTROFWWSY 44
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 ANAFLLXXLRDGLXRXCKXXQCSFXXARXIFKDAKRTKLFWISY 44

RESULT 6
ID AAY18302 standard; peptide; 44 AA.
XX
XX AC AAY18302;
XX
XX DT 17-AUG-1999 (first entry)
XX
XX DE Modified GLA domain of vitamin K-dependent protein.
XX
XX KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..44
XX FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
XX acid"
XX

```

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure; Page 15; 86pp; English.
 XX
 CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 XX Sequence 44 AA;
 SO
 Query Match 81.6%; Score 155; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 2.1e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ANGFLXXLRPGSLRXCRXXLCSPFXAFXIFRNXXRTQFWVS 44
 DB 1 ANGFLXXLRPGSLRXCRXXLCSPFXAHXIFRNXXRTQFWVS 44
 RESULT 2
 AAB36396 standard; peptide; 44 AA.
 ID AAB36396
 AC AAB36396;
 XX
 DT 27-FEB-2001 (first entry)
 DE Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.
 XX
 XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KM factor X; prothrombin; enhanced membrane binding affinity;
 KM clot formation; thrombolytic; haemostatic; bleeding disorder;
 KM thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KM liver disease.
 XX
 OS Bos taurus.
 XX
 PN WO200066753-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US11416.
 XX
 PR 29-APR-1999; 99US-0302239.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Neisestuen GL;
 XX
 PS WPI; 2001-007226/01.
 DR
 XX Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprises modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity
 XX
 PS Disclosure; Page 12; 81pp; English.
 XX
 CC The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified
 CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type bovine factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.
 XX
 XX Sequence 44 AA;
 SO
 Query Match 81.6%; Score 155; DB 22; Length 44;
 Best Local Similarity 95.5%; Pred. No. 2.1e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ANGFLXXLRPGSLRXCRXXLCSPFXAFXIFRNXXRTQFWVS 44
 DB 1 ANGFLXXLRPGSLRXCRXXLCSPFXAHXIFRNXXRTQFWVS 44
 RESULT 3
 AAY18312 standard; peptide; 44 AA.
 ID AAY18312
 AC AAY18312;
 XX
 DT 17-AUG-1999 (first entry)
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KM therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 acid"
 FT
 PN WO9920767-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Neisestuen GL;
 XX
 PS WPI; 1999-288309/24.
 DR
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 PT
 XX
 PS Disclosure; Page 80; 86pp; English.
 XX
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 XX Sequence 44 AA;
 SO
 Query Match 67.9%; Score 129; DB 20; Length 44;
 Best Local Similarity 77.3%; Pred. No. 4.4e-14;
 Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds
(without alignments)
186.869 Million cell updates/sec

Title: 10GLU28PHE_4
Perfect score: 190
Sequence: 1 ANGFLXLRREGSLRXCRXX.....XXAFXIFRNXXRQFWWSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	81.6	44	20	AAV18306
2	155	81.6	44	22	AAV18306
3	129	67.9	44	20	AAV18312
4	126	66.3	44	20	AAV18310
5	123	64.7	44	20	AAV18311
6	121	63.7	44	20	AAV18302
7	120	63.2	44	20	AAV18305
8	120	63.2	44	22	AAV18305
9	120	63.2	401	22	AAV18305
10	120	63.2	401	22	AAV18305

11	120	63.2	406	14	AAV18306	Factor VII (VII).
12	120	63.2	406	18	AAV14509	Modified blood coa
13	120	63.2	406	18	AAV14510	Modified blood coa
14	120	63.2	406	22	AAV17745	Human factor VIIa
15	120	63.2	406	22	AAV52171	Human FVII SEQ ID
16	120	63.2	406	22	AAV52172	Mammalian expresse
17	120	63.2	406	22	AAV52181	Human FVII mutant
18	120	63.2	406	22	AAV52182	Human FVII mutant
19	120	63.2	406	22	AAV52183	Human FVII mutant
20	120	63.2	406	22	AAV52184	Human FVII mutant
21	120	63.2	406	22	AAV52185	Human FVII mutant
22	120	63.2	406	22	AAV52186	Human FVII mutant
23	120	63.2	406	22	AAV52187	Human FVII mutant
24	120	63.2	406	22	AAV52188	Human FVII mutant
25	120	63.2	406	22	AAV52189	Human FVII mutant
26	120	63.2	406	22	AAV52190	Human FVII mutant
27	120	63.2	406	22	AAV52191	Human FVII mutant
28	120	63.2	406	22	AAV52192	Human FVII mutant
29	120	63.2	406	22	AAV52193	Human FVII mutant
30	120	63.2	406	22	AAV52194	Human FVII mutant
31	120	63.2	406	22	AAV52195	Human FVII mutant
32	120	63.2	406	22	AAV52196	Human FVII mutant
33	120	63.2	406	22	AAV52197	Human FVII mutant
34	120	63.2	406	22	AAV52198	Human FVII mutant
35	120	63.2	406	22	AAV52199	Human FVII mutant
36	120	63.2	406	22	AAV52200	Human FVII mutant
37	120	63.2	406	22	AAV52201	Human FVII mutant
38	120	63.2	406	22	AAV52202	Human FVII mutant
39	120	63.2	406	22	AAV52203	Human FVII mutant
40	120	63.2	406	22	AAV52204	Human FVII mutant
41	120	63.2	406	22	AAV52205	Human FVII mutant
42	120	63.2	406	22	AAV52206	Human FVII mutant
43	120	63.2	406	22	AAV52207	Human FVII mutant
44	120	63.2	406	22	AAV52208	Human FVII mutant
45	120	63.2	406	22	AAV52209	Human FVII mutant

ALIGNMENTS

RESULT 1	AAV18306	standard, peptide, 44 AA.
ID	AAV18306	standard, peptide, 44 AA.
AC	AAV18306	standard, peptide, 44 AA.
XX	AAV18306	standard, peptide, 44 AA.
DT	17-ANG-1999	(first entry)
XX	17-ANG-1999	(first entry)
DE	Bovine factor VII GLA domain.	
XX	Bovine factor VII GLA domain.	
KW	GLA domain; vitamin K-dependent protein; clotting disorder;	
XX	therapy.	
OS	Bos taurus.	
XX	Bos taurus.	
FN	Key	Location/Qualifiers
FT	Misc-difference 1..44	
FT	note="Xaa= gamma-carboxyglutamic acid, or glutamic acid"	
XX	W0920767-A1.	
XX	PD	29-APR-1999.
XX	PD	29-APR-1999.
PF	20-OCT-1998;	98WO-US22152.
XX	20-OCT-1998;	98WO-US22152.
PR	23-OCT-1997;	97US-0955636.
XX	23-OCT-1997;	97US-0955636.
PA	(MINV) UNIV MINNESOTA.	
XX	(MINV) UNIV MINNESOTA.	
PI	Nelaeetuen GL;	
XX	Nelaeetuen GL;	
DR	WPI; 1999-288309/24.	


```

DR PROSITE; PS01187; EGF_CA. 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match: 49.2%; Score 93; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 1.1e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLLXRLREGSLRXRCRXLLCSFXXAEXIFRNXXTRQFWWSY 44
DB 41 ANSFEEFKGNLERECMEICSYEVRRIFFEDDEKTEKWTXY 84

RESULT 9
ID 088947 PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TRENBLREL. 08, Created)
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; Pubmed=9684791;
RA Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129Sj;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of the murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC36345.1; -.
DR EMBL; AF211347; XAF22980.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

```

```

DR PROSITE; PS01187; EGF_CA. 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5EF9D271E CRC64;

Query Match: 49.2%; Score 93; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 1.1e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLLXRLREGSLRXRCRXLLCSFXXAEXIFRNXXTRQFWWSY 44
DB 41 ANSFEEFKGNLERECMEICSYEVRRIFFEDDEKTEKWTXY 84

RESULT 10
ID 014316 PRELIMINARY; PRT; 456 AA.
AC 014316;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1999 (TRENBLREL. 11, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, Christmas
DE disease, HAEMOPHILIA B) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RT Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; Pubmed=3416069;
RA Reitema P.A., Bertina R.M., Ploos van Amstel J.K., Riemsma A.,
RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; 1CFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.

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DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 5149 MW; 54E20A1B3964E234 CRC64;

Query Match 47.6%; Score 90; DB 4; Length 456;
Best Local Similarity 39.5%; Pred. No. 3.9e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRGSLKRXKXCLCSFYXAXEIRNXXRTQFWVSY 44
DB 49 SGKLEEFVQGNLERECMEKCSFEAREVFENTERTEFWKQY 86

RESULT 11

ID Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OC NCBI_TaxID=9598;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Gene Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; JOINED.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; G1a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 47.6%; Score 90; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 3.9e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRGSLKRXKXCLCSFYXAXEIRNXXRTQFWVSY 44
DB 49 SGKLEEFVQGNLERECMEKCSFEAREVFENTERTEFWKQY 91

RESULT 12

ID Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OC NCBI_TaxID=9598;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Gene Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; JOINED.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; G1a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 47.6%; Score 90; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 3.9e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRGSLKRXKXCLCSFYXAXEIRNXXRTQFWVSY 44
DB 49 SGKLEEFVQGNLERECMEKCSFEAREVFENTERTEFWKQY 91

RESULT 13

ID Q9GMD9 PRELIMINARY; PRT; 469 AA.
AC Q9GMD9;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Coagulation factor X.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OC NCBI_TaxID=9258;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=21015017; PubMed=11132153;
RA Poorafshar M., Aveskog M., Munday B., Hellman L.;
RT "Identification and structural analysis of four serine proteases in a

RT monochrome, the platypus, Ornithorhynchus anatinus.";
 RL Immunogenetics 52:19-28(2000).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC EMBL: AF275654; AAC00453.1; -.
 DR HSSP: P00742; 1XKB.
 DR MEROPS: S01.216; -.
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF 2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser protease_Try.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; gla_1.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00179; EGF_Ca_1.
 DR SMART: SM00001; EGF_like_2.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; TRYP_Spc_1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_Ca_1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 469 AA; 52196 MW; 4C66C23D0D758F6A CRC64;

Query Match 47.1%; Score 89; DB 6; Length 469;
 Best Local Similarity 34.1%; Pred. No. 6.1e-08;
 Matches 15; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRGSLRXRCRXXLCSPFXAEXIFRNXXRTROFWVS 44
 Db 41 ANSLFEELKKGNLERECNETCSYEAREVFEDTKTNEFWNTY 84

RESULT 14
 Q9SME8 PRELIMINARY; PRT; 49 AA.
 AC Q9SME8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Coagulation factor IX (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxId=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Mizlata M.N., Amaral E.J.;
 RT "Partial sequence of bovine F9 coding gene."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF394598; AAK77556.1; -.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00594; gla_1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 49
 SQ SEQUENCE 49 AA; 6023 MW; DISC6DE9CCBA4A14 CRC64;

Query Match 46.6%; Score 88; DB 6; Length 49;
 Best Local Similarity 37.2%; Pred. No. 1e-08;

Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXXLRGSLRXRCRXXLCSPFXAEXIFRNXXRTROFWVS 44
 Db 6 SGKLEFVRGNLERECKEKCSFEAREVFENTKTEFWKQY 48

RESULT 15
 Q28994 PRELIMINARY; PRT; 138 AA.
 AC Q28994;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Mature porcine factor IX (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxId=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96003866; PubMed=7568220;
 RA Brandstetter H., Bauer M., Huber R., Lollar P., Bode W.;
 RT "X-ray structure of clotting factor IXa: active site and module
 structure related to Xase activity and hemophilia B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9796-9800(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Lollar P.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U51135; AAA96318.1; -.
 DR HSSP: P00740; 1EDM.
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR000561; EGF_like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00008; gla_1.
 DR Pfam: PF00594; gla_1.
 DR PRINTS: PR00010; EGFBLDOD.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_Ca_1.
 DR SMART: SM00069; GLA_1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_Ca_1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
 FT NON_TER 1
 FT NON_TER 138
 SQ SEQUENCE 138 AA; 15515 MW; 793BABDE4D5FAFAD CRC64;

Query Match 42.9%; Score 81; DB 6; Length 138;
 Best Local Similarity 41.2%; Pred. No. 5.7e-07;
 Matches 14; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 11 GSILRXCRXXLCSPFXAEXIFRNXXRTROFWVS 44
 Db 4 GNLERECIEKCSFEAREVFENTKTEFWKQY 37

Search completed: March 19, 2003, 15:13:36
 Job time : 46.3125 secs

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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10GLU28GLU_4
Perfect score: 189
Sequence: 1 ANGFLXLRGSLXRCXCRXX.....XXAEXIFRNXXRTQFWWSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfill1es1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	82.5	44	3	US-08-955-636-4
2	129	68.3	44	3	US-08-955-636-26
3	126	65.7	44	3	US-08-955-636-27
4	124	65.6	44	3	US-08-955-636-30
5	123	65.1	44	3	US-08-955-636-3
6	123	65.1	406	1	US-08-293-778-24
7	123	65.1	406	1	US-08-295-411-5
8	123	65.1	406	1	US-08-955-471-5
9	123	65.1	406	5	PCT-US92-10242-5
10	123	65.1	444	1	US-08-475-845-2
11	123	65.1	444	2	US-08-327-690-2
12	123	65.1	444	2	US-08-660-289-2
13	123	65.1	444	2	US-08-537-807-2
14	123	65.1	444	2	US-08-871-003-2
15	123	65.1	444	2	US-08-464-233-2
16	123	65.1	444	4	US-09-189-607-2
17	123	65.1	444	4	US-09-378-907-2
18	123	65.1	444	5	PCT-US94-05779-2
19	123	65.1	466	1	US-07-882-202A-4
20	123	65.1	466	1	US-08-021-615A-4
21	123	65.1	466	4	US-08-321-777-4
22	123	65.1	466	4	US-09-009-217-14
23	123	65.1	466	4	US-09-009-656-14
24	123	65.1	466	5	PCT-US93-04493-4
25	120	63.0	44	3	US-08-955-636-28
26	119	63.0	44	3	US-08-955-636-29
27	109	57.7	41	1	US-08-229-280-4

28	101	53.4	139	1	US-08-330-978-2	Sequence 2, Appl1
29	101	53.4	139	1	US-08-474-042-2	Sequence 2, Appl1
30	101	53.4	139	1	US-08-484-558-2	Sequence 2, Appl1
31	101	53.4	139	1	US-08-774-592-2	Sequence 2, Appl1
32	101	53.4	437	1	US-08-487-037-2	Sequence 2, Appl1
33	101	53.4	437	1	US-08-487-037-2	Sequence 2, Appl1
34	101	53.4	488	1	US-08-487-037-1	Sequence 1, Appl1
35	98	51.9	44	3	US-08-955-636-23	Sequence 1, Appl1
36	98	51.9	44	3	US-08-955-636-35	Sequence 35, Appl1
37	97	51.3	44	3	US-08-955-636-2	Sequence 2, Appl1
38	96	50.8	448	1	US-08-295-411-3	Sequence 3, Appl1
39	96	50.8	448	2	US-08-955-471-3	Sequence 1, Appl1
40	96	50.8	448	5	PCT-US92-10068-1	Sequence 3, Appl1
41	96	50.8	448	5	PCT-US92-10242-3	Sequence 3, Appl1
42	95	50.3	44	3	US-08-955-636-24	Sequence 24, Appl1
43	93	49.2	41	1	US-08-229-280-5	Sequence 5, Appl1
44	93	49.2	42	2	US-08-745-254A-2	Sequence 2, Appl1
45	93	49.2	44	3	US-08-955-636-1	Sequence 1, Appl1

ALIGNMENTS

```
RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      82.5%; Score 156; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 5,2e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ANGFLXLRGSLXRCXCRXXLSFXAEXIFRNXXRTQFWWSY 44
DB      1 ANGFLXLRGSLXRCXCRXXLSFXAAXHIFRNXXRTQFWWSY 44

RESULT 2
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agria, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24

Query Match
Best Local Similarity 65.1%; Score 123; DB 1; Length 406;
52.3%; Pred. No. 2.4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRGSLRXRCRXLCSPXXAEXIFRNXXRTROFWYSY 44
Db 1 ANAFLYLRPGSLRYCKYQCSFYARIFDKAVRTKLFWISY 44

RESULT 7
US-08-295-411-5
Sequence 5, Application US/08295411
Patent No. 5679639

GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSER: Office of Patent Counsel, The Scripps
ADDRESSER: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-295-411-5

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Best Local Similarity 65.1%; Score 123; DB 1; Length 406;
52.3%; Pred. No. 2.4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRGSLRXRCRXLCSPXXAEXIFRNXXRTROFWYSY 44
Db 1 ANAFLELRPGSLRERCKEBCQSFERRRIFDKARTKLFWISY 44

RESULT 8
US-08-955-471-5
Sequence 5, Application US/08955471
Patent No. 5968751

GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSER: Office of Patent Counsel, The Scripps
ADDRESSER: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152

OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 65.1%; Score 123; DB 2; Length 406;
Best Local Similarity 52.3%; Pred. No. 2.4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLXRCRXXLCSEFXAEXIFRNXXRTROPFWVS 44
DB 1 ANAFLELRPGSLRBECKEQCSFEERARLIFKDAERIKLFWIS 44

RESULT 9
PCT-US92-10242-5

Sequence 5, Application PC/RUS9210242

GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10242

FILING DATE: 19921118

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/793,989

FILING DATE: 18-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCRO472P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 406 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: Region

LOCATION: 1..152

OTHER INFORMATION: /note= "Factor VII Light Chain"

NAME/KEY: Region

LOCATION: 153..406

OTHER INFORMATION: /note= "Factor VII Heavy Chain"

PCT-US92-10242-5

Query Match 65.1%; Score 123; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 2.4e-13;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
QY 1 ANGFLLXLRGSLXRCRXXLCSEFXAEXIFRNXXRTROPFWVS 44
DB 1 ANAFLELRPGSLRBECKEQCSFEERARLIFKDAERIKLFWIS 44

RESULT 10
US-08-475-845-2

Sequence 2, Application US/08475845

Patent No. 578965

GENERAL INFORMATION:

APPLICANT: Berkner, Kathleen L.

APPLICANT: Petersen, Lars C.

APPLICANT: Hart, Charles E.

APPLICANT: Hedner, Ulla

APPLICANT: Bregengaard, Claus

TITLE OF INVENTION: Modified Factor VII

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: One Market Plaza, Stewart Street Tower

CITY: San Francisco

STATE: CA

COUNTRY: U.S.A.

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,845

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/327,690

FILING DATE: 24-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/065,725

FILING DATE: 21-MAY-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/662,920

FILING DATE: 28-FEB-1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 13952-8-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 444 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-475-845-2

Query Match 65.1%; Score 123; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLXRCRXXLCSEFXAEXIFRNXXRTROPFWVS 44

DB 39 ANAFLELRPGSLRBECKEQCSFEERARLIFKDAERIKLFWIS 82

RESULT 11
US-08-327-690-2


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; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-690-2

Query Match          65.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRXCRXXLCSPFXAEXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFPDARTKLFWISY 82

RESULT 12
US-08-660-289-2
; Sequence 2, Application US/08660289
; Patent No. 5833982
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower

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; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,289
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2

Query Match          65.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRXCRXXLCSPFXAEXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFPDARTKLFWISY 82

RESULT 13
US-08-537-807-2
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-537-807-2

Query Match      65.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY      1 ANGFLXXLRGSLRXRCRXXLCSPFXAEXIFRNXXRTROFWVS 44
DB      39 ANAFLELRPGSLRECKEBCGCFEAREIFKDAERTKLFWISY 82

RESULT 14
US-08-871-003-2
; Sequence 2, Application US/08871003
; Patent No. 5997864
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/871,003
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-871-003-2

Query Match      65.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
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QY      1 ANGFLXXLRGSLRXRCRXXLCSPFXAEXIFRNXXRTROFWVS 44
DB      39 ANAFLELRPGSLRECKEBCGCFEAREIFKDAERTKLFWISY 82

RESULT 15
US-08-464-233-2
; Sequence 2, Application US/08464233
; Patent No. 6039944
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,233
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-464-233-2

Query Match      65.1%; Score 123; DB 3; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY      1 ANGFLXXLRGSLRXRCRXXLCSPFXAEXIFRNXXRTROFWVS 44
DB      39 ANAFLELRPGSLRECKEBCGCFEAREIFKDAERTKLFWISY 82

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OM protein - protein search, using sw model

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280.876 Million cell updates/sec

Title: 10GLU28GLU_4
Perfect score: 189
Sequence: 1 ANGFLXLRPGSLKRXCRXX.....XXAEXIFRNXXRTQFWVS 44

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13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	95	50.3	419	9	US-10-182-263-6
3	93	49.2	419	9	US-10-182-263-1
4	93	49.2	419	9	US-10-182-263-3
5	93	49.2	419	9	US-10-182-263-4
6	93	49.2	419	9	US-10-182-263-5
7	93	49.2	419	9	US-09-978-917A-4
8	93	49.2	461	9	US-10-182-263-2
9	93	49.2	461	9	US-09-978-917A-2
10	90	47.6	415	10	US-09-118-748-2
11	90	47.6	461	9	US-10-132-829-5
12	90	47.6	461	9	US-09-884-901-3
13	70	37.0	96	9	US-09-759-130B-313
14	70	37.0	209	9	US-09-759-130B-312
15	70	37.0	226	9	US-09-759-130B-110
16	53	28.0	95	9	US-09-759-130B-356
17	53	28.0	208	9	US-09-759-130B-355
18	53	28.0	225	9	US-09-759-130B-353
19	43	22.8	484	10	US-09-801-368-334

20	42	22.2	233	10	US-09-867-550-1024	Sequence 1024, App
21	40.5	21.4	197	9	US-10-076-622-516	Sequence 516, App
22	40.5	21.4	197	12	US-10-007-605-516	Sequence 516, App
23	40.5	21.4	232	9	US-10-076-622-517	Sequence 517, App
24	40.5	21.4	232	12	US-10-007-605-517	Sequence 517, App
25	40.5	21.4	243	9	US-09-938-418-7	Sequence 7, Appl1
26	40.5	21.4	243	9	US-10-045-992-4	Sequence 4, Appl1
27	40.5	21.4	243	9	US-10-063-547-122	Sequence 122, App
28	40.5	21.4	243	9	US-10-174-590-366	Sequence 366, App
29	40.5	21.4	243	9	US-10-176-758-366	Sequence 366, App
30	40.5	21.4	243	9	US-10-063-616-122	Sequence 122, App
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39	40.5	21.4	243	9	US-10-176-913-366	Sequence 366, App
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42	40.5	21.4	243	9	US-10-173-700-366	Sequence 366, App
43	40.5	21.4	243	9	US-10-174-572-366	Sequence 366, App
44	40.5	21.4	243	9	US-10-174-579-366	Sequence 366, App
45	40.5	21.4	243	9	US-10-174-582-366	Sequence 366, App

ALIGNMENTS

RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286 200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1
Query Match 65.1%; Score 123; DB 9; Length 406;
Best Local Similarity 75.0%; Pred. No. 1.3e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 ANGFLXLRPGSLKRXCRXXLCFFXAXEIPFNXXRTQFWVS 44
DB 1 ANAFLLXLRPGSLKRXCRXXCQCFXAXRTIFDAXRTKLFWSY 44
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E

```

; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          50.3%; Score 95; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRXCRXXLCSPFXAEXIFRNXXRTROFW 41
DB 1 ANSFLELRHGSLERECIETICDFEAKEIFEDVDTLAFW 41

RESULT 3
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRXCRXXLCSPFXAEXIFRNXXRTROFW 41
DB 1 ANSFLELRHGSLERECIETICDFEAKEIFEDVDTLAFW 41

RESULT 4
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRXCRXXLCSPFXAEXIFRNXXRTROFW 41
DB 1 ANSFLELRHGSLERECIETICDFEAKEIFEDVDTLAFW 41

RESULT 5
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXRXCRXXLCSPFXAEXIFRNXXRTROFW 41
DB 1 ANSFLELRHGSLERECIETICDFEAKEIFEDVDTLAFW 41

RESULT 6
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
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ORGANISM: Homo sapiens
US-10-182-263-5

Query Match 49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRCXKXLCSPXXAEXIFRNXXRTROFW 41
Db 1 ANSFLELRHSSLRECIIEICDFEAKKEIFQVDDTLAFW 41

RESULT 7
US-09-978-917A-4
Sequence 4, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT APPLICATION NUMBER: US/09/978, 917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT

ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match 49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRCXKXLCSPXXAEXIFRNXXRTROFW 41
Db 1 ANSFLELRHSSLRECIIEICDFEAKKEIFQVDDTLAFW 41

RESULT 8
US-10-182-263-2
Sequence 2, Application US/10182263
Publication No. US20030022354A1

GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182, 263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 49.2%; Score 93; DB 9; Length 461;
Best Local Similarity 46.3%; Pred. No. 2.5e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRCXKXLCSPXXAEXIFRNXXRTROFW 41
Db 43 ANSFLELRHSSLRECIIEICDFEAKKEIFQVDDTLAFW 83

RESULT 9

US-09-978-917A-2
Sequence 2, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT APPLICATION NUMBER: US/09/978, 917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens

NAME/KEY: SIGNAL
LOCATION: (1)...(42)
FEATURE:
NAME/KEY: CHAIN
LOCATION: (43)...(461)

US-09-978-917A-2

Query Match 49.2%; Score 93; DB 9; Length 461;
Best Local Similarity 46.3%; Pred. No. 2.5e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRCXKXLCSPXXAEXIFRNXXRTROFW 41
Db 43 ANSFLELRHSSLRECIIEICDFEAKKEIFQVDDTLAFW 83

RESULT 10
US-09-118-748-2
Sequence 2, Application US/09118748A
Patent No. US20020031799A1

GENERAL INFORMATION:
APPLICANT: Stafford, Darrel W.
APPLICANT: Chang, Jinli
TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
TITLE OF INVENTION: Actively
FILE REFERENCE: 5470-183
CURRENT APPLICATION NUMBER: US/09/118, 748A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053, 571
EARLIER FILING DATE: 1997-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-09-118-748-2

Query Match 47.6%; Score 90; DB 10; Length 415;
Best Local Similarity 39.5%; Pred. No. 7.4e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXXLRGSLXRCXKXLCSPXXAEXIFRNXXRTROFW 44
Db 3 SGKLEEFVQGNLERCEMEKCSFEARAEVFENTERTEFWKQY 45

RESULT 11
US-10-132-829-5
Sequence 5, Application US/10132829
Publication No. US20030044982A1

GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
TITLE OF INVENTION: with vesicle vector
FILE REFERENCE: 6627-PAL170

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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          47.6%; Score 90; DB 9; Length 461;
Best Local Similarity 39.5%; Pred. No. 8.3e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy      2 NGFLXXLREGSLXRXCRXXLCSPFXAEXIFRNXXRTROFWVS 44
Db      49 SGKLEEFVQGNLERECMEKCSFEAREVFENTERTTEFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18/2002
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-901-3

Query Match          47.6%; Score 90; DB 10; Length 461;
Best Local Similarity 39.5%; Pred. No. 8.3e-08;
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy      2 NGFLXXLREGSLXRXCRXXLCSPFXAEXIFRNXXRTROFWVS 44
Db      49 SGKLEEFVQGNLERECMEKCSFEAREVFENTERTTEFWKQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarty, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtz, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match          37.0%; Score 70; DB 9; Length 96;
Best Local Similarity 38.2%; Pred. No. 5.3e-05;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy      11 GSIXRCRXLLCSFXAEXIFRNXXRTROFWVS 44
Db      46 GNLERECNELCNVEAREIFVDEDDXTIAFWQRY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarty, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtz, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2000-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313
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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-312

Query Match      37.0%; Score 70; DB 9; Length 209;
Best Local Similarity 38.2%; Pred. No. 0.00012;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY      11  GSLKRXCRXXLCSPXXAEXIFRXXXRTROPWVS 44
DB      46  GNLERECNEELCNVEEARREIFVDEKTIAPWQEX 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirel, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MP100-5350NM1M
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-759-130B-310

Query Match      37.0%; Score 70; DB 9; Length 226;
Best Local Similarity 38.2%; Pred. No. 0.00013;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY      11  GSLKRXCRXXLCSPXXAEXIFRXXXRTROPWVS 44
DB      63  GNLERECNEELCNVEEARREIFVDEKTIAPWQEX 96
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Mar 20 14:51:57 2003

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

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(without alignments)
186.869 Million cell updates/sec

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Perfect score: 191
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Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	159	82.7	44	20	AAV18310
3	158	82.7	44	20	AAV18302
4	157	82.2	44	20	AAV18311
5	156	81.7	44	20	AAV18305
6	156	81.7	44	22	AAV18395
7	156	81.7	401	22	AAV18470
8	156	81.7	401	22	AAV18471
9	156	81.7	406	14	AAV15764
10	156	81.7	406	18	AAV14509

11	156	81.7	406	18	AAV14510	Modified blood coa
12	156	81.7	406	22	AAU77745	Human factor VIIA
13	156	81.7	406	22	AAM52171	Human FVII SEQ ID
14	156	81.7	406	22	AAM52172	Mammalian expresse
15	156	81.7	406	22	AAM52181	Human FVII mutant
16	156	81.7	406	22	AAM52182	Human FVII mutant
17	156	81.7	406	22	AAM52183	Human FVII mutant
18	156	81.7	406	22	AAM52184	Human FVII mutant
19	156	81.7	406	22	AAM52185	Human FVII mutant
20	156	81.7	406	22	AAM52186	Human FVII mutant
21	156	81.7	406	22	AAM52187	Human FVII mutant
22	156	81.7	406	22	AAV18486	Wild-type human bl
23	156	81.7	406	22	AAV18487	Mutant blood coagu
24	156	81.7	406	22	AAV18488	Mutant blood coagu
25	156	81.7	406	22	AAV18489	Mutant blood coagu
26	156	81.7	406	23	AAV18490	Human coagulation
27	156	81.7	406	23	AAV18491	Human coagulation
28	156	81.7	406	23	AAV18492	Human coagulation
29	156	81.7	406	23	AAV18493	Human coagulation
30	156	81.7	406	23	AAV18494	Human coagulation
31	156	81.7	406	23	AAV18495	Human coagulation
32	156	81.7	406	23	AAV18496	Human coagulation
33	156	81.7	406	23	AAV18497	Human coagulation
34	156	81.7	406	23	AAV18498	Human coagulation
35	156	81.7	406	23	AAV18499	Human coagulation
36	156	81.7	406	23	AAV18500	Human coagulation
37	156	81.7	406	23	AAV18501	Human coagulation
38	156	81.7	406	23	AAV18502	Human coagulation
39	156	81.7	406	23	AAV18503	Human coagulation
40	156	81.7	406	23	AAV18504	Human coagulation
41	156	81.7	406	23	AAV18505	Human coagulation
42	156	81.7	406	23	AAV18506	Human coagulation
43	156	81.7	406	23	AAV18507	Human coagulation
44	156	81.7	406	23	AAV18508	Human coagulation
45	156	81.7	406	23	AAV18509	Human coagulation

ALIGNMENTS

RESULT 1		
AAV18312		
ID	AAV18312	standard; peptide; 44 AA.
XX		
AC	AAV18312;	
XX		
DT	17-AUG-1999	(first entry)
XX		
DE	Modified GIA domain of vitamin K-dependent protein.	
XX		
KW	GIA domain; muten; vitamin K-dependent protein; clotting disorder;	
XX	therapy.	
OS		
OS	Homo sapiens.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference	1..44
FT	FT	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX		
PN	WO9920767-A1.	
XX		
PD	29-APR-1999.	
XX		
PF	20-OCT-1998;	98WO-US22152.
XX		
PR	23-OCT-1997;	97US-0955636.
XX		
PA	(MINU) UNIV MINNESOTA.	
XX		
PI	Nelaeuten GL;	
XX		

DR WPI; 1999-288309/24.
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure; Page 80; 86bp; English.
 XX
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SO Sequence 44 AA;
 Query Match 86.4%; Score 165; DB 20; Length 44;
 Best Local Similarity 97.7%; Pred. No. 1.6e-20;
 Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRGSLRXKCKXQCSFXXAFIFKDAKRTKLFWISY 44
 DB 1 ANAFLLXLRGSLRXKCKXQCSFXXAFIFKDAKRTKLFWISY 44
 RESULT 2
 ID AAY18310 standard; peptide; 44 AA.
 AC AAY18310;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 FT
 XX
 PN WO9920767-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsestuen GL;
 XX
 DR WPI; 1999-288309/24.
 XX
 PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure; Page 80; 86bp; English.
 XX
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC disorder by decreasing or increasing clot formation. Modification of the

CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SO Sequence 44 AA;
 Query Match 83.2%; Score 159; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 1.7e-19;
 Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRGSLRXKCKXQCSFXXAFIFKDAKRTKLFWISY 44
 DB 1 ANAFLLXLRGSLRXKCKXQCSFXXAFIFKDAKRTKLFWISY 44
 RESULT 3
 ID AAY18302 standard; peptide; 44 AA.
 AC AAY18302;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 FT
 XX
 PN WO9920767-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsestuen GL;
 XX
 DR WPI; 1999-288309/24.
 XX
 PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Claim 11; Page 81; 86bp; English.
 XX
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SO Sequence 44 AA;
 Query Match 82.7%; Score 158; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 2.5e-19;
 Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRGSLRXKCKXQCSFXXAFIFKDAKRTKLFWISY 44
 DB 1 ANAFLLXLRGSLRXKCKXQCSFXXAFIFKDAKRTKLFWISY 44

```

RESULT 4
AA18311
ID AA18311 standard; peptide; 44 AA.
AC AA18311;
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KM therapy.
XX
OS Homo sapiens.
XX
PI Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
acid"
XX
XX MO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
PI Nelsstuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 80; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;
XX
Query Match 82.2%; Score 157; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 3.6e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Oy 1 ANAFLXLRPGSLXRXCKXQCSFXAXFIFKDAKRTKLFWISY 44
Db 1 ANAFLXLRPGSLXRXCKXQCSFXAXFIFKDAKRTKLFWISY 44
XX
RESULT 5
AA18305
ID AA18305 standard; peptide; 44 AA.
XX
XX AA18305;
XX
XX 17-AUG-1999 (first entry)
XX
XX Human factor VII GLA domain.
XX
XX GLA domain; vitamin K-dependent protein; clotting disorder;
XX therapy.

```

```

XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 1..44
XX /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
XX acid"
XX
XX MO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsstuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 15; 86pp; English.
XX
XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;
XX
Query Match 81.7%; Score 156; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 5.4e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Oy 1 ANAFLXLRPGSLXRXCKXQCSFXAXFIFKDAKRTKLFWISY 44
Db 1 ANAFLXLRPGSLXRXCKXQCSFXAXFIFKDAKRTKLFWISY 44
XX
RESULT 6
AAB36395
ID AAB36395 standard; peptide; 44 AA.
XX
XX AAB36395;
XX
XX 27-FEB-2001 (first entry)
XX
XX Human factor VII gamma-carboxyglutamic acid domain SPQ ID NO:3.
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
XX factor X; prothrombin; enhanced membrane binding affinity;
XX clot formation; thrombolytic; haemostatic; bleeding disorder;
XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX liver disease.
XX
XX Homo sapiens.
XX
XX MO20006753-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11416.
XX
XX 29-APR-1999; 99US-0302239.

```

XX (MINU) UNIV MINNESOTA.
 PA
 XX
 PI Neisetsuen GL;
 XX
 XX WPI; 2001-007226/01.
 XX
 XX Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprises modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity -
 XX
 XX Disclosure; Page 12; 81pp; English.
 PS
 XX
 XX The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot
 CC formation in a mammal, a factor VII or factor IX containing a modified
 CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type human factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.
 CC
 XX
 XX Sequence 44 AA;

Query Match 81.7%; Score 156; DB 22; Length 44;
 Best Local Similarity 95.5%; Pred. No. 5.4e-19;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQSGSLRXCKXCCSFXXAFKIFPDARTKLFWISY 44
 Db 1 ANAFLLXLRPGSLRXCKXCCSFXXARXIFPDARTKLFWISY 44

RESULT 7
 AAB84870
 ID AAB84870 standard; Protein; 401 AA.
 AC AAB84870;
 XX
 XX 31-JUL-2001 (first entry)
 DT
 XX
 DE Mutant blood coagulant factor VII (FVII-31).
 DE
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutcin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX

Key Location/Qualifiers
 FH Misc-difference 311..317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
 FT
 XX

JP2001061479-A.

13-MAR-2001.

24-AUG-1999; 99JP-0237610.

24-AUG-1999; 99JP-0237610.

(KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

WPI; 2001-310677/33.

N-PSDB; AAH19463.

XX

PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 XX
 XX
 PS Claim 14; Page 20-21; 29pp; Japanese.
 XX

CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.
 XX

Sequence 401 AA;

Query Match 81.7%; Score 156; DB 22; Length 401;
 Best Local Similarity 72.7%; Pred. No. 5.1e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQSGSLRXCKXCCSFXXAFKIFPDARTKLFWISY 44
 Db 1 ANAFLELRPGSLRCKEBCQSFEDARIFPDARTKLFWISY 44

RESULT 8
 AAB84871
 ID AAB84871 standard; Protein; 401 AA.
 AC AAB84871;
 XX
 XX 31-JUL-2001 (first entry)
 DT
 XX
 DE Mutant blood coagulant factor VII (FVII-39).
 DE
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutcin.
 XX

OS Homo sapiens.
 OS Synthetic.
 OS
 XX

Key Location/Qualifiers
 FH Misc-difference 235..239
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
 FT Asp-Arg-Lys-Thr-Leu"
 FT
 FT Misc-difference 311..317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
 FT
 XX

JP2001061479-A.

13-MAR-2001.

24-AUG-1999; 99JP-0237610.

24-AUG-1999; 99JP-0237610.

(KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

WPI; 2001-310677/33.

N-PSDB; AAH19464.

PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 XX

Claim 16; Page 23-24; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.
 XX

Sequence 401 AA;

Query Match 81.7%; Score 156; DB 22; Length 401;
 Best Local Similarity 72.7%; Pred. No. 5.1e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

FT	Disulfide-bond	91..102	
FT	Disulfide-bond	98..112	
FT	Disulfide-bond	114..127	
FT	Disulfide-bond	135..162	
FT	Cleavage-site	143..144	/note= "proteolytic site"
FT	Modified-site	145	/note= "glycosylation site"
FT	Disulfide-bond	159..164	
FT	Disulfide-bond	178..194	
FT	Active-site	193	
FT	Active-site	242	
FT	Active-site	344	
FT	Cleavage-site	290..291	/note= "proteolytic site in unmodified factor VII"
FT	Misc-difference	290	/note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"
FT	Disulfide-bond	310..329	
FT	Cleavage-site	315..316	/note= "proteolytic site"
FT	Modified-site	322	/note= "glycosylation site"
FT	Disulfide-bond	340..368	
FT	Cleavage-site	341..342	/note= "proteolytic site"
FT	Cleavage-site	392..393	/note= "proteolytic site"
FT	Cleavage-site	396..397	/note= "proteolytic site"
FT	Cleavage-site	402..403	/note= "proteolytic site"
XX	US5580560-A.		
XX	03-DEC-1996.		
XX	13-NOV-1989;	89US-0434149.	
XX	09-AUG-1993;	93US-0104509.	
PR	13-NOV-1989;	89US-0434149.	
PR	12-JUN-1992;	92US-0898248.	
PR	22-AUG-1994;	94US-0293778.	
XX	(NOVO) NOVO-NORDISK AS.		
XX	Bjorn SE, Nicolaissen EM, Wiberg FC, Woodbury R;		
XX	WPI; 1997-033523/03.		
DR	Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability		
XX	Example 3; Page -; 28pp; English.		
XX	Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an amino acid that provides a proteolytically more stable peptide bond, provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser. The modified proteins are useful for treating bleeding disorders such as thrombocytopenia and von Willebrand's disease. They are also suitable for addition to plasma substitutes. The present sequence is a specific example of a modified factor VII protein.		
CC	Sequence	406 AA;	

[illegible]

```
FT Modified-site 145 /note= "glycosylation site"
FT FT Disulfide-bond 159..164
FT Disulfide-bond 178..194
FT Active-site 193
FT Active-site 242
FT Active-site 344
FT Cleavage-site 290..291
FT Cleavage-site /note= "proteolytic site"
FT Disulfide-bond 310..329
FT Cleavage-site 315..316
FT FT Misc-difference 315 /note= "proteolytic site in unmodified factor VII"
FT /note= "native Arg115 has been substituted by Ser to
FT provide a proteolytically more stable peptide
FT bond"
FT Modified-site 322 /note= "glycosylation site"
FT FT Disulfide-bond 340..368
FT Cleavage-site 341..342
FT /note= "proteolytic site"
FT Cleavage-site 392..393 /note= "proteolytic site"
FT Cleavage-site /note= "proteolytic site"
FT Cleavage-site 396..397 /note= "proteolytic site"
FT Cleavage-site /note= "proteolytic site"
FT Cleavage-site 402..403 /note= "proteolytic site"
FT FT
FT XX US5580560-A.
FT PN 03-DEC-1996.
FT PD 13-NOV-1989; 89US-0434149.
FT XX
FT PE 09-AUG-1993; 93US-0104509.
FT PR 13-NOV-1989; 89US-0434149.
FT PR 12-JUN-1992; 92US-0898248.
FT PR 22-AUG-1994; 94US-0293778.
FT XX
FT PA (NOVO ) NOVO-NORDISK AS.
FT XX
FT XX Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
FT XX WPI; 1997-033523/03.
FT DR
FT XX Mutated human factor VII or VIIa proteins - with amino acid
FT substitutions to improve proteolytic stability
FT XX
FT PS Example 4; Page -: 28pp; English.
FT XX
CC Modified human factor VII or VIIa proteins are stabilised against
CC proteolytic cleavage by substitution of one of the residues Lys32,
CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
CC Lys341 by an amino acid that provides a proteolytically more stable
CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
CC bleeding disorders such as thrombocytopenia and von Willebrand's
CC disease. They are also suitable for addition to plasma substitutes.
CC The present sequence is a specific example of a modified factor VII
CC protein.
CC XX
SQ Sequence 406 AA;
Query Match 81.7%; Score 156; DB 18; Length 406;
Best Local Similarity 72.7%; Pred. No. 5.1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
AAU77745
ID AAU77745 standard; protein; 406 AA.
XX
XX AC AAU77745;
XX
XX 05-JUN-2002 (first entry)
XX
XX Human factor VIIa active site mutant.
XX
XX Factor VIIa; human; shock heat treatment; protein stability;
XX protein manufacture; protein conformation; mutant; mutein.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Active-site 193 /note= "Member of the factor VIIa catalytic triad"
XX Active-site 242 /note= "Member of the factor VIIa catalytic triad"
XX Active-site 344 /note= "Member of the factor VIIa catalytic triad"
XX Active-site 344 /note= "Member of the factor VIIa catalytic triad"
XX Misc-difference 344 /label= Gly, Met, Thr
XX /note= "Preferably Ala. wild type Ser"
XX
XX W0200177141-A1.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-DK00234.
XX
XX 06-APR-2000; 2000DK-0000573.
XX 17-APR-2000; 2000US-197650P.
XX
XX (NOVO ) NOVO NORDISK AS.
XX
XX Mathiesen F;
XX WPI; 2001-657162/75.
XX
XX Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX involves a shock heat treatment -
XX
XX Disclosure; Page -: 22pp; English.
XX
XX The invention describes a method of stabilising a polypeptide involving
XX shock heat treatment of the polypeptide. The method is useful in a
XX pharmaceutical composition, in the industrial or large scale method of
XX manufacturing a polypeptide, also as a unit operation during preparation,
XX purification, recovery and/or formulation of polypeptides. The shock heat
XX treatment improves the protein stability without substantial loss of
XX biological activity. The method can be applied to change polypeptide
XX conformation in a very fast and non-invasive manner. The polypeptide
XX formed is stable. The method is also useful for decreasing the
XX association of the polypeptide. This sequence represents a modified
XX human factor VIIa protein, mutated at the catalytic site, described
XX in the invention.
XX Note: This sequence does not appear in the specification but has
XX been obtained using information given in the invention.
XX
SQ Sequence 406 AA;
Query Match 81.7%; Score 156; DB 22; Length 406;
Best Local Similarity 72.7%; Pred. No. 5.1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

RESULT 12

RESULT 13


```

PR 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
PI Andersen KV, Pedersen AH, Bornaes C;
XX WPI; 2001-581807/65.
DR N-PSDB; AA199983.
XX
PT New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX
PS Disclosure; Page 85-86; 89pp; English.
XX
CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections.
CC
XX
SQ Sequence 406 AA;
XX
XX
Query Match 81.7%; Score 156; DB 22; Length 406;
Best Local Similarity 72.7%; Pred. No. 5.1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Cy 1 ANAFPLXLRGSLRXCKXKXOCSEFXAFIFMDARTKLFWISY 44
Db 1 ANAFLEELRPSGLRECKECCFEAREIFDARTKLFWISY 44
RESULT 15
AAM52181
ID AAM52181 standard; Procein; 406 AA.
XX
XX AAM52181;
AC
XX
XX 07-FEB-2002 (first entry)
DT
XX
XX Human FVII mutant T106N.
DB
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KW mutuin.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
FH Key Location/Qualifiers
FT FT Misc-difference 6 /label= Glu, OTHER
FT FT Misc-difference 7 /note= "OTHER = gamma carboxylutamic acid"
FT FT Misc-difference 7 /label= Glu, OTHER
FT FT Misc-difference 14 /note= "OTHER = gamma carboxylutamic acid"
FT FT Misc-difference 14 /label= Glu, OTHER
FT FT Misc-difference 16 /note= "OTHER = gamma carboxylutamic acid"
FT FT Misc-difference 16 /label= Glu, OTHER

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FT FT /note= "OTHER = gamma carboxylutamic acid"
FT FT 19 /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxylutamic acid"
FT FT 20 /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxylutamic acid"
FT FT 25 /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxylutamic acid"
FT FT 26 /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxylutamic acid"
FT FT 29 /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxylutamic acid"
FT FT 35 /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxylutamic acid"
FT FT 52 /note= "OTHER = gamma carboxylutamic acid"
FT FT 60 /note= "O-glycosylated"
FT FT /note= "O-glycosylated"
FT FT 106 /note= "O-glycosylated"
FT FT /note= "O-glycosylated"
FT FT 145 /note= "wild-type Thr substituted by Asn"
FT FT /note= "N-glycosylated"
FT FT 152.153 /note= "proteolytic cleavage site converting FVII zymogen
FT FT to an activated form, comprising two chains
FT FT linked by a single disulphide bridge"
FT FT 322 /note= "N-glycosylated"
FT FT
XX
XX Modified-site 322 /note= "N-glycosylated"
XX
XX W0200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-DK0094.
XX
XX 11-FEB-2000; 2000DK-0000218.
XX
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
PI Andersen KV, Pedersen AH, Bornaes C;
XX
XX WPI; 2001-581807/65.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently
XX attached to polypeptide group -
XX
XX Example 3; Page -; 89pp; English.
XX
CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a human FVII mutant,
CC having an addition in vivo glycosylation site and tested for its
CC amidolytic activity.

```

CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC (AAM52171).

XX
SQ Sequence 406 AA;

Query Match 81.7%; Score 156; DB 22; Length 406;
Best Local Similarity 95.5%; Pred. No. 5.1e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANAFLLXLRQGSIXRXCXXQCSFXXAFXIFKDXRRKLFWISY 44
|||
DB 1 ANAFLLXLRQGSIXRXCXXQCSFXXAFXIFKDXRRKLFWISY 44

Search completed: March 19, 2003, 14:51:09
Job time : 31.4375 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10GLN28PHE
Perfect score: 191
Sequence: 1 ANAFLLXRLRGSLXRCCKX.....XXAFXIFKDXRTLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.73:*
2: pir1:*
3: pir2:*
4: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	466	1 KFHU7	coagulation factor
2	122	63.9	443	2 I46932	coagulation factor
3	114	59.7	407	1 KFB07	coagulation factor
4	99	51.8	492	1 EXBO	coagulation factor
5	97	50.8	461	1 UX0210	protein C (activat
6	96	50.3	461	1 S18994	protein C (activat
7	96	50.3	461	1 EXHU	coagulation factor
8	94	49.2	622	1 TBUH	thrombin (EC 3.4.2
9	90	47.1	482	1 EXRT	coagulation factor
10	90	47.1	617	2 S10511	thrombin (EC 3.4.2
11	90	46.6	475	2 A35827	thrombin (EC 3.4.2
12	89	46.6	475	1 EXCH	coagulation factor
13	88	46.1	456	1 KXBO	protein C (activat
14	81	42.4	461	1 KXHU	protein C (activat
15	80	41.9	461	1 KFB0	coagulation factor
16	79	41.4	416	1 KFB0	coagulation factor
17	74	38.7	625	1 TBBO	thrombin (EC 3.4.2
18	71	37.2	452	1 A30351	coagulation factor
19	71	37.2	459	2 U00419	coagulation factor
20	67	35.1	642	2 S53433	plasma protein S p
21	62	32.5	642	2 S53434	plasma protein S p
22	62	32.5	676	1 KXHUS	plasma protein S p
23	60	31.4	675	1 KXBOS	plasma protein S p
24	58	30.4	396	1 KXBOS	plasma protein S p
25	58	30.4	646	2 S38819	plasma protein S -
26	57	29.8	676	1 KXRTS	plasma protein S p
27	55.5	29.1	575	2 G96763	probable MAP kinase
28	53	27.7	422	1 KXHUZ	plasma protein 2 p
29	53	27.7	673	2 A48089	growth arrest-spec

30	51	26.7	674	2 I55476	growth potentiating
31	51	26.7	678	2 B48089	growth arrest-spec
32	50	26.2	675	1 KXMS	plasma protein S p
33	49.5	25.9	594	2 D84859	probable MAP kinase
34	49.5	25.9	603	2 C96575	probable MAP kinase
35	47.5	24.9	271	2 S66591	probable membrane
36	45.5	23.8	83	2 T17839	hypothetical prote
37	45	23.6	52	2 T19574	hypothetical prote
38	45	23.6	879	2 S55864	hypothetical prote
39	45	23.6	907	2 T15792	hypothetical prote
40	44	23.0	306	2 I49068	protein kinase STY
41	43	22.5	394	1 S30286	tetracycline resist
42	43	22.5	440	2 C70198	conserved hypothe
43	42	22.0	486	2 T06770	cellulase (EC 3.2.
44	42	22.0	1559	2 T07757	probable DNA (cyto
45	41.5	21.7	161	2 F82637	conserved hypothe

ALIGNMENTS

RESULT 1

KFHU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000

C:Accession: A28322; A28819; A31186; B31186; S63524

R:O'Hara, P.J.; Grant, F.J.; Halldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murte

Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987

A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend

A:Reference number: A28322; MUID:87260948; PMID:3037537

A:Accession: A28322

A:Molecule type: DNA

A:Residues: 1-466 <OHA>

A:Cross-references: GB:U02933; NID:G180333; PIDN:AAA51983.1; PID:G180334

R:Hagen, F.S.; Gray, C.L.; O'Hara, P.J.; Grant, F.J.; Saarl, G.C.; Woodbury, R.G.; Hart, C

Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986

A:Title: Characterization of a cDNA coding for human factor VII.

A:Reference number: A28819; MUID:86205965; PMID:3486420

A:Accession: A28819

A:Molecule type: mRNA

A:Residues: 1-466 <HAG>

A:Cross-references: GB:M13232; NID:G182729; PIDN:AAA8040.1; PID:G182801

R:Thim, L.; Bioern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.

Biochemistry 27, 7785-7793, 1988

A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a fr

A:Reference number: A90539; MUID:89088153; PMID:3264725

A:Accession: A31186

A:Molecule type: protein

A:Residues: 61-212 <THI>

A:Accession: B31186

A:Molecule type: protein

A:Residues: 213-466 <TH2>

R:Bioern, S.; Foster, D.C.; Thim, L.; Wlberg, F.C.; Christensen, M.; Komiyama, Y.; Peders

J. Biol. Chem. 266, 11051-11057, 1991

A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at

A:Reference number: A40529; MUID:91250411; PMID:1904059

A:Contents: annotation; carbohydrate binding sites

R:Persson, E.; Petersen, L.C.

Eur. J. Biochem. 234, 293-300, 1995

A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy

A:Reference number: S63524; MUID:96096752; PMID:8529655

A:Accession: S63524

A:Molecule type: protein

A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>

C:Genetics:

A:Gene: GDB:F7

A:Cross-references: GDB:119897; OMIM:227500

A:Map position: 13q34-13q34

A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1

C:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen

coagulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-20/Domain: signal sequence #status predicted <PRO>
 F:21-60/Domain: propeptide #status predicted <PRO>
 F:61-104/Domain: Gla domain homology <Gla>
 F:161-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
 F:110-141/Domain: EGF homology <EG1>
 F:151-187/Domain: EGF homology <EG2>
 F:213-447/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F:213-447/Domain: trypsin homology <TRY>
 F:66-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxylglutamic acid (Glu) #status
 F:77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
 F:112/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
 F:205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:213-213/Cleavage site: Arg-1le (coagulation factor X1a) #status experimental
 F:253,302,404/Active site: His, Asp, Ser #status predicted
 F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 81.7%; Score 156; DB 1; Length 466;
 Best Local Similarity 72.7%; Pred. No. 7, 6e-19;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLLXLRQSLRXCKKXQCSFXXAFKFDAXRTKLFMISY 44
 DB 61 ANAFLEELRPGSLRECKECCQCFEBAKRFKDAKTKLFMISY 104

RESULT 2
 146932
 coagulation factor VII - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
 C:Accession: 146932
 R:Brothers, A.B.; Clarke, B.D.; Sheffield, W.P.; Blajchman, M.A.
 Thromb. Res. 69, 231-238, 1993
 A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
 A:Reference number: 146932; MUID:93190306; PMID:8383365
 A:Accession: 146932
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-443 <BRO>
 A:Cross-references: GB:S56300; NID:9266294; PID:9266295
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 F:24-83/Domain: Gla domain homology <Gla>
 F:89-120/Domain: EGF homology <EG1>
 F:130-166/Domain: EGF homology <EG2>
 F:192-425/Domain: trypsin homology <TRY>

Query Match 63.9%; Score 122; DB 2; Length 443;
 Best Local Similarity 54.5%; Pred. No. 5, 2e-13;
 Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANAFLLXLRQSLRXCKKXQCSFXXAFKFDAXRTKLFMISY 44
 DB 40 ANAFLEELRPGSLRECKECCQCFEBAKRFKDAKTKLFMISY 83

RESULT 3
 KFB07
 coagulation factor VIIa (BC 3.4.21.21) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
 C:Accession: A31979; C20274
 R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamachi, Y.; Miyata, T.; Iwanaga, S.
 J. Biol. Chem. 263, 14868-14877, 1988
 A:Title: Bovine factor VII. Its purification and complete amino acid sequence.
 A:Reference number: A31979; MUID:89008362; PMID:3049594
 A:Accession: A31979
 A:Molecule type: protein
 A:Residues: 1-407 <TAK>
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; MUID:83308813; PMID:6688526
 A:Accession: C20274
 A:Molecule type: protein
 A:Residues: 58-62, 'X', 64-68 <MCN>
 A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid
 A:Hoce, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.
 J. Biochem. 104, 867-868, 1988
 A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
 A:Reference number: A44556; MUID:89213999; PMID:3149637
 A:Contents: annotation
 A:Note: structure and location of covalently bound carbohydrate
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen
 gulation factor IX in the presence of calcium and tissue factor
 A:Pathway: blood coagulation extrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>
 F:1-44/Domain: Gla domain homology (fragment) <Gla>
 F:50-81/Domain: EGF homology <EG1>
 F:91-127/Domain: EGF homology <EG2>
 F:153-387/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F:153-407/Product: coagulation factor <TRY>
 F:67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxylglutamic acid (Glu) #status
 F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/
 F:52/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
 F:145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:152-153/Cleavage site: Arg-1le (coagulation factor X1a) #status experimental
 F:193,242,344/Active site: His, Asp, Ser #status predicted
 F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 59.7%; Score 114; DB 1; Length 407;
 Best Local Similarity 50.0%; Pred. No. 1, 1e-11;
 Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANAFLLXLRQSLRXCKKXQCSFXXAFKFDAXRTKLFMISY 44
 DB 1 ANAFLEELRPGSLRECKECCQCFEBAKRFKDAKTKLFMISY 44

RESULT 4
 EXB0
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine
 N:Alternate names: Stuart factor
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
 C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
 R:Pung, M.R.; Campbell, R.M.; MacGillivray, T.A.
 Nucleic Acids Res. 12, 4481-4492, 1984
 A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
 A:Reference number: A22867; MUID:84247315; PMID:6330671
 A:Accession: A22867
 A:Molecule type: mRNA
 A:Residues: 1-487 <FNU>
 A:Cross-references: GB:X00673; NID:9192; PID:CAA25286.1; PID:9193
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Tlani, K.
 Biochemistry 19, 659-667, 1980
 A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A:Reference number: A14997; MUID:80130563; PMID:6766735
 A:Accession: A14997
 A:Molecule type: protein
 A:Residues: 41-102, 'N', 104-180 <ENF>
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; MUID:83308813; PMID:6688526
 A:Contents: annotation; revision to residue 103
 R:Tlani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.

A:Reference number: A12030; MUID:76053069; PMID:105093

A:Molecule type: protein

A:Residues: 183-232,294-295,'GDE',299-334,336-348,'AE',351-354,356-441,'GKGF',446-492 <T>

A:Note: carboxylate binding sites and disulfide bonds were determined

R:Person, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlén, A.K.; Stenflo, J.

J: Biol. Chem. 264, 16897-16904, 1989

A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal

A:Reference number: A14412; MUID:89380326; PMID:2789221

A:Accession: A34412

A:Molecule type: protein

A:Residues: 85-126 <PBR>

A:Note: beta-hydroxyaspartic acid site

R:Imoue, K.; Morita, T.

Eur. J. Biochem. 218, 153-163, 1993

A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of

A:Reference number: S39414; MUID:94062825; PMID:8243461

A:Accession: S39414

A:Molecule type: protein

A:Residues: 183-196,199-209,216-233 <INO>

A:Note: carboxylate binding sites

R:Tiliani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neutra, H.; D

Biochemistry 11, 4899-4903, 1972

A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammalian

A:Reference number: A12453; MUID:73053314; PMID:4264286

A:Contents: annotation; active site

R:Fujikawa, K.; Tilani, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975

A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to

A:Reference number: A13504; MUID:76053121; PMID:1059122

A:Contents: annotation; activation

R:Snogo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.

J. Biol. Chem. 259, 5705-5710, 1984

A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamidic

A:Reference number: A38024; MUID:84185716; PMID:6546930

A:Contents: annotation; calcium binding

R:Morita, T.; Jackson, C.M.

J. Biol. Chem. 261, 4008-4014, 1986

A:Reference number: A38025; MUID:86140210; PMID:3949800

A:Contents: annotation; sulfate binding

C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.

C:Comment: The two chains are formed from a single-chain precursor by the excision of tw

C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c

activation.

C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro

C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C:Genetics:

A:Gene: F10

A:Map position: 13q34

C:Function:

A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the p

A:Pathway: blood coagulation

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutac

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-40/Domain: propeptide #status predicted <PPO>

F:25-84/Domain: Gla domain homology <Gla>

F:41-180/Product: coagulation factor X light chain #status experimental <LCH>

F:90-121/Domain: BGF homology <BGI>

F:123-164/Domain: EGF homology <EG2>

F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>

F:183-233/Domain: activation peptide #status experimental <APr>

F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>

F:234-461/Domain: trypsin homology <TRY>

F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #

F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:200/Binding site: sulfite (Tyr) (covalent) (partial) #status experimental

F:208,465/Binding site: carboxylate (Thr) (covalent) #status experimental

F:218/Binding site: carboxylate (Asn) (covalent) #status experimental

F:223-234/Cleavage site: Arg-Tile (coagulation factor IXa, coagulation factor VIIa) #stat

F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental

F:275,331,418/Active site: His, Asp, Ser #status predicted

```

Query Match          51.8%; Score 99; DB 1; Length 492;
Best Local Similarity 43.2%; Pred No.5.2e-09;
Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

Qy      1 ANAFLLXLRQGSLRXRCXXKCSFXXAFAFIKDXARTKLFWISY 44
        ||::|||::|||::|||::|||::|||::|||::|||::|||
Db       41 ANSFLEEVVQGNLERECLEBACGLEEARFEVFEDAEQDFDEWSKY 84

RESULT 5
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N.Alternate names: vitamin K-dependent serine proteinase
C.Species: Mus musculus (house mouse)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 16-Jun-2000
Accession: JX0210
R.Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A.Title: Isolation and characterization of a mouse protein C cDNA.
A.Reference number: JX0210; MUID:92316897; PMID:1618739
A.Accession: JX0210
A.Molecule type: mRNA
A.Residues: 1-461 <TA>
A.Cross-references: GB:D10445; NID:g220385; PIDN:BAA01235.1; PID:g220386
C.Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg

B.
C.Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C.Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutami
F.1-33/Domain: signal sequence #status predicted <SIG>
F.27-85/Domain: Gla domain homology <Gla>
F.34-41/Domain: propeptide #status predicted <PRO>
F.42-196/199-461/Product: protein C #status predicted <PC>
F.42-196/Domain: light chain #status predicted <PCL>
F.91-130/Domain: EGF homology <EG1>
F.139-174/Domain: EGF homology <EG2>
F.199-461/Domain: heavy chain #status predicted <PCH>
F.199-211/Domain: activation peptide #status predicted <ACT>
F.212-461/Product: vitamin K-dependent serine proteinase #status predicted <VT>
F.212-445/Domain: trypsin homology <TRY>
F.47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxylglutamic acid (Glu) #status i
F.112/Modified site: eythro-beta-hydroxyaspartic acid (Asp) #status predicted
F.121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Isoulfide bonds: #statu
F.214,299,355/Binding site: carbohydrate (asn) (covalent) #status predicted
F.253,299,402/Active site: His, Asp, Ser #status predicted

Query Match          50.8%; Score 97; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No.1.1e-08;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy      1 ANAFLLXLRQGSILRXRCXXKCSFXXAFAFIKDXARTKLFWISY 44
        ||::|||::|||::|||::|||::|||::|||::|||::|||
Db       42 ANSFLEEMRPGLSRLRECEMEICDPEBAQEIFQNVEDTLAWIKY 85

RESULT 6
S18994
protein C (activated) (EC 3.4.21.69) precursor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 29-Oct-1999
Accession: S18994; S24312
R.Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A.Description: The cDNA cloning and mRNA expression of rat protein C.
A.Reference number: S18994
A.Accession: S18994
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-461 <OK>
A.Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
R.Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
```

A>Title: The cDNA cloning and mRNA expression of rat protein C.
A:Reference number: S24312; MUID:92329550; PMID:1627650
A:Accession: S24312
A:Molecule type: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <OKR2>
A:Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA5617.1; PID:g56963
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydroxylase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <GLA>
F:33-42/Domain: propeptide #status predicted <PRO>
F:43-461/Product: protein C #status predicted <PRC>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:213-445/Domain: trypsin homology <TRY>
F:477-48-55-57-60-61-66-67-70-76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #sta
F:215,291,335/binding site: carbohydate (Asn) (covalent) #status predicted
F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 50.3%; Score 96; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 1.6e+08;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

CY 1 ANAFPLXLRQSGSLRXCKXXQCSFPXXAFIFPKDAXRTKFLWISY 44
|||::|||::|||::|||::|||:
DB 42 ANSFLEEVAGSLERCMEMELCDPEAQEITPQNVEDTLIAFWIKY 85
|||||::|||::|||::|||::|||:

RESULT 7
EXHU
coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
N.Alternate names: Stuart factor
C.Species: Homo sapiens (man)
C.Date: 15-Nov-1984 #sequence revision 02-May-1994 #text change 08-Dec-2000
A:Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A005
R.Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5102, 1986
A>Title: Gene for Human Factor X: a blood coagulation factor whose gene organization is
A:Reference number: A24478; MUID:87026600; PMID:3768336
A:Accession: A24478
A:Molecule type: DNA
A:Residues: 1-488 <LEY>
A:Cross-references: GB:M14327; NID:g459809; PIDN:AAA52764.1; PID:g182831
R.Meessier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
A>Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag
A:Reference number: J00917; MUID:91216473; PMID:1902434
A:Accession: J00917
A:Molecule type: mRNA
A:Residues: 1-488 <MES>
A:Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390
R.Mingo, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
J. Biol. Chem. 267, 7395-7401, 1992
A>Title: Liver-specific expression of the gene coding for human factor X, a blood coagul
A:Reference number: A42485; MUID:92218390; PMID:1333796
A:Accession: A42485
A:Molecule type: DNA
A:Residues: 1-15 <MIA>
A:Experimental source: liver
A>Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:93787)
R.Kaul, R.K.; Hildebrand, B.; Roberts, S.; Usgadeeswararn, P.
Gene 41, 311-314, 1986
A>Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A:Reference number: A25853; MUID:86221713; PMID:3011603
A:Accession: A25853
A:Molecule type: mRNA
A:Residues: 19-284, 'E', 289-488 <KAU>
A:Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A:Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X.
A:Reference number: A22208; MUID:85216545; PMID:2582420
A:Accession: A22208
A:Molecule type: mRNA
A:Residues: 13-441, 'S', 443-488 <FUN>
A:Cross-references: GB:K0194; NID:G182840; PIDN:AAA52490.1; PID:G182841
R:McNallen, B.A.; Fujikawa, K.; Kisiel, W.; Sasaegawa, T.; Howald, W.N.; Kwa, E.Y.; Weinstein, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
A:Title: Characterization of a cDNA coding for human factor X.
A:Reference number: A21284; MUID:84222026; PMID:6587384
A:Accession: A21284
A:Molecule type: mRNA
A:Residues: 13-284, 'E', 289-488 <LE2>
A:Cross-references: GB:K0186
R:McNallen, B.A.; Fujikawa, K.; Kisiel, W.; Sasaegawa, T.; Howald, W.N.; Kwa, E.Y.; Weinstein, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, E.W.
Biochemistry 22, 2875-2884, 1983
A:Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.
A:Reference number: A20362; MUID:83357207; PMID:6871167
A:Accession: A20362
A:Molecule type: protein
A:Residues: 41-179 <MCM>
R:Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of factor X.
A:Reference number: S39414; MUID:94062825; PMID:8243461
A:Accession: S39415
A:Molecule type: protein
A:Residues: 183-234 <INO>
A:Note: glycosylation sites
A:Note: identification and characterization of beta-hydroxyaspartic acid
R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.U.; Hameshushanham, K.; Lyman, G.
Gene 84, 517-519, 1989
A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X.
A:Reference number: 154051; MUID:90128299; PMID:2612918
A:Accession: 154051
A:Status: translation not shown; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-23 <RES>
A:Cross-references: GB:M31297; NID:G183860; PIDN:AAA52636.1; PID:G553330
R:Padmanabhan, K.; Padmanabhan, K.P.; Tullinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blumberg, P.M.
J. Mol. Biol. 232, 947-966, 1993
A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A:Reference number: A49458; MUID:93360277; PMID:8355219
A:Contents: annotation; X-ray crystallography, 2.2 angstroms
C:Comment: The two chains held together by one disulfide bond are formed from a single-chain polypeptide. The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or factor XIa (in the extrinsic pathway).
C:Genetics:
A:Gene: GDB:F10
A:Cross-references: GDB:119890; OMIM:227600
A:Map position: 13q34-13q34
A:Introns: 24/1, 77/3; 86/1, 124/1, 150/3; 249/3; 289/1
A:Note: deficiency of this factor causes Stuart disease
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V and calcium ions.
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylutamic acid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-84/Domain: propeptide #status predicted <PRO>
F:85-84/Domain: Gla domain homology <GLA>
F:41-179/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EGF>
F:129-164/Domain: EGF homology <EG2>
F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F:183-234/Domain: activation peptide #status experimental <APT>
F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F:46-47, 54, 56, 65, 66, 67, 72, 79/Modified site: gamma-carboxylutamic acid (Glu) #status experimental <ACT>
F:57-62/Disulfide bonds: #status predicted
F:90-101, 95-110, 112-121, 129-140, 136-149, 151-166, 172-342, 241-246, 261-277, 390-404, 415-443/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:199, 211/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:221, 231/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 50.3%; Score 96; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 1,7e-08;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

1 ANAFLLXLRGSLKRCXKXCFXAFKIFKDXRTLFWISY 44
Db 41 ANFLERKMKGLRERCEETCTSEAREVFEDSDKTNEFWNKY 84

RESULT 8
TBHU
Chrombin (EC 3.4.21.5) precursor [validated] - human
N/Alternate names: coagulation factor II
N/Contains: prothrombin
C/Species: Homo sapiens (man)
C/Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000
C/Accession: A29351; A00914; B00914; A37549; A37550; I51952
R/Degen, S.J.F.; Davie, E.W.
Biochemistry 26, 6165-6177, 1987
A/Title: Nucleotide sequence of the gene for human prothrombin.
A/Reference number: A29351; MUID:88077877; PMID:2825773
A/Accession: A29351

A/Molecule type: DNA
A/Residues: 1-622 <DEG>
A/Cross-references: GB:M17262; GB:M3691; NID:G558069; PIDN:AA63054.1; PID:G339641
R/Degen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.
Biochemistry 22, 2087-2097, 1983
A/Title: Characterization of the complementary deoxyribonucleic acid and gene coding for
A/Reference number: A00914; MUID:83231469; PMID:6305407
A/Accession: A00914

A/Molecule type: mRNA
A/Residues: 8-163, 'N', 165-622 <DE2>
A/Cross-references: GB:V00595; GB:U00307; NID:G37128; PIDN:CAA23842.1; PID:G1335344
A/Accession: B00914

A/Molecule type: DNA
A/Residues: 186-311 <DE3>
R/Malz, D.A.; Hewitt-Emmett, D.; Seegers, W.H.
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
A/Reference number: A37549; MUID:77193964; PMID:266717
A/Accession: A37549

A/Molecule type: protein
A/Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-308,
R/Butkowski, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.
J. Biol. Chem. 252, 4942-4957, 1977
A/Title: Primary structure of human prothrombin 2 and alpha-thrombin.
A/Reference number: A37550; MUID:77207112; PMID:873923
A/Accession: A37550

A/Molecule type: protein
A/Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
R/Rabier, M.J.; Blashill, A.; Furtle, B.; Furtle, B.C.
J. Biol. Chem. 261, 13210-13215, 1986
A/Reference number: A37551; MUID:87008532; PMID:3759958
A/Contents: annotation; activation cleavages
R/MacGillivray, R.T.; Irwin, D.M.; Guinto, E.R.; Stone, J.C.
Ann. N. Y. Acad. Sci. 485, 73-79, 1986
A/Title: Recombinant genetic approaches to functional mapping of thrombin.
A/Reference number: I51952; MUID:87182874; PMID:3471151
A/Accession: I51952

A/Status: translated from GB/EMBL/DBDUT
A/Molecule type: mRNA
A/Residues: 1-2, 'RI', 5-100 <RES>
A/Cross-references: GB:M33021; NID:G190723; PIDN:AAA60220.1; PID:G190724
C/Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
C/Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
C/Comment: removed either by factor Xa or thrombin; the cleavage into light and heavy chain
ter 314-Arg, are released in natural blood clotting.
C/Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
C/Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
C/Comment: interaction with the negatively charged phospholipid membrane surface.
C/Comment: The prothrombin precursor is synthesized in the liver.

C/Genetics:
A/Gene: GDB:F2
A/Cross-references: GDB:119894; OMIM:176930

A/Map position: 11p11-11q12
A/Intons: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552/
C/Superfamily: thrombin; Gla domain homology; Kringle homology; trypsin homology
C/Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; duplic
F:124/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-87/Domain: Gla domain homology <Gla>
F:44-622/Product: prothrombin #status experimental <MAT>
F:44-327/Domain: activation peptide #status experimental <APT>
F:108-186/Domain: kringle homology <KR1>
F:213-291/Domain: kringle homology <KR2>
F:328-363/Product: thrombin light chain #status experimental <LCH>
F:364-622/Product: thrombin heavy chain #status experimental <HCH>
F:364-613/Domain: trypsin homology <TRY>
F:49,50,57,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Dissulfide bonds: #status
F:121,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F:336-482,536-550,564-594/Dissulfide bonds: #status predicted
F:331-407/Dissulfide bonds: #status experimental
F:406,462/Active site: His, Asp #status predicted
F:416/Binding site: carboxylate (Asn) (covalent) #status experimental
F:568/Active site: Ser #status experimental

Query Match 49.2%; Score 94; DB 1; Length 622;
Best Local Similarity 38.6%; Pred. No. 4.6e-08;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

1 ANAFLLXLRGSLKRCXKXCFXAFKIFKDXRTLFWISY 44
Db 44 ANFLERKMKGLRERCEETCTSEAREVFEDSDKTNEFWNKY 87

RESULT 9
EXRT
Coagulation factor Xa (EC 3.4.21.6) precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text change 08-Dec-2000
C/Accession: S49075; JC4670; PS0191; PS0190; 162745
R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A/Title: Evidence for competition between vitamin K-dependent clotting factors for intrac
A/Reference number: A58498; MUID:96093366; PMID:8578539
A/Accession: S49075

A/Molecule type: mRNA
A/Residues: 1-482 <STRA>
A/Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601
A/Note: submitted to the EMBL Data Library, June 1994
A/Note: neither the complete nucleic acid sequence nor the complete translation are show
R/Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A/Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A/Reference number: JC4670; MUID:96194815; PMID:8647460
A/Accession: JC4670

A/Molecule type: mRNA
A/Residues: 1-482 <STRA>
A/Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601
A/Experimental source: Cos-1 cell
R/Enyoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A/Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plas
A/Reference number: PS0190; MUID:92041742; PMID:1718949
A/Accession: PS0190

A/Molecule type: protein
A/Residues: 41-58, 'X', 60-65 <ENU1>
A/Accession: PS0190

A/Molecule type: protein
A/Residues: 183-186, 'X', 188-207 <ENU2>
R/Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A/Title: Analysis of the partial nucleotide sequences and deduced primary structures of t

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A:Reference number: 146196; MUID:944222160; PMID:8168596
A:Accession: I62745
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 295-383; 'G', 385-455 <MUR>
A:Cross-references: GB:D21215; NID:9415309; PIDN:BA04756.1; PID:9455396
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:41-179/Domain: EGF homology factor X light chain #status predicted <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>
F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F:183-231/Domain: activation peptide #status predicted <APT>
F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F:232-460/Domain: trypsin homology <TRY>
F:46-47,54,56,65,66,67,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat
F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:187/Binding site: carboxylate (Asn) (covalent) #status experimental
F:208/Binding site: carboxylate (Thr) (covalent) #status predicted
F:218/Binding site: carboxylate (Asn) (covalent) #status predicted
F:231-232/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stat
F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match          47.1%  Score 90;  DB 1;  Length 482;
Best Local Similarity 38.6%  Pred. No. 18e-07;
Matches 17;  Conservative 8;  Mismatches 19;  Indels 0;  Gaps 0;

Cy 1 ANAFLXLRGSLRXKCKXQCSFXXAFIFKDXATKLFMISY 44
    |||::|::|::|::|::|::|::|::|::|::|::|::|
Db 41 ANSFEEIKKGNRECEVEICSFEEAREVEFENETTEMWNY 84

RESULT 10
S10511
thrombin (EC 3.4.21.5) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1993 #sequence revision 07-May-1993 #text_change 03-May-2002
C:Accession: S10511; A60576; B42696
R:Dihaatch, M.; Monard, D.
Nucleic Acids Res. 18, 4251, 1990
A:Title: cDNA sequence of rat prothrombin.
A:Reference number: S10511; MUID:90332426; PMID:2377469
A:Accession: S10511
A:Molecule type: mRNA
A:Residues: 1-617 <DIH>
A:Cross-references: EMBL:X52835; NID:956969; PIDN:CA37017.1; PID:956970
R:Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A:Title: Prothrombin levels are increased in the estrogen-created immature rat uterus.
A:Reference number: A60576; MUID:90091942; PMID:2293980
A:Accession: A60576
A:Molecule type: protein
A:Residues: 44-58 <HEN>
A>Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute
R:Banfield, D.K.; Macgillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Accession: B42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 383-617, 'E' <BAN>
A:Cross-references: GB:M81397
C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hydr
F:1-24/Domain: signal sequence #status predicted <SIG>

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```

F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-617/Product: prothrombin #status experimental <PMAT>
F:109-187/Domain: kringe homology <KRI>
F:215-293/Domain: kringe homology <KR2>
F:360-609/Domain: trypsin homology <TRY>
F:51,55,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylglutamic acid (Glu) #status
F:61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,54
F:402,458,564/Active site: His, Asp, Ser #status predicted

Query Match          47.1%  Score 90;  DB 2;  Length 617;
Best Local Similarity 39.5%  Pred. No. 2.2e-07;
Matches 17;  Conservative 6;  Mismatches 20;  Indels 0;  Gaps 0;

Cy 2 NAFLXLRGSLRXKCKXQCSFXXAFIFKDXATKLFMISY 44
    :|||::|::|::|::|::|::|::|::|::|::|::|::|
Db 46 SGFLBELRGKNRECEVEICSFEEAREVEFENETTEMWNY 88

RESULT 11
A35827
thrombin (EC 3.4.21.5) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text_change 03-May-2002
C:Accession: A35827; A42696; S12081
R:Deegen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pat, J.A.
DNA Cell Biol. 9, 487-498, 1990
A:Title: Characterization of the cDNA coding for mouse prothrombin and localization of th
A:Reference number: A35827; MUID:91025551; PMID:2222810
A:Accession: A35827
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-618 <DEG>
A:Cross-references: GB:X52308; NID:953813; PIDN:CA36548.1; PID:953814
A:Experimental source: strain C57BL/6
A>Note: the data were obtained from females resulting from the cross of M. domesticus and
R:Banfield, D.K.; Macgillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Accession: A42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 384-618, 'E' <BAN>
A:Cross-references: GB:M81394
C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hydr
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-618/Product: prothrombin B #status predicted <MAT>
F:109-187/Domain: kringe homology <KRI>
F:215-293/Domain: kringe homology <KR2>
F:361-610/Domain: trypsin homology <TRY>
F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylglutamic acid (Glu) #status
F:61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,54
F:403,459,565/Active site: His, Asp, Ser #status predicted

Query Match          47.1%  Score 90;  DB 2;  Length 618;
Best Local Similarity 39.5%  Pred. No. 2.2e-07;
Matches 17;  Conservative 6;  Mismatches 20;  Indels 0;  Gaps 0;

Cy 2 NAFLXLRGSLRXKCKXQCSFXXAFIFKDXATKLFMISY 44
    :|||::|::|::|::|::|::|::|::|::|::|::|::|
Db 46 SGFLBELRGKNRECEVEICSFEEAREVEFENETTEMWNY 88

RESULT 12
EXCH
coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N:Alternate names: virus-activating proteinase
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 16-Jul-1999

```


Proc.Natl. Acad.Sci. U.S.A. 80, 1802-1806, 1983

A>Title: beta-hydroxyaspartic acid in vitamin K-dependent protein C.

A|Reference number: A19316; MUID:83169769; PMID:6572939

A|Contents: annotation; revision 110

R|Stenflo, J.; Fernlund, P.

J Biol. Chem. 257, 12180-12190, 1982

A>Title: Amino acid sequence of the heavy chain of bovine protein C.

A|Reference number: A18386; MUID:83007326; PMID:6696877

A|Accession: A18386

A|Molecule type: protein

A|Residues: 197-454,'PV' <STB>

R|Esmon, N.L.; DeBaill, L.E.; Esmon, C.T.

J Biol. Chem. 258, 5548-5553, 1983

A>Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless p

A|Reference number: A37541; MUID:83213513; PMID:6304092

A|Contents: annotation; activation; calcium binding

R|Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.

J Biol. Chem. 258, 5554-5560, 1983

A>Title: Structural changes required for activation of protein C are induced by Ca2+ bindi

A|Reference number: A37542; MUID:83213514; PMID:6406503

A|Contents: annotation; activation; calcium binding

C|Comment: protein C is the zymogen of the vitamin K-dependent serine proteinase that reg

s.

C|Comment: Protein C is synthesized in the liver as a single chain precursor, which is c

bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reactio

C|Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro

cognition of the thrombin-thrombomodulin complex.

C|Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

G|Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C|Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding

F11-29/Domain: signal sequence (fragment) #status predicted <SIG>

F124-83/Domain: Gla domain homology <GLA>

F130-39/Domain: propeptide #status predicted <PRO>

F140-194/Product: protein C light chain #status experimental <LCH>

F198-128/Domain: EGF homology <EGF>

F137-117/Domain: EGF homology <EG2>

F197-456/Product: protein C heavy chain #status experimental <HCH>

F197-210/Domain: activation peptide #status experimental <APR>

F211-440/Domain: trypsin homology <TRY>

F145,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #statu

F110/Modified site: eythro-beta-hydroxyaspartic acid (Asp) #status experimental

F1138-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #statu

F1136,288,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

F1252,296,397/Active site: His, Asp, Ser #status predicted

F1366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.1%; Score 88; DB 1; Length 456;

Best Local Similarity 40.9%; Pred. No. 3 8e-07;

Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

CY 1 ANAFLLXLRQSLRXKXXQCSPFXAXFIKDXARTKLFWISY 44
||:||:||||:||||:||||:
DB 40 ANSFLEELRGVNERECSEVECFEEAREIFQNTEDIMAFWSFY 83
||:||||:||||:||||:

RESULT 14

KKHU

protein C (activated) (EC 3.4.21.69) precursor - human

N|Alternate names: autoprothrombin IIA; plasma protein C

C|Species: Homo sapiens (man)

C|Date: 17-Mar-1987 #sequence,revision 17-Mar-1987 #text-change 16-Jul-1999

C|Accession: A22331; A25426; A21781; A23789; A00927

R|Foster, D.C.; Yoshitake, S.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985

A>Title: The nucleotide sequence of the gene for human protein C.

A|Reference number: A22331; MUID:85270390; PMID:2991887

A|Accession: A22331

A|Molecule type: DNA

A|Residues: 1-461 <FSM1>

A|Cross-references: GB:M1228; NID:g190333; PIN:AAA60166.1; PID:g190334

R|Plutzky, J.; Hosking, J.A.; Long, G.L.; Crabtree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986

A>Title: Evolution and organization of the human protein C gene.

A:Reference number: A25426; MUID:86120978; PMID:3511471
A:Accession: A25426
A:Molecule type: DNA
A:Residues: 1-445, 'L', 446-461 <PU>
A:Cross-references: GB:M12712; NID:9190330; PIDN:AAA60165.1; PID:9190332
R:Poster, D.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
A:Title: Characterization of a cDNA coding for human protein C.
A:Reference number: A21781; MUID:84272714; PMID:6589623
A:Accession: A21781
A:Molecule type: mRNA
A:Residues: 'Q', 107-461 <POS>
A:Cross-references: GB:K02059; NID:9190322; PIDN:AAA60164.1; PID:9190323
R:Beckmann, R.U.; Schmidt, R.J.; Sautter, R.F.; Plutzky, J.; Crabtree, G.R.; Long, G.L.
Nucleic Acids Res. 13, 5233-5247, 1985
A:Title: The structure and evolution of a 461 amino acid human protein C precursor and
A:Reference number: A23789; MUID:85269639; PMID:2991859
A:Accession: A23789
A:Molecule type: mRNA
A:Residues: 1-461 <BEC>
A:Cross-references: GB:X02750; NID:935689; PIDN:CAA26528.1; PID:9763120
R:Milliet, J.P.; Broze Jr., G.U.
J. Biol. Chem. 265, 11397-11404, 1990
A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation
A:Reference number: A44605; MUID:90293094; PMID:1694179
A:Accession: A44605
A:Contents: annotation; carbohydrate binding sites; activation peptide
A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
R:Harrie, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor
A:Reference number: A44605; MUID:92184750; PMID:1544894
A:Accession: A44605
A:Contents: annotation; beta-hydroxyaspartic acid
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
activation of factor Va is strongly enhanced by complexing with protein S. Protein C also
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is
b1n, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
C:Genetics:
A:Gene: GDB:PROC
A:Cross-references: GDB:120317; OMIM:176860
A:Map position: 2q13-2q21
A:Interon: 24/1, 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F:1-12/Domain: signal sequence #status predicted <SID>
F:27-86/Domain: Gla domain homology <GUA>
F:33-42/Domain: propeptide #status predicted <PRO>
F:43-197/Product: protein C light chain #status predicted <LCH>
F:92-131/Domain: EGF homology <EG1>
F:140-175/Domain: EGF homology <EG2>
F:200-461/Product: protein C heavy chain #status predicted <HCH>
F:200-211/Domain: activation peptide #status experimental <APT>
F:212-445/Domain: trypsin homology <TRY>
F:48, 49, 56, 61, 62, 67, 68, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
F:59-64, 92-105, 101-120, 122-131, 140-151, 147-160, 162-175, 183-319, 238-254, 373-387, 398-426/D
F:106-111/Disulfide bonds: #status predicted
F:110/Binding site: carbohydrate (Thr) (covalent) #status absent
F:113/Modified site: eythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:139, 290, 335/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
F:253, 299, 402/Active site: His, Asp, Ser #status predicted
F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 42.4%; Score 81; DB 1; Length 461;
Best Local Similarity 43.9%; Pred. No. 6, 1e-06;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

1 ANAFLXLRGSGLRKCKKXQGFXXAFKFXKXRTKLFM 41
Db 43 ANSFLERHSHSLRECEIEICDFEAKKEIFQVNDTLAFW 83
RESUL 15
KFHU

coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
N:Alternate names: antihemophilic factor B; Christmas factor
C:Species: Homo sapiens (man)
C:Date: 17-Dec-1982 #sequence_revision 30-Jun-1987 #text_change 15-Sep-2000
A:Accession: A00922; A37570; A30511; A32989; A26673; A21337; A37546; A30623; A60486; A20
R:Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
Biochemistry 24, 3736-3750, 1985
A:Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
A:Reference number: A00922; MUID:8600558; PMID:29947716
A:Accession: A00922
A:Molecule type: DNA
A:Residues: 1-461 <POS>
A:Cross-references: GB:K02402; NID:9182612; PIDN:AAA59620.1; PID:9182613
R:Ranson, D.S.; Choo, K.H.; Ree, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Bro
EMBO J. 3, 1053-1060, 1984
A:Title: The gene structure of human anti-haemophilic factor IX.
A:Reference number: A37570; MUID:84236100; PMID:6329734
A:Accession: A37570
A:Molecule type: DNA
A:Residues: 1-461 <ANS>
A:Cross-references: GB:K02048
R:Reitsma, P.H.; Bertina, R.W.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
Blood 72, 1074-1076, 1988
A:Title: The putative factor IX gene promoter in hemophilia B Leyden.
A:Reference number: A30511; MUID:88327116; PMID:3416069
A:Accession: A30511
A:Molecule type: DNA
A:Residues: 8-24 <REL>
A:Cross-references: ENBL:X55008; NID:9311288; PIDN:CAB38245.2; PID:94469253
R:Koeberl, D.D.; Bottema, C.D.K.; Buerschede, J.M.; Sommer, S.S.
Am. J. Hum. Genet. 45, 448-457, 1989
A:Title: Functionally important regions of the factor IX gene have a low rate of polymor
A:Reference number: A32989; MUID:88371752; PMID:2773937
A:Accession: A32989
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-92 <KOE>
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
A:Reference number: A26673; MUID:85190593; PMID:3857619
A:Accession: A26673
A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <MCG>
A:Cross-references: GB:M11309; NID:9180552; PIDN:AAA52023.1; PID:9180553
A:Note: the authors translated the codon ACA for residue 29 as Tyr
R:Jay, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Findel, A.; Tolstosh
Nucleic Acids Res. 11, 2325-2335, 1983
A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
A:Reference number: A21337; MUID:83220788; PMID:6687940
A:Accession: A21337
A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <JAY>
A:Cross-references: GB:J00137; NID:9182610; PIDN:AAA52763.1; PID:9182611
R:Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A:Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
A:Reference number: A37546; MUID:84300526; PMID:6089357
A:Accession: A37546
A:Molecule type: mRNA
A:Residues: 38-193, 'T', 195-326 <JAG>
A:Cross-references: GB:M35672
R:Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A:Title: Isolation and characterization of a cDNA coding for human factor IX.
A:Reference number: A30623; MUID:83065193; PMID:6959130
A:Accession: A30623
A:Molecule type: mRNA
A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',
A:Cross-references: GB:J00136; NID:9182608; PIDN:AAA98726.1; PID:9182609
R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 58, 21-29, 1990

A>Title: Development of an immunoaffinity process for factor IX purification.
 A:Reference number: A60486; MUID:90194857; PMID:2316207
 A:Accession: A60486
 A:Molecule type: protein
 A:Residues: 47-52,'XX',55-60,'X',62,'XX',65 <THA>
 R:McMullen, B.A.; Fujikawa, K.; Kiesel, W.
 A:Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX.
 A:Reference number: A20274; MUID:83308813; PMID:6688526
 A:Accession: A20274
 A:Molecule type: protein
 A:Residues: 105-109,'X',111-115 <MCM>
 R:Ballard, A.; Faure, T.; Carvalho, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle, J.
 A:Biochem. Biophys. Res. Commun. 172, 565-572, 1988
 A>Title: Characterisation of two differently processed forms of human recombinant factor IX.
 A:Reference number: S02527; MUID:88166735; PMID:3280312
 A:Accession: S02527
 A:Molecule type: protein
 A:Residues: 29-63 <BAL>
 A:Note: Processed forms expressed in recombinant system
 R:Jallat, S.; Perraud, F.; Dalemans, W.; Ballard, A.; Dieterle, A.; Faure, T.; Meullen, E.MBO J. 9, 3295-3301, 1990
 A>Title: Characterization of recombinant human Factor IX expressed in transgenic mice and in human placenta.
 A:Reference number: S12058; MUID:9106024; PMID:2209546
 A:Accession: S12058
 A:Molecule type: mRNA; protein
 A:Residues: 1-68 <JAL>
 A:Note: processed forms expressed in recombinant system
 R:Handford, P.A.; Barton, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe E.MBO J. 9, 475-480, 1990
 A>Title: The first EGF-like domain from human factor IX contains a high-affinity calcium binding site.
 A:Reference number: S12377; MUID:90151623; PMID:2406129
 A:Accession: S12377
 A:Molecule type: protein
 A:Residues: 92-130 <HAN>
 A:Note: NMR detection of calcium binding by domain expressed in recombinant system
 R:de la Salle, C.; Charmanlier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum, Thromb. Haemost. 70, 370-371, 1993
 A>Title: A deletion located in the 3' non translated part of the factor IX gene responsi
 A:Reference number: I59612; MUID:94054330; PMID:8236150
 A:Accession: I59612
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 444-461 <RES>
 A:Cross-references: GB:S66752; NID:9439773; PIDN:AA828588.1; PID:9439774
 R:Stoflet, E.S.; Koebberl, D.D.; Sarkar, G.; Sommer, S.S.
 A>Title: Genomic amplification with transcript sequencing.
 A:Reference number: I59529; MUID:88127096; PMID:3340835
 A:Accession: I59529
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 290-359 <RE2>
 A:Cross-references: GB:M9063; NID:9182622; PIDN:AA52456.1; PID:9182623
 R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw Biochemstry 33, 5167-5171, 1994
 A>Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin
 A:Reference number: A54255; MUID:94227047; PMID:8172892
 A:Accession: A54255
 A:Molecule type: protein
 A:Residues: 'D',204,'X',206-211,212,'D',214,'X',216-221,'D' <AGA>
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrate
 R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.
 A:J. Clin. Invest. 61, 1528-1538, 1978
 A>Title: Activation of human factor IX (Christmas factor).
 A:Reference number: A18483; MUID:78194509; PMID:659613
 A:Contents: annotation; activation; active site; carbohydrate binding
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W. Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
 A:Reference number: A37569
 A:Contents: annotation
 A:Note: 194-Thr was also found
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.

J. Biol. Chem. 259, 5698-5704, 1984
 A>Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding site.
 A:Reference number: A37543; MUID:84185715; PMID:6425296
 A:Contents: annotation; calcium binding
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A:Reference number: A37544
 A:Contents: annotation; calcium binding, correction
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A>Title: Defective propeptide processing of blood clotting factor IX caused by mutation
 A:Reference number: A37545; MUID:86189947; PMID:3009023
 A:Contents: annotation; signal sequence cleavage site
 R:Sunhito, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya, J. Biol. Chem. 264, 21257-21265, 1989
 A>Title: Blood clotting factor IX (BIM) Nagoya: substitution of arginine 180 by tryptophan
 A:Reference number: A30622; MUID:90078223; PMID:2552373
 A:Contents: annotation; sequence of mutant BIM Nagoya
 A:Note: carboxylation, glycosylation, and cleavage sites
 R:Barton, M.; Norman, D.G.; Harvey, T.S.; Handford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee submitted to the Brookhaven Protein Data Bank, November 1991
 A:Reference number: A51252; PDB:1IXA
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A:Note: recombinant form expressed in yeast
 C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
 A:Gene: GDB:F9
 A:Cross-references: GDB:119900; OMIM:306900
 A:Map position: Xq27.1-Xq27.2
 A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-88/Domain: signal sequence #status predicted <SIG>
 F:29-46/Domain: propeptide #status experimental <PPT>
 F:31-91/Domain: Gla domain homology <GLA>
 F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:134-170/Domain: EGF homology <EGF>
 F:192-226/Domain: activation peptide #status experimental <ACT>
 F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F:227-454/Domain: trypsin homology <TRY>
 F:53,54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #st
 F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,352-368,382-396,407-435/D
 F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:191-192/Cleavage site: Arg-Ala (coagulation factor IXa) #status experimental
 F:203,213/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:205,215/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental

Query Match 41.9%; Score 80; DB 1; Length 461;
 Best Local Similarity 42.9%; Pred. No. 9 1e-06;
 Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
 10 QGSLRXCKXXQCSEFXAFXIFKDXRTKLFWISY 44
 DB 57 QGNLERECMEKCSFEARVEFEMTERTFEWMQY 91

Search completed: March 19, 2003, 15:00:50
 Job time : 30.125 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10GLN28PHE
Sequence: 1 ANAFLLXLRQGLXRCCKXX.....XXAFYIFKDXKRTLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	466	1	FA7_HUMAN
2	122	63.9	444	1	FA7_RABIT
3	114	59.7	407	1	FA7_BOVIN
4	111	58.1	446	1	FA7_MOUSE
5	102	53.4	490	1	FA10_RABIT
6	98	51.3	459	1	FA10_BOVIN
7	97	50.8	218	1	TMG1_HUMAN
8	97	50.8	461	1	PRTG_MOUSE
9	96	50.3	461	1	PRTG_RAT
10	96	50.3	488	1	FA10_HUMAN
11	94	49.2	622	1	THRB_HUMAN
12	94	49.2	617	1	THRB_RAT
13	90	47.1	618	1	THRB_MOUSE
14	90	47.1	617	1	THRB_MOUSE
15	89	46.6	231	1	TMG3_HUMAN
16	89	46.6	475	1	FA10_CHICK
17	88	46.1	456	1	PRTG_BOVIN
18	81	42.4	458	1	PRTG_RABIT
19	81	42.4	461	1	PRTG_HUMAN
20	80	41.9	461	1	FA9_HUMAN
21	79	41.4	416	1	FA9_BOVIN
22	76	39.8	376	1	FA10_TROCA
23	74	38.7	625	1	THRB_BOVIN
24	73	38.2	202	1	TMG2_HUMAN
25	71	37.2	452	1	FA9_MOUSE
26	71	37.2	459	1	FA9_MOUSE
27	66.5	34.8	226	1	TMG4_HUMAN
28	62	32.5	649	1	PRTS_MAKNU
29	62	32.5	676	1	PRTS_HUMAN
30	60	31.4	396	1	PRTZ_BOVIN
31	58	30.4	646	1	PRTS_RABIT
32	58	30.4	675	1	PRTS_RAT
33	57	29.8	675	1	PRTS_RAT

34	53	27.7	400	1	PRTZ_HUMAN	P22891	homo sapien
35	50	26.2	675	1	PRTS_MOUSE	Q08761	mus musculus
36	47.5	24.9	271	1	MD12_YEAST	Q92328	saccharomyc
37	45	23.6	879	1	YN65_YEAST	P42837	saccharomyc
38	43	22.5	394	1	TCR4_SALOR	P33733	salmonella
39	43	22.5	440	1	Y788_BORBU	O51728	borrelia bu
40	41	21.5	263	1	PFLA_STRMU	O68575	streptococc
41	41	21.5	393	1	DPS5_PINSY	Q02323	pinus sylve
42	41	21.5	616	1	JEN1_YEAST	P36035	saccharomyc
43	40	20.9	343	1	HMD_METVO	O50840	methanococc
44	40	20.9	353	1	HMD_METTL	O50759	m coenzyme
45	40	20.9	602	1	VE1_CRPVK	P03112	cottoncattal

ALIGNMENTS

RESULT 1
ID FA7_HUMAN STANDARD; PRT; 466 AA.
AC P08709: 014339;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
conversion accelerator) (Eptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.;"
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.;"
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A. AND VARIANTS THR-352; GLN-413 AND LYS-445.
RX Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RX Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjorn S., Christensen M., Nicolaissen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.;"
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Thim L., Wlberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.;"
RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;

RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.;
 RA "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [7]
 RN STRUCTURE OF CARBOHYDRATE ON SSR-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598993;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [9]
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPT mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RN STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=968367502; PubMed=9692950;
 RA Muryani A., Finn B.E., Gipeert G.P., Forzen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RN VARIANT GLN-364.
 RP MEDLINE=91300046; PubMed=2070047;
 RX O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [12]
 RN VARIANTS GLN-364 AND PHE-370.
 RP MEDLINE=92340074; PubMed=1634227;
 RX Marchetti G., Patrascchini P., Gemmati D., Denosa V., Pinotti M.,
 RA Roderigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RN VARIANT TYR-238.
 RP MEDLINE=93372811; PubMed=8364544;
 RX Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.,
 RA "A missense mutation (178Cys->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RN VARIANTS.
 RP MEDLINE=94061028; PubMed=8242057;
 RX Takamiya O., Kembail-Cook G., Marin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RN VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE=94264305; PubMed=8204879;
 RA Chating S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [16]
 RN VARIANT VAL-354.
 RP MEDLINE=95072589; PubMed=7981691;
 RX Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala->Val) and X (334Ser->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RN VARIANT MET-HIS-307.
 RP MEDLINE=95064662; PubMed=7974346;
 RX Ohlwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Met: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg (247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RN VARIANT MET-419.
 RP MEDLINE=96247510; PubMed=8652821;
 RX Arbini A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [19]
 RN VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RP MEDLINE=97001216; PubMed=8844208;
 RX Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RN VARIANT VAL-304.
 RP MEDLINE=97037613; PubMed=8883260;
 RX Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaitov R., Seligson U.;
 RT "A1a244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RN VARIANTS MALTA THR-194 AND VAL-304.
 RP MEDLINE=98112461; PubMed=9452082;
 RX Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -1- PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

FA7_BOVIN
ID FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OC NCBI_Taxid=9913;
OX NCBI_Taxid=9913;
RN [1]
RP MEDLINE=89008362; PubMed=3049594;
RX Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.;
RA Iwanaga S.;
RT "Bovine factor VII. Its purification and complete amino acid sequence."
RT J. Biol. Chem. 263:14868-14877(1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T., Miyata T., Iwanaga S., Takao T., Shimomichi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX."
RT J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=9134709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."
RT Adv. Exp. Med. Biol. 281:121-131(1990).
RL Adv.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
DR PIR: A31979; A31979.
DR HSSP: P08709; 1BP9.
DR MEROPS: S01.215;
DR Interpro: IPR000152; Asx_hydroxyl.
DR Interpro: IPR001314; Chymotrypsin.
DR Interpro: IPR000561; EGF-like.
DR Interpro: IPR000742; EGF 2.
DR Interpro: IPR001881; EGF-Ca.
DR Interpro: IPR001438; EGF-II.
DR Interpro: IPR002383; GLA_blood.
DR Interpro: IPR001254; Ser_protease_Try.
DR Interpro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF 2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00001; GLABLOD.
DR SMART: SM00179; EGF CA; 1.
DR SMART: SM00001; EGF_like; 1.

DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_spec; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF 2; 2.
DR PROSITE: PS01187; EGF CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; KW EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
FT DOMAIN 153 407 FACTOR VII HEAVY CHAIN.
FT DOMAIN 46 82 GLA-RICH.
FT DOMAIN 87 128 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 153 407 SERINE PROTEASE.
FT SITE 152 153 CLEAVAGE (BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR THROMBIN).
FT ACT_SITE 193 193 BY SIMILARITY.
FT ACT_SITE 242 242 BY SIMILARITY.
FT ACT_SITE 344 344 BY SIMILARITY.
FT BINDING 338 338 SUBSTRATE (BY SIMILARITY).
FT DISULFID 17 22 BY SIMILARITY.
FT DISULFID 50 61 BY SIMILARITY.
FT DISULFID 55 70 BY SIMILARITY.
FT DISULFID 72 81 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 98 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 135 262 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 178 194 BY SIMILARITY.
FT DISULFID 310 329 BY SIMILARITY.
FT DISULFID 340 368 BY SIMILARITY.
FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 52 52 O-LINKED (GLCNAc).
FT CARBOHYD 145 145 N-LINKED (GLCNAc).
FT CARBOHYD 203 203 N-LINKED (GLCNAc).
SQ SEQUENCE 407 AA, 44431 MW, 703E1FE0636F7F10 CRC64;
Query Match 59.7%; Score 114; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 2,3e-12;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
QY 1 ANAFLLKRGSLKRCXKXGCSFXAFLIPDKARTKTFWISY 44
DB 1 ANGFLLELLPSLIERCRELCSFEFAHDFPNEERTQFWISY 44
RESULT 4
FA7_MOUSE STANDARD; PRT; 446 AA.
ID FA7_MOUSE
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97127167; PubMed=8972017;
 RX Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood
 coagulation factor VII gene."
 RL Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR Xa
 BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; U66079; AAC3796.1; -.
 DR HSSP; P08709; 1BF9.
 DR MEROPS; S01.215; -.
 DR MCD; MGI:109325; F7.
 DR InterPro; IPR000152; Aex_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS001187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 24
 FT PROPEP 25 41
 FT CHAIN 42 193
 FT CHAIN 194 446
 FT DOMAIN 47 76
 FT DOMAIN 87 123

FT DOMAIN 128 169
 FT DOMAIN 194 446
 FT SITE 193 194
 FT ACT SITE 234 234
 FT ACT SITE 283 283
 FT ACT SITE 385 385
 FT BINDING 379 379
 FT DISULFID 58 63
 FT DISULFID 91 102
 FT DISULFID 96 111
 FT DISULFID 113 122
 FT DISULFID 132 143
 FT DISULFID 139 153
 FT DISULFID 155 168
 FT DISULFID 176 203
 FT DISULFID 200 205
 FT DISULFID 219 235
 FT DISULFID 351 370
 FT DISULFID 381 409
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 76 76
 FT MOD_RES 104 104
 FT CARBOHYD 186 186
 FT CARBOHYD 244 244
 FT SEQUENCE 446 AA; 50276 MW; 2512E44A5C9C96E CMC64;
 Query Match 58.1%; Score 111; DB 1; Length 446;
 Best Local Similarity 54.5%; Pred. No. 8.3e-12;
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;
 Oy 1 ANAFLLXLRQGSLLKRXCKXQCSFYKXAFYTRDAMRTLFMISY 44
 Db 42 ANSLLEELWPGSLRECNBEOCSFEAREIFKSPERTQFMWIV 85
 RESULT 5
 ID FA10_RABIT STANDARD; PRT; 490 AA.
 AC O19045;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97256311; PubMed=9101642;
 RX Pendurthi U.R., Anderson K.D., James H.L.;
 RT "Characterization of a full-length cDNA for rabbit factor X.";
 RL Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 converts prothrombin to thrombin in the presence of factor Va,
 calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC		CALCIUM (BY SIMILARITY).
CC	-1-PTM; N- AND O-GLYCOSYLATED (BY SIMILARITY).	
CC	-1-PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIIA (IN THE EXTRINSIC PATHWAY) (BY SIMILARITY).	
CC	MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.	
CC	-1- SIMILARITY: BELONGS TO PERTIDASE FAMILY S1.	
CC	-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.	
CC	-----	
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CC	EMBL; AF003200; AAB62542.1; --	
DR	HSSP; P00742; IHCG.	
DR	MEROPE; S01_216; --	
DR	InterPro; IPR000152; Asx_hydroxy1.	
DR	InterPro; IPR001314; Chymotrypsin.	
DR	InterPro; IPR000561; EGF-like.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR002383; GLA_blood.	
DR	InterPro; IPR001254; Ser_protease_Try.	
DR	InterPro; IPR002394; Vltk_dep_GLA.	
DR	pfam; PF00008; EGF_2.	
DR	pfam; PF00089; trypsin; 1.	
DR	pfam; PF00594; gla; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	PRINTS; PR00001; GLABLOOD.	
DR	SMART; SM00179; EGF_CA; 1.	
DR	SMART; SM00001; EGF_Like; 1.	
DR	SMART; SM00069; GLA; 1.	
DR	SMART; SM00020; TRY_SPC; 1.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.	
DR	PROSITE; PS00022; EGF_1; 1.	
DR	PROSITE; PS01186; EGF_2; 2.	
DR	PROSITE; PS01187; EGF_CA; 1.	
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.	
DR	PROSITE; PS00240; TRYPsin_DOM; 1.	
DR	PROSITE; PS00134; TRYPsin_HIS; 1.	
DR	PROSITE; PS00135; TRYPsin_SER; 1.	
KW	Glycoprotein; Hydroxylase; Serine protease; Plasma; Blood coagulation;	
KW	Gamma-carboxyglutamic acid; Hydroxylase; Calcium-binding; Vitamin K;	
KW	Signal; Zymogen; EGF-like domain; Repeat.	
FT	SIGNAL	1 20
FT	PROPEP	21 40
FT	CHAIN	41 180
FT	PROPEP	184 490
FT	CHAIN	184 490
FT	PROPEP	184 490
FT	DOMAIN	86 122
FT	DOMAIN	125 165
FT	DOMAIN	233 490
FT	MOD_RES	46 46
FT	MOD_RES	47 47
FT	MOD_RES	54 54
FT	MOD_RES	56 56
FT	MOD_RES	59 59
FT	MOD_RES	60 60
FT	MOD_RES	65 65
FT	MOD_RES	66 66
FT	MOD_RES	66 66

[illegible]

RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [4]
 RX SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=105993;
 RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
 RA Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 RT chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 RN [5]
 RX SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE=7305314; PubMed=4264286;
 RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 RL Biochemistry 11:4899-4903(1972).
 RN [7]
 RP PROCESSING.
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Titani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN [8]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN [9]
 RP SULFATION.
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN [10]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
 RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN [11]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Telemann O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN [12]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1527084;
 RA Selander M., Ullner M., Persson E., Telemann O.,
 RA Stenflo J., Drakenberg T.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
 RL J. Biol. Chem. 267:19642-19649(1992).

RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Trewhella J.;
 RT "The relative orientation of Glu and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";
 RL Biochemistry 35:11547-11559(1996).
 RN [14]
 RP FUNCTION. Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC [15]
 CC CATALYTIC ACTIVITY. Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC [16]
 CC SUBUNIT. THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC [17]
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC [18]
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC [19]
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC [20]
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC [21]
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 CC [22]
 CC EMBL; X00673; CAA25286.1; -.
 CC PIR; A00925; EXBO.
 CC PDB; 1APO; 31-JAN-94.
 CC PDB; 1CCF; 31-MAY-94.
 CC PDB; 1WHE; 15-MAY-97.
 CC PDB; 1WHE; 15-MAY-97.
 CC MEROPS; S01.216; -.
 CC Glycosylated; P00743; -.
 CC InterPro; IPR000152; Asx_hydroxyl.
 CC InterPro; IPR001314; Chymotrypsin.
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR000742; EGF 2.
 CC InterPro; IPR001881; EGF Ca.
 CC InterPro; IPR002383; Gla_blood.
 CC InterPro; IPR001254; Ser_protease_Try.
 CC InterPro; IPR000294; VitK_dep_Gla.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00089; trypsin; 1.
 CC Pfam; PF00594; Gla; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00179; EGF_CA; 1.
 CC SMART; SM00001; EGF_like; 1.
 CC SMART; SM00659; Gla; 1.
 CC SMART; SM00020; Tryp_SPC; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS01187; EGF_CA; 1.
 CC PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE; PS02040; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 CC [23]
 CC SIGNAL
 CC 1
 CC 23
 CC POTENTIAL.

```

FT PROBE 24 40 FACTOR X LIGHT CHAIN.
FT CHAIN 41 180 FACTOR X HEAVY CHAIN.
FT SMIN 183 492 ACTIVATION PEPTIDE.
FT PROBE 183 233 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT CHAIN 234 492 MAY BE REMOVED BUT IS NOT NECESSARY FOR
FT PROBE 476 492 ACTIVATION.
FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 234 492 SERINE PROTEASE.
FT ACT_SITE 275 492 CHARGE RELAY SYSTEM.
FT ACT_SITE 321 321 CHARGE RELAY SYSTEM.
FT ACT_SITE 418 418 CHARGE RELAY SYSTEM.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

Query Match 51.8%; Score 99; DB 1; Length 492;
Best Local Similarity 43.2%; Pred. No. 1.2e-09;
Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANAFLLXLAQGSIXKXKXKQCFXAXFKFKAXTKLFWISY 44
Db 41 ANSFLFEVKGNNLERECLEACSLBEAREVFEDEQTDERWSKY 84

RESULT 7
PRTC_PTC STANDARD; PRT; 459 AA.
ID PRTC_PTC
AC Q9GHP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoprotechomoin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
DE PROC.
GN Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCB1_TaxID=9823;
RN NCB1_TaxID=9823;
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
RA Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
RT protein modeling of membrane binding sites and comparative anatomy of
RT domain."
RU Cell. Mol. Life Sci. 58:148-159(2001).
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the Glu domain. This Glu-independent binding
CC site is necessary for the recognition of the

```

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CC thrombin-thrombomodulin complex.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL, AF191307; AAC28380.1; -.
CC HSP; P04070; 1PCU.
CC MEROPS: S01.218; -.
CC InterPro: IPR000152; Axx_hydroxyl.
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR001881; EGF_Ca.
CC InterPro: IPR002383; Glu_blood.
CC InterPro: IPR001254; Ser_protease_Try.
CC InterPro: IPR00294; Vitk_dep_Glu.
CC Pfam: PF00008; EGF; 2.
CC Pfam: PF00089; trypsin; 1.
CC Pfam: PF00594; Glu; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00001; GLABLOOD.
CC SMART: SM00181; EGF; 2.
CC SMART: SM00001; EGF-like; 2.
CC SMART: SM00069; Glu; 1.
CC SMART: SM00020; Tryp_Spc; 1.
CC PROSITE: PS00010; ASX_HYDROXYL; 1.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS01186; EGF_2; 2.
CC PROSITE: PS01187; EGF_Ca; 1.
CC PROSITE: PS00011; Glu_CARBOXYLATION; 1.
CC PROSITE: PS00240; TRYPSIN_DOM; 1.
CC PROSITE: PS00134; TRYPSIN_HIS; 1.
CC PROSITE: PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Glycoprotein; Serine protease;
CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
CC EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
CC SIGNAL.
CC PROBE 19 41 BY SIMILARITY.
CC CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.
CC CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY
CC SIMILARITY).
CC CHAIN 199 459 PROTEIN C HEAVY CHAIN (BY
CC SIMILARITY).
CC PEPTIDE 199 213 ACTIVATION PEPTIDE (BY SIMILARITY).
CC SITE 213 214 CLEAVAGE (BY THROMBIN) (BY
CC SIMILARITY).
CC DOMAIN 96 131 EGF-LIKE 1.
CC DOMAIN 135 175 EGF-LIKE 2.
CC DOMAIN 214 459 SERINE PROTEASE.
CC MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).
CC MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
CC SIMILARITY).

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FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 255 255 CHARGE RELAY SYSTEM.
FT ACT_SITE 301 301 CHARGE RELAY SYSTEM.
FT ACT_SITE 400 400 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).
FT DISULFID 240 256 BY SIMILARITY.
FT DISULFID 371 385 BY SIMILARITY.
FT DISULFID 396 424 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

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Query Match 51.3%; Score 98; DB 1; Length 459;
Best Local Similarity 45.5%; Pred. No. 1.6e-09;
Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

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Qy 1 ANAFLLXLRQSLKRCXKXQCSFXAFAFKDAXRTLFWISY 44
Db 42 ANGFLEELRPSSELRCKEETCTDEBARERFQNTENTWAFMSKY 85

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RESULT 8

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TMGL_HUMAN STANDARD; PRT; 218 AA.

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AC 014668;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
1).
GN PRG1 OR TMG1 OR PRGP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; Pubmed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
gamma-carboxyglutamic acid proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
modifications of glutamic acid by a vitamin K-dependent gamma-
carboxylase.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF009242; AAB67070.1; -.
CC HSSP; P00740; ICFH.
CC Genew; HGNC:9469; PRG1.
CC MTM; 604428;
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR002294; VltK_dep_GLA.
CC Pfam; PF00594; gla; 1.
CC PRINTS; PR00001; GLABLOOD.

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DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20 POTENTIAL.
FT CHAIN 21 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 21 83 PROTEIN 1.
FT TRANSMEM 84 106 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 107 218 POTENTIAL.
FT DOMAIN 24 61 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 131 135 GLA-RICH.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

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Query Match 50.8%; Score 97; DB 1; Length 218;
Best Local Similarity 40.9%; Pred. No. 1.2e-09;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

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Qy 1 ANAFLLXLRQSLKRCXKXQCSFXAFAFKDAXRTLFWISY 44
Db 21 ANGFLEELRPSSELRCKEETCTDEBARERFQNTENTWAFMSKY 64

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RESULT 9
PRTC_MOUSE STANDARD; PRT; 461 AA.

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AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
factor XIV).
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92316897; Pubmed=1618739;
RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
RT "Isolation and characterization of a mouse protein C cDNA.";
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SvJ;
RC MEDLINE=98152576; Pubmed=9493582;
RA Jalbert L.R., Rosen E.D., Liesens A., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding
anticoagulant protein C.";
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE OF 274-434 FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94318474; Pubmed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nino Y.;
RT "A comparative study of partial primary structures of the catalytic
region of mammalian protein C.";
RL Br. J. Haematol. 86:590-600(1994).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILLA
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
and Villia.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.

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[illegible][illegible]

CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: X64336; CAA45617.1; -.
 DR PIR: S18994; S18994.
 DR PIR: S24312; S24312.
 DR HESP: P04070; 1PCU.
 DR MEROPS: S01.218; -.
 DR InterPro: IPR000152; Asx_hydroxyl-
 DR InterPro: IPR000314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin_1.
 DR Pfam: PF00594; gla_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM000179; EGF_Ca_1.
 DR SMART: SM00001; EGF_like_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; TRYP_SPC_1.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS50240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS_1.
 DR PROSITE: PS00135; TRYPSIN_SER_1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 32
 FT PROPEP 33 41
 FT CHAIN 42 196
 FT PEPTIDE 199 461
 FT SITE 212 213
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 213 461
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70

FT MOD_RES 112 112 (BY SIMILARITY).
 FT ACT_SITE 254 254 HYDROXYLATION (BY SIMILARITY).
 FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
 FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
 FT DISULFID 58 63 BY SIMILARITY.
 FT DISULFID 91 110 BY SIMILARITY.
 FT DISULFID 100 105 BY SIMILARITY.
 FT DISULFID 104 119 BY SIMILARITY.
 FT DISULFID 121 130 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 146 159 BY SIMILARITY.
 FT DISULFID 161 174 BY SIMILARITY.
 FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 239 255 BY SIMILARITY.
 FT DISULFID 373 387 BY SIMILARITY.
 FT DISULFID 398 426 BY SIMILARITY.
 FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF9364BDACD5 CRC64;
 Query Match 50.3%; Score 96; DB 1; Length 461;
 Best Local Similarity 45.3%; Pred. No. 3,7e-09;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 ANAFLLXLRGSLRXCCKXXQCFXAFIFKDXARTKLPISY 44
 Db 42 ANSFLEERFAGSLERECMEETCFEEAOFIFQNVEDTLAFWIKY 85
 ID PA10_HUMAN STANDARD; PRT; 488 AA.
 AC P00742; Q14340;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91216473; PubMed=1902434;
 RA Messier T.L., Plitman D.D., Long G.L., Kaufman R.J., Church W.R.;
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
 RL human coagulation factor X.";
 RN Gene 99:291-294(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87026600; PubMed=3768336;
 RA Leytue S.P., Foster D.C., Kurachi K., Davie B.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RL protein C.";
 RL Biochemistry 25:5098-5102(1986).
 RN [3]
 RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Pung M.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RT blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";

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RL Gene 41:311-314(1986).
RN
RP SEQUENCE OF 41-179.
RX MEDLINE=83257207; PubMed=6871167;
RA McMillen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,
RA Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
RT coagulation factor X: evidence for identification of residue 63 as
RT beta-hydroxyaspartic acid.";
RL Biochemistry 22:2875-2884(1983).
RN
RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=LIVER;
RX MEDLINE=84222026; PubMed=6587384;
RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
RN
RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN
RP SEQUENCE OF 1-23 FROM N.A.
RX MEDLINE=90128299; PubMed=2612918;
RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hameedhushanam K., Lyman G.;
RT "Cloning and characterization of the 5' end (exon 1) of the gene
RT encoding human factor X.";
RL Gene 84:517-519(1989).
RN
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=93360277; PubMed=8355279;
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
RL J. Mol. Biol. 232:947-966(1993).
RN
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=98283982; PubMed=9618463;
RA Kanata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
RT "Structural basis for chemical inhibition of human blood coagulation
RT factor Xa.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HEID TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- PTM: N- AND O-GLYCOSYLATED.
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VITA (IN THE EXTRINSIC PATHWAY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; K03194; AAA52490.1; -.

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DR EMBL; M57285; AAA52421.1; -.
DR EMBL; L29433; AAA52764.1; -.
DR EMBL; L00390; AAA52764.1; JOINED.
DR EMBL; L00391; AAA52764.1; JOINED.
DR EMBL; L00392; AAA52764.1; JOINED.
DR EMBL; L00393; AAA52764.1; JOINED.
DR EMBL; L00394; AAA52764.1; JOINED.
DR EMBL; L00395; AAA52764.1; JOINED.
DR EMBL; L00396; AAA52764.1; JOINED.
DR EMBL; M22613; AAA51984.1; -.
DR EMBL; K01886; AAA52486.1; -.
DR EMBL; M33297; AAA52636.1; -.
DR PIR; A00924; EXHU.
DR PIR; A25853; A25853.
DR PIR; A24478; A24478.
DR PDB; 1HCG; 08-MAY-95.
DR PDB; 1FAX; 29-OCT-97.
DR PDB; 1FXY; 17-JUN-98.
DR PDB; 1XKA; 23-MAR-99.
DR PDB; 1XKB; 23-MAR-99.
DR MEROPS; S01.216; -.
DR GlycoSuiteDB; P00742; -.
DR Genew; HGNC:3528; F10.
DR MIM; 134530; -.
DR MIM; 227600; -.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
FT SIGNAL 1 31
FT PROPEP 32 40
FT CHAIN 41 179
FT CHAIN 183 488
FT PROPEP 183 234
FT CHAIN 235 488
FT DOMAIN 86 122
FT DOMAIN 125 165
FT DOMAIN 235 488
FT MOD_RES 46 46
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FT MOD_RES 55 56
FT MOD_RES 59 59
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FT MOD_RES 65 65
FT MOD_RES 66 66
FT MOD_RES 69 69
FT MOD_RES 72 72
FT MOD_RES 79 79
FT MOD_RES 79 79

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FT MOD RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .)
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .)
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .)
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .)
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .)
FT ACT_SITE 276 276 /FTID=CAR 000013.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110 CHARGE RELAY SYSTEM.
FT DISULFID 112 121 CHARGE RELAY SYSTEM.
FT DISULFID 129 140 CHARGE RELAY SYSTEM.

Query Match 50.3%; Score 96; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 3.9e-09;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXKXCFXAFXPFDARTLFTMSY 44
DB 41 ANSFLEMKKHLREKMEFTCSYEAREVFEDSDKTNEFMNKY 84

RESULT 12
THRB HUMAN STANDARD; PRT; 622 AA.
AC P00734;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId:9606;
RN [1]
RX MEDLINE=8807877; PubMed=2825773;
RA Degen S.J.F., Davie E.W.;
RT "Nucleotide sequence of the gene for human prothrombin."
RL Biochemistry 26:6165-6177(1987).
RN [2]
RX MEDLINE=83231469; PubMed=6105407;
RA Degen S.J.F., McMillivray R.T.A., Davie E.W.;
RT "Characterization of the complementary deoxyribonucleic acid and gene
coding for human prothrombin."
RL Biochemistry 22:2087-2097(1983).
RN [3]
RX MEDLINE=83231469; PubMed=6105407;
RA Degen S.J.F., McMillivray R.T.A., Davie E.W.;
RT "Characterization of the complementary deoxyribonucleic acid and gene
coding for human prothrombin."
RL Biochemistry 22:2087-2097(1983).
RN [4]
RX MEDLINE=77193964; PubMed=266717;
RA Walz D.A., Hewett-Evans D., Seegers W.H.;
RT "Amino acid sequence of human prothrombin fragments 1 and 2."
RL Proc. Natl. Acad. Sci. U.S.A. 74:1963-1972(1977).
RN [5]
RX MEDLINE=77207112; PubMed=8739323;
RA Butkowsky R.J., Elion J., Downing M.R., Mann K.G.;
RT "Primary structure of human prothrombin 2 and alpha-thrombin."
RL J. Biol. Chem. 252:4942-4957(1977).
RN [6]
RX MEDLINE=87008532; PubMed=3759958;
RA Rabiet M.J., Blachill A., Furie B.C.;
RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin
activation in human plasma."
RL J. Biol. Chem. 261:13210-13215(1986).
RN [7]
RX MEDLINE=90059942; PubMed=2583108;
RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
RT "The refined 1.9 A crystal structure of human alpha-thrombin:
interaction with D-Phe-Pro-Arg chloromethylketone and significance of
the Tyr-Pro-Tip insertion segment."
RL EMBO J. 8:3467-3475(1989).
RN [8]
RX MEDLINE=90327074; PubMed=2374926;
RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
RT "The structure of a complex of recombinant hirudin and human alpha-
thrombin."
RL Science 249:277-280(1990).
RN [9]
RX MEDLINE=94350942; PubMed=8071320;
RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
RT "Crystallographic structure of human gamma-thrombin."
RL J. Biol. Chem. 269:22000-22006(1994).
RN [10]
RX MEDLINE=97357286; PubMed=9214615;
RA van de Loch A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,
RT "The thrombin E192Q-BPI complex reveals gross structural
rearrangements: implications for the interaction with antithrombin
and thrombomodulin."
RL EMBO J. 16:2977-2984(1997).
RN [11]
RX MEDLINE=99162521; PubMed=10051558;
RA Guineto E.R., Gaccia S., Rose T., Fuetterer K., Waksman G., di Cera E.;
RT "Unexpected crucial role of residue 225 in serine proteases."
RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
RN [12]
RX MEDLINE=87037379; PubMed=3771562;
RA Rabiet M.-J., Furie B.C., Furie B.;
RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine
for arginine at residue 273."
RL J. Biol. Chem. 261:15045-15048(1986).
RN [13]
RX MEDLINE=95313001; PubMed=7792730;
RA Degen S.J.F., McDowell S.A., Sparks L.W., Scharer I.;
RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by
substitution of Glu-466 by Ala."
RL Thromb. Haemost. 73:203-209(1995).
RN [14]
RX MEDLINE=93043342; PubMed=1421398;
RA Morishita E., Saito M., Kumabashiri I., Asakura H., Matsuda T.,
RT "Prothrombin Himi: a compound heterozygote for two dysfunctional
prothrombin molecules (Met-337-->Thr and Arg-388-->His)."
RL Blood 80:2275-2280(1992).
RN [15]
RX MEDLINE=95169898; PubMed=7865694;
RA James H.L., Kim D.J., Zheng D.-Q., Girolami A.;
RT "Prothrombin Padua I: incomplete activation due to an amino acid
substitution at a factor Xa cleavage site."
RL Blood Coagul. Fibrinolysis 5:841-844(1994).
RN [16]
RX MEDLINE=89207504; PubMed=3242619;
RA Henriksen R.A., Mann K.G.;
RT "Identification of the primary structural defect in the dysprothrombin
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RT thrombin Quick I: substitution of cysteine for arginine-382.";
 RL Biochemistry 27:9160-9165(1988).
 RN [17]
 RP VARIANT QUICK-2.
 RX MEDLINE=89247398; PubMed=2719946;
 RA Henriksen R.A., Mann K.G.;
 RT "Substitution of valine for glycine-558 in the congenital dysfibrinogen
 RL Biochemistry 28:2078-2082(1989).
 RN [18]
 RP VARIANT SALAKTA.
 RX MEDLINE=92378975; PubMed=1354985;
 RA Miyata T., Aruga R., Uneyama H., Bezeaud A., Guillin M.-C.,
 RA Iwanaga S.;
 RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
 RL Biochemistry 31:7457-7462(1992).
 RN [19]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=87185407; PubMed=3567158;
 RA Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,
 RA Iwanaga S.;
 RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
 RL Biochemistry 26:1117-1122(1987).
 RN [20]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=87101511; PubMed=3801671;
 RA Inomoto T., Shirakami A., Kawauchi S., Shigekiyo T., Saito S.,
 RA Miyoshi K., Morita T., Iwanaga S.;
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
 RL Biochem Biophys Res Commun 191:565-569(1997).
 RN [21]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=92256895; PubMed=1349838;
 RA Iwahana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,
 RA Itakura M.;
 RT "Detection of a single base substitution of the gene for prothrombin
 RL Tokushima. The application of PCR-SSCP for the genetic and molecular
 RL Int. J. Hematol. 55:93-100(1992).
 RN [22]
 RP VARIANT TYPE-3.
 RX MEDLINE=83204687; PubMed=6405779;
 RA Board P.G., Shaw D.C.;
 RT "Determination of the amino acid substitution in human prothrombin
 RL type 3 (157 glu leads to lys) and the localization of a third
 RL thrombin cleavage site";
 RL Br. J. Haematol. 54:245-254(1983).
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- CATALYTIC ACTIVITY: preferential cleavage: Arg-|-Gly: activates
 CC fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER, FOUND IN PLASMA.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC -1- DISEASE: DEFECTS IN F2 ARE THE CAUSE OF VARIOUS FORMS OF
 CC DYSFIBRINOGENEMIA.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.

CC -1- MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION
 CC PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN
 CC NATURAL BLOOD CLOTTING.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO, DOES
 CC NOT
 CC Query Match 49.2%; Score 94; DB 1; Length 622;
 CC Best Local Similarity 38.6%; Pred. No. 1.1e-08;
 CC Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
 CC
 CC QY 1 ANAPFLXLRQSLXRXCKXQCSFXAFIFPDAXRTKLFMTSY 44
 CC Db 44 ANTFLEVRKGLNERCVCETCSYGEAFEALESSTATDVFMFKY 87
 CC
 CC RESULT 13
 CC THRB RAT STANDARD; PRT; 617 AA.
 CC AC P18252;
 CC DT 01-NOV-1990 (Rel. 16, Created)
 CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Prothrombin precursor (EC 3.4.21.5).
 CC GN F2.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_TaxID=10116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 CC RX MEDLINE=90332426; PubMed=2377469;
 CC RA Dihanich M., Monard D.;
 CC RT "cDNA sequence of rat prothrombin";
 CC RL Nucleic Acids Res. 18:4251-4251(1990).
 CC RN [2]
 CC RP SEQUENCE OF 383-617 FROM N.A.
 CC RC TISSUE=Liver;
 CC RX MEDLINE=92212913; PubMed=1557383;
 CC RA Banfield D.K., Macgillivray R.T.;
 CC RT "Partial characterization of vertebrate prothrombin cDNAs:
 CC RT amplification and sequence analysis of the B chain of thrombin from
 CC RT nine different species";
 CC RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
 CC CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- CATALYTIC ACTIVITY: preferential cleavage: Arg-|-Gly: activates
 CC fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTRAINS 2 KRINGLE DOMAINS.
 CC -----
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FT DISULFID 264 287 BY SIMILARITY.
FT DISULFID 332 478 INTERCHAIN (BY SIMILARITY).
FT DISULFID 387 403 BY SIMILARITY.
FT DISULFID 532 546 BY SIMILARITY.
FT DISULFID 560 590 BY SIMILARITY.
SQ SEQUENCE 617 AA; 70411 MM; AD27D1B71445DB1D CRC64;

Query Match 47.1% Score 90; DB 1; Length 617;
Best Local Similarity 39.5% Pred. No. 5.5e-08;
Matches 17; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

OY 2 NAFELXLRQGSILRXCKKXOCSPXAXFIFPDAXRTKLFWISY 44
Db 46 SGFEELRKGNLRECEVBEQCSYEAEFAELASPODIDVFMANKY 88

RESULT 14
THRB_MOUSE STANDARD; PRI; 618 AA.
ID_THRB_MOUSE
AC P19221;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2 OR CF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91025551; PubMed=2228210;
RA Friezner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
RA Fitzgibbon J.J., Pal J.-A., Chapman V.M., Elliott R.W.;
RT "Characterization of the cDNA coding for mouse prothrombin and
RT localization of the gene on mouse chromosome 2.";
RL DNA Cell Biol. 9:1487-1498 (1990).
[2]
RP SEQUENCE OF 384-618 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=155783;
RA Bantfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783 (1992).
RU
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C,
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
CC -----
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DR EMBL; X52308; CAA36548.1; -
 DR EMBL; M81394; AAA40435.1; -
 DR PIR; A35827; A35827.
 DR HSSP; P00734; 1B7X.
 DR MEROPS; S01.217; -.
 DR MCD; MGI:88380; F2.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR002383; GLA blood.
 DR InterPro; IPR000001; Kringele.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00051; kringele; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringele; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00011; GLT CARBOXYLATION; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
 KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
 KW Hydrolyase; Serine protease; Kringele; Signal.
 KW SIGNAL 1 24 POTENTIAL.
 FT PROPEP 25 43
 FT CHAIN 44 618 PROTHROMBIN.
 FT PEPTIDE 44 200 ACTIVATION PEPTIDE (FRAGMENT 1).
 FT PEPTIDE 201 324 ACTIVATION PEPTIDE (FRAGMENT 2).
 FT CHAIN 325 360 THROMBIN LIGHT CHAIN (A).
 FT CHAIN 361 618 THROMBIN HEAVY CHAIN (B).
 FT DOMAIN 109 187 KRINGLE 1.
 FT DOMAIN 215 292 KRINGLE 2.
 FT SITE 361 618 SERINE PROTEASE.
 FT SITE 200 201 CLEAVAGE (BY THROMBIN).
 FT SITE 324 325 CLEAVAGE (BY FACTOR XA).
 FT SITE 360 361 CLEAVAGE (BY THROMBIN).
 FT ACT_SITE 403 403 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 459 459 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 565 565 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 63 63 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
 FT DISULFID 61 66 BY SIMILARITY.
 FT DISULFID 91 104 BY SIMILARITY.
 FT DISULFID 109 187 BY SIMILARITY.
 FT DISULFID 130 170 BY SIMILARITY.
 FT DISULFID 158 182 BY SIMILARITY.
 FT DISULFID 215 293 BY SIMILARITY.
 FT DISULFID 236 276 BY SIMILARITY.
 FT DISULFID 264 288 BY SIMILARITY.
 FT DISULFID 333 479 INTERCHAIN (BY SIMILARITY).

FT DISULFID 388 404 BY SIMILARITY.
 FT DISULFID 533 547 BY SIMILARITY.
 FT DISULFID 561 591 BY SIMILARITY.
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 618 AA; 70268 MW; B89F719AAFD6D1ED CRC64;

Query Match 47.1%; Score 90; DB 1; Length 618;
 Best Local Similarity 39.5%; Pred. No. 5.5e-08;
 Matches 17; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 2 NAFLLXRGSLXRXCKXQSEFXAXAFIKDAXTKFWISY 44
 Db 46 SGLEBLKKNLRECEVEBQCSYBFAFALBSPQTDVFWAKY 88

RESULT 15
 TMG3 HUMAN STANDARD; PRT; 231 AA.
 AC Q9BZD7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
 GN TMG3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=spinal cord;
 RX MEDLINE=21117044; Pubmed=11719571;
 RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
 RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
 RT proteins expressed broadly in fetal and adult tissues.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
 CC -1- PTM: Gla residues are produced after subsequent posttranslational
 CC modifications of glutamic acid by a vitamin K-dependent gamma-
 CC carboxylase.

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 DR EMBL; AF326350; AAK00955.1; -
 DR HSSP; P00740; ICFH.
 DR InterPro; IPR002383; GLA blood.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00069; GLA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
 FT PROPEP 1 19 POTENTIAL.
 FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
 FT DOMAIN 20 78 PROTEIN 3.
 FT TRANSMEM 79 101 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 102 231 POTENTIAL.
 FT DOMAIN 23 60 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 23 60 GLA-RICH.
 SQ SEQUENCE 231 AA; 25848 MW; 8A573E4848490D81 CRC64;

Query Match 46.6%; Score 89; DB 1; Length 231;
 Best Local Similarity 38.6%; Pred. No. 3.2e-08;

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model1

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10Gln28PNE
Perfect score: 191
Sequence: 1 ANAFILXRLRGSLRXCKXX.....XXAFILFKDAXRTKLFWISY 44

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	701	4 Q96PQ8	Q96PQ8 homo sapien
2	111	58.1	446	1 Q61109	Q61109 mus musculu
3	97	50.8	460	11 Q91WN8	Q91WN8 mus musculu
4	94	49.2	100	4 Q15253	Q15253 homo sapien
5	91	47.6	460	11 Q99PC6	Q99PC6 mus musculu
6	90	47.1	482	11 Q63207	Q63207 ractus norv
7	88	46.1	456	6 Q9TRR0	Q9TRR0 canis fam1
8	88	46.1	469	6 Q9GMD9	Q9GMD9 ornithorhyn
9	88	46.1	481	11 Q54740	Q54740 mus musculu
10	88	46.1	481	11 Q99L32	Q99L32 mus musculu
11	88	46.1	481	11 Q88947	Q88947 mus musculu
12	80	41.9	456	4 Q14316	Q14316 homo sapien
13	80	41.9	461	6 Q95ND7	Q95ND7 pan troglod
14	79	41.4	49	6 Q95ME8	Q95ME8 bos taurus
15	79	41.4	49	6 Q95ME8	Q95ME8 bos taurus
16	73	38.2	179	4 Q8TAS3	Q8TAS3 homo sapien

17	73	38.2	198	11 Q8R182	Q8R182 mus musculu
18	72	37.7	138	6 Q28994	Q28994 sus scrofa
19	72	37.7	608	13 Q9PTW7	Q9PTW7 struthio ca
20	69	36.1	607	13 Q91001	Q91001 gallus gall
21	67	35.1	443	13 Q90YK1	Q90YK1 brachydanio
22	67	35.1	648	6 Q29094	Q29094 sus scrofa
23	64	33.5	399	11 Q9COW3	Q9COW3 mus musculu
24	62	32.5	98	13 P82807	P82807 notechis sc
25	62	32.5	650	4 Q9NSD0	Q9NSD0 homo sapien
26	62	32.5	650	4 Q16519	Q16519 homo sapien
27	57.5	30.1	542	5 Q8T613	Q8T613 halocynthia
28	55.5	29.1	431	10 Q94EY5	Q94EY5 arabidopsis
29	55.5	29.1	492	10 Q9SMJ7	Q9SMJ7 cicier ariet
30	55.5	29.1	543	10 Q9MB23	Q9MB23 arabidopsis
31	55.5	29.1	576	10 Q9C9U4	Q9C9U4 arabidopsis
32	55.5	29.1	589	10 Q9LMS2	Q9LMS2 arabidopsis
33	55	28.8	25	11 Q9QVH6	Q9QVH6 ractus sp.
34	54.5	28.5	196	10 Q04284	Q04284 selaginella
35	53.5	28.0	459	10 Q9SEB22	Q9SEB22 oryza sativ
36	53	27.7	673	11 Q61592	Q61592 mus musculu
37	53	27.7	674	11 Q99K57	Q99K57 mus musculu
38	52.5	27.5	506	10 Q9SEF0	Q9SEF0 oryza sativ
39	52.5	27.5	506	10 Q9SEB23	Q9SEB23 oryza sativ
40	52.5	27.5	567	10 Q8W4J2	Q8W4J2 arabidopsis
41	51.5	27.0	510	10 Q9MB22	Q9MB22 arabidopsis
42	51.5	27.0	619	10 Q9LV37	Q9LV37 arabidopsis
43	51	26.7	674	11 Q63772	Q63772 ractus sp.
44	51	26.7	678	4 Q14393	Q14393 homo sapien
45	49.5	25.9	588	10 Q9LM33	Q9LM33 arabidopsis

ALIGNMENTS

RESULT 1

Q96PQ8	PRELIMINARY;	PRT;	701 AA.
ID Q96PQ8			
AC Q96PQ8:			
DT 01-DEC-2001 (TREMURel. 19, Created)			
DT 01-DEC-2001 (TREMURel. 19, Last sequence update)			
DT 01-MAR-2002 (TREMURel. 20, Last annotation update)			
DE Factor VII active site mutant immunocoujugate.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX NCBI_taxonomy=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21477448; PubMed=11593034;			
RA Hu Z., Garen A.;			
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor			
RT cells for immunotherapy in mouse models of prostatic cancer.";			
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185 (2001).			
DR EMBL; AF272774; AKS58686.1; -			
DR InterPro; IPR000152; Asx hydroxyl.			
DR InterPro; IPR000561; EGF-like.			
DR InterPro; IPR007742; EGF_2.			
DR InterPro; IPR001881; EGF_Ca.			
DR InterPro; IPR003006; IG_MHC.			
DR InterPro; IPR001254; Ser protease Try.			
DR InterPro; IPR000294; VitK_dep_GLA.			
DR Pfam; PF00008; EGF_2.			
DR Pfam; PF00594; Gla_1.			
DR Pfam; PF00047; IG_2.			
DR Pfam; PF00089; trypsin_1.			
DR SMART; SM00181; EGF_2.			
DR PROSITE; PS00002; ASX_HYDROXYL; UNKNOWN_1.			
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.			
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.			
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.			
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.			
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.			
DR PROSITE; PS50240; TRYPSIN_DOM_1.			

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydroxylase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 81.7%; Score 156; DB 4; Length 701;
Best Local Similarity 72.7%; Pred. No. 1.9e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQGSLLRXCKXKXCSFXXAFIFPDARTKLFWISY 44
Db 61 ANAFLEELRPGSLERCKECCSFEEAREIFPDARTKLFWISY 104

RESULT 2

Q61109 PRELIMINARY; PRT; 446 AA.
ID Q61109;
AC Q61109;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Coagulation factor VII.
DE F7 OR FVII.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96276538; PubMed=8701412;
RA Idnagoge E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RL "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487 (1996).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; U4795; AAC52570.1; -.
DR HSSP; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001114; Chymotrypsin.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR00561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00025; CRYSTALLIN BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylase; Repeat;
KM Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEPDA6870 CRC64;

Query Match 58.1%; Score 111; DB 11; Length 446;

Best Local Similarity 54.5%; Pred. No. 3.2e-12;
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQGSLLRXCKXKXCSFXXAFIFPDARTKLFWISY 44
Db 42 ANSLLEELMPGSLERCKNECCSFEEAREIFKSPERTQFWIV 85

RESULT 3

Q91WN8 PRELIMINARY; PRT; 460 AA.
ID Q91WN8;
AC Q91WN8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to protein C.
DE PROC.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC013896; AAH13896.1; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydroxylase; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 0117F265B8FCC274 CRC64;

Query Match 50.8%; Score 97; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 1.4e-09;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQGSLLRXCKXKXCSFXXAFIFPDARTKLFWISY 44
Db 42 ANSFLERMPGSLERCKNEICDFEEAOEIFQVEDTLAFWIKY 85

RESULT 4

Q15253 PRELIMINARY; PRT; 100 AA.
ID Q15253;
AC Q15253;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Thrombin precursor (Fragment).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; PubMed=3471151;
RA Macgillivray R.T., Irwin D.M., Guinto E.R., Stone J.C.;


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GN F10 OR FA10.
OS Mus musculus (Mouse).
OG Plasmid pluscript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=9845493; PubMed=9783672;
RA Heidemann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AJ222677; CAA10933.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00889; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_CA; 1.
DR SMART; SM00017; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702D5EF9D97AE CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.2e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFPLXLRGSLRXKCKXKXCSFXAFIFPDAXRTKLFMTSY 44
Db 41 ANSFEEFKGNLREKCMELCSYEVRREIFEDDEKTKYWTXY 84

RESULT 10
O99132 PRELIMINARY; PRT; 481 AA.
AC O99132;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; BC003877; AA03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00889; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_CA; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88B96CA0B7E7F CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.2e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFPLXLRGSLRXKCKXKXCSFXAFIFPDAXRTKLFMTSY 44
Db 41 ANSFEEFKGNLREKCMELCSYEVRREIFEDDEKTKYWTXY 84

RESULT 11
O88947 PRELIMINARY; PRT; 481 AA.
AC O88947;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX STRAIN=C57BL6 X CBA; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen B.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=129SJ;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of the Murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC36345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSB; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MG1:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00063; GLA; 1.
DR SMART; SM00020; TRYD_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 1 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5EF9D271E CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.2e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXXQCSFXXAFXIFKDXRTKLFWISY 44
DB 41 ANSFEEFKKGNLRECMERICSYEEVREIFEDDEKTKYWTXY 84

RESULT 12
Q14316 PRELIMINARY; PRT; 456 AA.
AC Q14316;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-AUG-1999 (TREMBlrel. 11, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (plasma THROMBOPLASTIC component, Christmas
DE disease, HAEMOPHILIA B)) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RA [1]
RA SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 3-19 FROM N.A.
RP MEDLINE=88327116; PubMed=3416069;
RX Reitema P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,

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RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSB; P00740; 1CFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR001438; EGF-11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00063; GLA; 1.
DR SMART; SM00020; TRYD_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 41.9%; Score 80; DB 4; Length 456;
Best Local Similarity 42.9%; Pred. No. 2.2e-06;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 10 QGSLXRXCKXXQCSFXXAFXIFKDXRTKLFWISY 44
DB 52 QGNLERECMEKXCSFEAREVFENTERITTEFWKQY 86

RESULT 13
Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RA [1]
RA SEQUENCE FROM N.A.
RA STRAIN=504;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.

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DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS0240; TRYPsin; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
KM Hydrolyase; Serine protease.
SQ SEQUENCE 461 AA; 5164 MW; 30C2F857C0F77F45 CRC64;

Query Match 41.9%; Score 80; DB 6; Length 461;
Best Local Similarity 42.9%; Pred. No. 2.2e-06;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 10 QGSLRXKXKXQCSFXXAFIFKDXRTKLFWISY 44
Db 57 QGNLERCEMEKCSFEAREVFEKTEKTEFWKQY 91

RESULT 14

ID Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Hominidae).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Saita Y.;
RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; -.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS0240; TRYPsin; 1.

DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
KM Hydrolyase; Serine protease.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A5250F65B5 CRC64;

Query Match 41.9%; Score 80; DB 6; Length 461;
Best Local Similarity 42.9%; Pred. No. 2.2e-06;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 10 QGSLRXKXKXQCSFXXAFIFKDXRTKLFWISY 44
Db 57 QGNLERCEMEKCSFEAREVFEKTEKTEFWKQY 91

RESULT 15

ID Q95ME8 PRELIMINARY; PRT; 49 AA.
AC Q95ME8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizlana M.N., Amara E.J.;
RT "Partial sequence of bovine F9 coding gene."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394598; AAK7556.1; -.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6023 MW; DISC6DE9CCBA4A14 CRC64;

Query Match 41.4%; Score 79; DB 6; Length 49;
Best Local Similarity 40.0%; Pred. No. 3.4e-07;
Matches 14; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 10 QGSLRXKXKXQCSFXXAFIFKDXRTKLFWISY 44
Db 14 QGNLERCEMEKCSFEAREVFEKTEKTEFWKQY 48

Search completed: March 19, 2003, 15:13:31
Job time : 47.3125 secs

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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10GLN28PHE
Perfect score: 191
Sequence: 1 ANAFLLXLRQGSLLRXCKX.....XXAFXIFPDAXRTLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	165	86.4	44	3	US-08-955-636-28
2	159	83.2	44	3	US-08-955-636-26
3	158	82.7	44	3	US-08-955-636-30
4	157	82.2	44	3	US-08-955-636-27
5	156	81.7	44	3	US-08-955-636-3
6	156	81.7	406	1	US-08-293-778-24
7	156	81.7	406	1	US-08-295-411-5
8	156	81.7	406	1	US-08-955-471-5
9	156	81.7	406	5	PCT-US92-10242-5
10	156	81.7	444	1	US-08-475-845-2
11	156	81.7	444	2	US-08-327-690-2
12	156	81.7	444	2	US-08-660-289-2
13	156	81.7	444	2	US-08-537-807-2
14	156	81.7	444	2	US-08-871-003-2
15	156	81.7	444	3	US-08-464-233-2
16	156	81.7	444	4	US-09-189-607-2
17	156	81.7	444	4	US-09-378-907-2
18	156	81.7	444	5	PCT-US94-05779-2
19	156	81.7	466	1	US-07-882-202A-4
20	156	81.7	466	1	US-08-021-615A-4
21	156	81.7	466	1	US-08-321-777-4
22	156	81.7	466	4	US-09-009-217-14
23	156	81.7	466	4	US-09-009-656-14
24	156	81.7	466	3	PCT-US93-04493-4
25	150	78.5	44	3	US-08-955-636-29
26	141	73.8	41	1	US-08-229-280-4
27	122	63.9	44	3	US-08-955-636-4

28	105	55.0	139	1	US-08-330-978-2	Sequence 2, Appli
29	105	55.0	139	1	US-08-474-042-2	Sequence 2, Appli
30	105	55.0	139	1	US-08-484-558-2	Sequence 2, Appli
31	105	55.0	139	1	US-08-774-592-2	Sequence 2, Appli
32	105	55.0	437	1	US-08-487-037-2	Sequence 2, Appli
33	105	55.0	437	1	US-08-487-037-3	Sequence 3, Appli
34	105	55.0	488	1	US-08-487-037-1	Sequence 1, Appli
35	99	51.8	44	3	US-08-955-636-18	Sequence 18, Appli
36	99	51.8	487	1	US-08-469-486-53	Sequence 53, Appli
37	99	51.8	487	2	US-08-469-658-53	Sequence 53, Appli
38	99	51.8	492	1	US-08-469-486-2	Sequence 2, Appli
39	99	51.8	492	2	US-08-469-658-2	Sequence 2, Appli
40	97	50.8	44	3	US-08-955-636-24	Sequence 24, Appli
41	96	50.3	448	1	US-08-295-411-3	Sequence 3, Appli
42	96	50.3	448	2	US-08-955-471-3	Sequence 3, Appli
43	96	50.3	448	5	PCT-US92-10068-1	Sequence 1, Appli
44	96	50.3	448	5	PCT-US92-10242-3	Sequence 3, Appli
45	95	49.7	44	3	US-08-955-636-25	Sequence 25, Appli

ALIGNMENTS

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RESULT 1
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955, 636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28

Query Match      86.4%; Score 165; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 3.1e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ANAFLLXLRQGSLLRXCKXQCSFXAXIFPDAXRTLFWISY 44
Db      1 ANAFLLXLRQGSLLRXCKXQCSFXAXIFPDAXRTLFWISY 44

RESULT 2
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955, 636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match 83.2%; Score 159; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 3.2e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXKQCSFXXAFKFDAXRTKLFWISY 44
DB 1 ANAFLLXLRQSLRXCKXKQCSFXXARXIFKDXARTKLFWISY 44

RESULT 3
US-08-955-636-30
Sequence 30, Application US/08955636A
Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelisseu, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FaastSeq for Windows Version 3.0

SEQ ID NO 30

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-30

Query Match 82.7%; Score 158; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 4.8e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXKQCSFXXAFKFDAXRTKLFWISY 44
DB 1 ANAFLLXLRQSLRXCKXKQCSFXXARXIFEDAXRTKLFWISY 44

RESULT 4
US-08-955-636-27

Sequence 27, Application US/08955636A
Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelisseu, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FaastSeq for Windows Version 3.0

SEQ ID NO 27

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-27

Query Match 82.2%; Score 157; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 7.1e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXKQCSFXXAFKFDAXRTKLFWISY 44
DB 1 ANAFLLXLRQSLRXCKXKQCSFXXARXIFKDXARTKLFWISY 44

RESULT 5
US-08-955-636-3
Sequence 3, Application US/08955636A
Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelisseu, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FaastSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-3

Query Match 81.7%; Score 156; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 1e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXKQCSFXXAFKFDAXRTKLFWISY 44
DB 1 ANAFLLXLRQSLRXCKXKQCSFXXARXIFKDXARTKLFWISY 44

RESULT 6
US-08-293-778-24

Sequence 24, Application US/08293778
Patent No. 5580560

GENERAL INFORMATION:

APPLICANT: Nicolaisen, Else M.

APPLICANT: Bjorn, Soren E.

APPLICANT: Wibe, Finn C.

TITLE OF INVENTION: MODIFIED FACTOR VII/VIII

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSER: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.

STREET: 405 Lexington Avenue, 62nd Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/293,778

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/104,509

FILING DATE:

APPLICATION NUMBER: DK 3235/87

FILING DATE: 25-JUN-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/434,149

FILING DATE: 13-NOV-1989

PRIOR APPLICATION DATA:


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: APPLICATION NUMBER: PCT/DK88/00103
: FILING DATE: 24-JUN-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/898,248
: FILING DATE: 12-JUN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Agria, Cheryl H.
: REGISTRATION NUMBER: 34,086
: REFERENCE/DOCKET NUMBER: 3129,224-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-867-0298
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-293-778-24

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Query Match      81.7%; Score 156; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy 1 ANAFLLXLRGSLXRXCKXOCSPFXAFIFPDAXRTKLFWISY 44
Db 1 ANAFLLYLRPGSLYRCKYQCSFYARIFRDAIRTKLFWISY 44

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RESULT 7

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: Sequence 5, Application US/08295411
: Patent No. 5679639

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: GENERAL INFORMATION:
: APPLICANT: Griffin, John H.
: APPLICANT: Mesters, Rolf M.
: TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
: TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
: TITLE OF INVENTION: for Inhibiting Coagulation
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Office of Patent Counsel, The Scripps
: ADDRESSEE: Research Institute
: STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA

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: ZIP: 92037

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: COMPUTER READABLE FORM:

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: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/295,411
: FILING DATE: 22-AUG-1994
: CLASSIFICATION: 530

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: PRIOR APPLICATION DATA:

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: APPLICATION NUMBER: US 07/793,989
: FILING DATE: 18-NOV-1991
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: TSR1263,0C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312

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: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: TYPE: amino acid

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: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..152
: OTHER INFORMATION: /note= "Factor VII Light Chain"
: FEATURE:
: NAME/KEY: Region
: LOCATION: 153..406
: OTHER INFORMATION: /note= "Factor VII Heavy Chain"
: US-08-295-411-5

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Query Match      81.7%; Score 156; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy 1 ANAFLLXLRGSLXRXCKXOCSPFXAFIFPDAXRTKLFWISY 44
Db 1 ANAFLELRPGSLRERCKEEOCSFEAREIFRDAIRTKLFWISY 44

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: Sequence 5, Application US/08955471
: Patent No. 5968751

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: GENERAL INFORMATION:
: APPLICANT: Griffin, John H.
: APPLICANT: Mesters, Rolf M.
: TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
: TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
: TITLE OF INVENTION: for Inhibiting Coagulation
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Office of Patent Counsel, The Scripps
: ADDRESSEE: Research Institute
: STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA

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: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/955,471
: FILING DATE:
: CLASSIFICATION:

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: PRIOR APPLICATION DATA:

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: APPLICATION NUMBER: 08/295,411
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: TSR1263,0C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312

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: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO

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: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..152

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OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153...406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 81.7%; Score 156; DB 2; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQGSIXRCKXQCSFXAXFIFDAXRTKLFWISY 44
Db 1 ANAFLEELRPGSLERCKEKCQCSFEAREIFDARTKLFWISY 44

RESULT 9
PCT-US92-10242-5

Sequence 5, Application PC/TUS9210242

GENERAL INFORMATION:
APPLICANT: Griffin, John H.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242

FILING DATE: 19921118

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989

FILING DATE: 18-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SC0472P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 406 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: Protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: Region

LOCATION: 1..152

OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153...406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match 81.7%; Score 156; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.1e-18;

Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRQGSIXRCKXQCSFXAXFIFDAXRTKLFWISY 44
Db 1 ANAFLEELRPGSLERCKEKCQCSFEAREIFDARTKLFWISY 44

RESULT 10
US-08-475-845-2

Sequence 2, Application US/08475845
Patent No. 578965

GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/327,690

FILING DATE: 24-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/662,920

FILING DATE: 28-FEB-1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 19952-8-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 444 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-475-845-2

Query Match 81.7%; Score 156; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQGSIXRCKXQCSFXAXFIFDAXRTKLFWISY 44
Db 39 ANAFLEELRPGSLERCKEKCQCSFEAREIFDARTKLFWISY 82

RESULT 11
US-08-327-690-2

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; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-690-2

Query Match      81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,289
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2

Query Match      81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY      1 ANAFLLXLRGSLRXCKXKQCSFXAIFKDXARTKLFWISY 44
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Db      39 ANAFLELRPGSLRECKEKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 13
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRQSLXRXCKXQCSFYXAFIFPDARTKLFWISY 44
Db 39 ANAFLEELRPGSLERCKEKEQCSFEAREIFPDARTKLFWISY 82

RESULT 14
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRQSLXRXCKXQCSFYXAFIFPDARTKLFWISY 44
Db 39 ANAFLEELRPGSLERCKEKEQCSFEAREIFPDARTKLFWISY 82

RESULT 15
US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match 81.7%; Score 156; DB 3; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRQSLXRXCKXQCSFYXAFIFPDARTKLFWISY 44
Db 39 ANAFLEELRPGSLERCKEKEQCSFEAREIFPDARTKLFWISY 82

Search completed: March 19, 2003, 15:16:14
Job time : 9.75 secs

GenCore version 5.1.4 p5 4578
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OW protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10Gln28PNE
Perfect score: 191
Sequence: 1 ANAFLLXLRQGSILRXCKXX.....XKAFIFKDXRTLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 22153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 22153

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCRT NEW PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	81.7	406	9	US-10-109-498-1
2	97	50.8	419	9	US-10-182-263-6
3	92	48.2	419	9	US-10-182-263-3
4	92	48.2	419	9	US-10-182-263-4
5	92	48.2	419	9	US-10-182-263-5
6	81	42.4	419	9	US-10-182-263-1
7	81	42.4	419	9	US-09-978-917A-4
8	81	42.4	461	9	US-10-182-263-2
9	81	42.4	461	9	US-09-978-917A-2
10	80	41.9	415	10	US-09-118-748-2
11	80	41.9	461	9	US-10-132-829-5
12	80	41.9	461	10	US-09-884-901-3
13	66.5	34.8	96	9	US-09-759-130B-313
14	66.5	34.8	209	9	US-09-759-130B-310
15	66.5	34.8	226	9	US-09-759-130B-310
16	51.5	27.0	908	9	US-09-759-130B-356
17	51.5	27.0	208	9	US-09-759-130B-355
18	51.5	27.0	225	9	US-09-759-130B-353
19	45.5	23.8	729	9	US-10-145-396-11

20	44.5	23.3	347	10	US-09-780-053-4	Sequence 4, Appli
21	44.5	23.3	730	9	US-10-145-396-12	Sequence 12, Appli
22	44.5	23.3	730	10	US-09-780-053-2	Sequence 2, Appli
23	41	21.5	88	10	US-09-811-284-194	Sequence 194, App
24	40	20.9	240	9	US-09-782-504-4	Sequence 4, Appli
25	40	20.9	447	10	US-09-815-242-13490	Sequence 13490, A
26	40	20.9	447	10	US-09-815-242-13612	Sequence 13612, A
27	40	20.9	447	10	US-09-735-564-2	Sequence 2, Appli
28	39	20.4	115	9	US-09-883-152-21	Sequence 21, Appli
29	39	20.4	115	9	US-09-986-480-192	Sequence 192, App
30	39	20.4	130	9	US-09-986-480-345	Sequence 345, App
31	39	20.4	254	9	US-10-104-019-21	Sequence 21, Appli
32	39	20.4	873	9	US-10-200-154-2	Sequence 2, Appli
33	39	20.4	873	10	US-09-954-043-2	Sequence 2, Appli
34	38.5	20.2	111	10	US-09-899-896-7	Sequence 7, Appli
35	38.5	20.2	206	10	US-09-970-711-13	Sequence 13, Appli
36	38	19.9	47	10	US-09-739-254-109	Sequence 109, App
37	38	19.9	47	10	US-09-904-615-109	Sequence 109, App
38	38	19.9	176	9	US-10-078-770-106	Sequence 106, App
39	38	19.9	273	9	US-09-764-668-968	Sequence 968, App
40	38	19.9	333	9	US-09-738-626-5683	Sequence 5683, Ap
41	38	19.9	400	9	US-10-078-770-114	Sequence 114, App
42	38	19.9	608	10	US-09-908-664-5	Sequence 2, Appli
43	38	19.9	1266	9	US-09-931-969A-2	Sequence 2, Appli
44	38	19.9	1266	9	US-10-079-699-2	Sequence 2, Appli
45	38	19.9	1266	10	US-09-757-781-63	Sequence 63, Appli

ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286, 200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/261,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      81.7%; Score 156, DB 9; Length 406;
Best local Similarity 95.5%; Pred. No. 5.36-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 ANAFLLXLRQGSILRXCKXXCSPFXAXFIFKDXRTLFWISY 44
Db 1 ANAFLLXLRPGSLRXCKXXCSPFXAXFIFKDXRTLFWISY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E
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ORGANISM: Homo sapiens
US-10-182-263-1

Query Match 42.4%; Score 81; DB 9; Length 419;
Best Local Similarity 43.9%; Pred. No. 1.5e-06;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFIXLRQGSIXKXCKXQCSFXKAFIFKDXARTKLFW 41
DB 1 ANSFLELRHSSLERECEIEICDFEAKEIFQNVDDTLAFW 41

RESULT 7

US-09-978-917A-4
Sequence 4, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT

ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match 42.4%; Score 81; DB 9; Length 419;
Best Local Similarity 43.9%; Pred. No. 1.5e-06;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFIXLRQGSIXKXCKXQCSFXKAFIFKDXARTKLFW 41
DB 1 ANSFLELRHSSLERECEIEICDFEAKEIFQNVDDTLAFW 41

RESULT 8

US-10-182-263-2
Sequence 2, Application US/10182263
Publication No. US2003002354A1

GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan B
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT

ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 42.4%; Score 81; DB 9; Length 461;
Best Local Similarity 43.9%; Pred. No. 1.7e-06;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFIXLRQGSIXKXCKXQCSFXKAFIFKDXARTKLFW 41
DB 43 ANSFLELRHSSLERECEIEICDFEAKEIFQNVDDTLAFW 83

RESULT 9

US-09-978-917A-2
Sequence 2, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT

ORGANISM: Homo sapiens

NAME/KEY: SIGNAL
LOCATION: (1)...(42)
FEATURE:
NAME/KEY: CHAIN
LOCATION: (43)...(461)
US-09-978-917A-2

Query Match 42.4%; Score 81; DB 9; Length 461;
Best Local Similarity 43.9%; Pred. No. 1.7e-06;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFIXLRQGSIXKXCKXQCSFXKAFIFKDXARTKLFW 41
DB 43 ANSFLELRHSSLERECEIEICDFEAKEIFQNVDDTLAFW 83

RESULT 10

US-09-118-748-2
Sequence 2, Application US/09118748A
Patent No. US20020031799A1

GENERAL INFORMATION:
APPLICANT: Stafford, Darrel W.
APPLICANT: Chang, Jinli
TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
FILE REFERENCE: 5470-183
CURRENT APPLICATION NUMBER: US/09/118,748A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,571
EARLIER FILING DATE: 1997-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 415
TYPE: PRT

ORGANISM: Homo sapiens
US-09-118-748-2

Query Match 41.9%; Score 80; DB 10; Length 415;
Best Local Similarity 42.9%; Pred. No. 2.3e-06;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

OY 10 QGSLRXCKXKXQCSFXKAFIFKDXARTKLFWISY 44
DB 11 QGNLERCEMEKCSFEAREVFEVNTERTTEFWKQY 45

RESULT 11

US-10-132-829-5
Sequence 5, Application US/10132829
Publication No. US20030044982A1

GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII
FILE REFERENCE: 6627-PAL170

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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match
Best Local Similarity 41.9%; Score 80; DB 9; Length 461;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 10 QGSLKRXCKXQCSFYXAFIFDAXRTKLFWISY 44
Db 57 QGNLERECMEKCSFEAREVFENTERTEFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: USFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO: 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-901-3

Query Match
Best Local Similarity 41.9%; Score 80; DB 10; Length 461;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 10 QGSLKRXCKXQCSFYXAFIFDAXRTKLFWISY 44
Db 57 QGNLERECMEKCSFEAREVFENTERTEFWKQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtel, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match
Best Local Similarity 34.8%; Score 66.5; DB 9; Length 96;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

Qy 2 NAF-LXXLRGSLKRXCKXQCSFYXAFIFDAXRTKLFWISY 44
Db 36 NRPDELFTPTGNLERECMEKCSFEAREVFENTERTEFWKQY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtel, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-10-19
```



```

; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-312

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Query Match      34.8%; Score 66.5; DB 9; Length 209;
Best Local Similarity 36.4%; Pred. No. 0.00029;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

```

```

QY      2 NAF-LXXLRQSLXRCXXCSPFXAIFKDXARTKLFWISY 44
DB      36 NRPDLLEFTPGNLERECNEELCNYEAREIFVDEDKTIAFWQY 79

```

RESULT 15

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US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT

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```

; ORGANISM: Homo sapiens
US-09-759-130B-310

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```

Query Match      34.8%; Score 66.5; DB 9; Length 226;
Best Local Similarity 36.4%; Pred. No. 0.00031;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

```

```

QY      2 NAF-LXXLRQSLXRCXXCSPFXAIFKDXARTKLFWISY 44
DB      53 NRPDLLEFTPGNLERECNEELCNYEAREIFVDEDKTIAFWQY 96

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Search completed: March 20, 2003, 13:30:11
Job time : 9.375 secs

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds
(without alignments)
186.869 Million cell updates/sec

Title: 10GLU28GLU
Perfect score: 190
Sequence: 1 ANAFLLXRLREGSLXRXCKX.....XXAEXIFMDAXRTKLFWISY 44

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_101002.*
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	86.8	44	20	AAV18310
2	162	85.3	44	20	AAV18311
3	159	83.7	44	20	AAV18305
4	159	83.7	44	22	AAAB36395
5	159	83.7	401	22	AAAB84870
6	159	83.7	401	22	AAAB84871
7	159	83.7	406	14	AAAB35764
8	159	83.7	406	18	AAW14509
9	159	83.7	406	18	AAW14510
10	159	83.7	406	22	AAU77745

11	159	83.7	406	22	AAW52171	Human FVII SEQ ID
12	159	83.7	406	22	AAW52172	Mammalian expresse
13	159	83.7	406	22	AAW52181	Human FVII mutant
14	159	83.7	406	22	AAW52182	Human FVII mutant
15	159	83.7	406	22	AAW52183	Human FVII mutant
16	159	83.7	406	22	AAW52184	Human FVII mutant
17	159	83.7	406	22	AAW52185	Human FVII mutant
18	159	83.7	406	22	AAW52186	Human FVII mutant
19	159	83.7	406	22	AAW52187	Human FVII mutant
20	159	83.7	406	22	AAW52188	Wild-type human b1
21	159	83.7	406	22	AAW52189	Mutant blood coagu
22	159	83.7	406	22	AAW52190	Mutant blood coagu
23	159	83.7	406	22	AAW52191	Mutant blood coagu
24	159	83.7	406	22	AAW52192	Human coagulation
25	159	83.7	406	22	AAW52193	Human coagulation
26	159	83.7	406	22	AAW52194	Human coagulation
27	159	83.7	406	22	AAW52195	Human coagulation
28	159	83.7	406	22	AAW52196	Human coagulation
29	159	83.7	406	22	AAW52197	Human coagulation
30	159	83.7	406	22	AAW52198	Human coagulation
31	159	83.7	406	22	AAW52199	Human coagulation
32	159	83.7	406	22	AAW52200	Human coagulation
33	159	83.7	406	22	AAW52201	Human coagulation
34	159	83.7	406	22	AAW52202	Human coagulation
35	159	83.7	406	22	AAW52203	Human coagulation
36	159	83.7	406	22	AAW52204	Human coagulation
37	159	83.7	406	22	AAW52205	Human coagulation
38	159	83.7	406	22	AAW52206	Human coagulation
39	159	83.7	406	22	AAW52207	Human coagulation
40	159	83.7	406	22	AAW52208	Human coagulation
41	159	83.7	406	22	AAW52209	Human coagulation
42	159	83.7	406	22	AAW52210	Human coagulation
43	159	83.7	406	22	AAW52211	Human coagulation
44	159	83.7	406	22	AAW52212	Human coagulation
45	159	83.7	406	22	AAW52213	Human coagulation

ALIGNMENTS

RESULT 1	AAV18310	standard; peptide; 44 AA.
ID	AAV18310	
AC	AAV18310;	
XX		
DT	17-AUG-1999	(first entry)
XX		
DE	Modified GLA domain of vitamin K-dependent protein.	
XX		
KW	GLA domain; muten; vitamin K-dependent protein; clotting disorder;	
KW	therapy.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 1..44	
FT	FT	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX		
PN	WO9920767-A1.	
XX		
PD	29-APR-1999.	
XX		
PF	20-OCT-1998;	98WO-US22152.
XX		
PR	23-OCT-1997;	97US-0955636.
XX		
PA	(MINU) UNIV MINNESOTA.	
XX		
PI	Nelstuen GL;	
XX		

```
DR WP1; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 80; 86pp; English.
XX
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;
Query Match 86.8%; Score 165; DB 20; Length 44;
Best Local Similarity 97.7%; Pred. No. 2e-20;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps
CY 1 ANAFPLXLRBGSILKRXCKXCOCSPFXAXEJFKDAXRTKLFWISY 44
1 ANAFPLXLRBGSILKRXCKXCOCSPFXAXEJFKDAXRTKLFWISY 44
ID AAY18311 standard; peptide; 44 AA.
XX
XX AAY18311;
AC 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KM therapy.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
FT
XX
XX WO9920767-A1.
XX
XX PD 29-APR-1999.
XX
XX PF 20-OCT-1998; 98WO-US22152.
XX
XX PR 23-OCT-1997; 97US-0955636.
XX
XX PA (MINU ) UNIV MINNESOTA.
XX
XX PI Neibeetuen GL;
XX
XX WP1; 1999-288309/24.
XX
XX DR Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 80; 86pp; English.
```

CC	GLA domain results in a protein which has enhanced membrane binding	
CC	affinity as compared to the native protein.	
xx		
xx		
SO	Sequence	44 AA;
	Query Match	85.3%; Score 162; DB 20; Length 44;
	Best Local Similarity	95.5%; Pred. No. 6,3e-20;
	Matches	42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy	1	ANAFLLXLRGSLRXKXQCSFXXAEXIFKDAKRTKLFWISY 44
		: : : : : :
Db	1	ANAFLLXLRDGSILRXKXQCSFXXAEXIFKDAKRTKLFWISY 44
		: : : : : :
RESULT 3		
ID	AAI18305	standard; peptide; 44 AA.
xx	AAI18305;	
AC	AAI18305;	
xx	17-AUG-1999	(first entry)
DT	xx	
xx	xx	
DE	Human factor VII GLA domain.	
xx	xx	
KM	GLA domain; vitamin K-dependent protein; clotting disorder;	
KW	therapy.	
xx	xx	
OS	Homo sapiens.	
xx	xx	
PH	Key	Location/Qualifiers
FT	Misc-difference	1..44
FT	/note=	"Xaa= gamma-carboxyglutamic acid, or glutamic acid"
xx	xx	
PN	MO9920767-A1.	
xx	xx	
PD	29-APR-1999.	
xx	xx	
PF	20-OCT-1998;	98WC-US22152.
xx	xx	
PR	23-OCT-1997;	97US-0955636.
xx	xx	
PA	(MINU) UNIV MINNESOTA.	
xx	xx	
PI	Nelsetuen GL;	
xx	xx	
DR	WPI. 1999-288309/24.	
xx	xx	
PT	Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic	
xx	acid domain, useful for treating clotting disorders	
PS	Disclosure; Page 15; 86pp; English.	
xx	xx	
CC	This sequence is the factor VII GLA (gamma-carboxyglutamic acid)	
CC	domain. The invention relates to a vitamin K-dependent polypeptide	
CC	comprising a modified GLA domain containing an amino acid substitution	
CC	which enhances membrane binding of the modified polypeptide as compared	
CC	to the native polypeptide. The polypeptide is used to treat a clotting	
CC	disorder by decreasing or increasing clot formation. Modification of the	
CC	GLA domain results in a protein which has enhanced membrane binding	
CC	affinity as compared to the native protein.	
xx	xx	
xx	xx	
SO	Sequence	44 AA;
	Query Match	83.7%; Score 159; DB 20; Length 44;
	Best Local Similarity	95.5%; Pred. No. 2e-19;
	Matches	42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1	ANAFLLXLRGSLRXKXQCSFXXAEXIFKDAKRTKLFWISY 44
		: : : : : :
Db	1	ANAFLLXLRPGSLRXKXQCSFXXAEXIFKDAKRTKLFWISY 44
		: : : : : :

RESULT 4
 AAB36395
 ID AAB36395 standard; peptide; 44 AA.
 XX
 AC AAB36395;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX
 KW Vitamin K-dependent protein; factor VII; protein C; GIIA domain;
 KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KW factor X; prothrombin; enhanced membrane binding affinity;
 KW clot formation; thrombolytic; haemostatic; bleeding disorder;
 KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KW liver disease.
 XX
 OS Homo sapiens.
 XX
 PN MO20006753-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US11416.
 XX
 PR 29-APR-1999; 99US-0302239.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Neiseetuen GL;
 XX
 DR WPI, 2001-007226/01.
 XX
 DT Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprising modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity -
 XX
 PS Disclosure: Page 12; 81pp; English.
 XX
 CC The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GIIA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot
 CC formation in a mammal, a factor VII or factor IX containing a modified
 CC GIIA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type human factor VII GIIA domain sequence, given in
 CC the exemplification of the present invention.
 CC
 XX
 SQ Sequence 44 AA;
 XX
 Query Match 83.7%; Score 159; DB 22; Length 44;
 Best Local Similarity 95.5%; Pred. No. 2e-19; Indels 0; Gaps 0;
 Matches 42; Conservative 0; Mismatches 2;
 Oy 1 ANAFLXLRGSLXRXCKXQCSFYXAEIIFPDARTKLFWISY 44
 |||||
 Db 1 ANAFLXLRGSLXRXCKXQCSFYXAEIIFPDARTKLFWISY 44
 |||||
 RESULT 5
 AAB84870
 ID AAB84870 standard; Protein; 401 AA.
 XX
 AC AAB84870;
 XX
 DT 31-JUL-2001 (first entry)
 XX

DE Mutant blood coagulant factor VII (FVII-31).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 311..317
 FT /note= "Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
 -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX
 PD JP2001061479-A.
 XX
 PF 13-MAR-2001.
 XX
 PF 24-AUG-1999; 99JP-0237610.
 XX
 PR 24-AUG-1999; 99JP-0237610.
 XX
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 DR WPI, 2001-310677/33.
 DR N-PSDB; AAH19463.
 XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 XX
 PS Claim 14; Page 20-21; 29pp; Japanese.
 XX
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.
 CC
 XX
 SQ Sequence 401 AA;
 XX
 Query Match 83.7%; Score 159; DB 22; Length 401;
 Best Local Similarity 72.7%; Pred. No. 1.9e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Oy 1 ANAFLXLRGSLXRXCKXQCSFYXAEIIFPDARTKLFWISY 44
 |||||
 Db 1 ANAFLXLRGSLXRXCKXQCSFYXAEIIFPDARTKLFWISY 44
 |||||
 RESULT 6
 AAB84871
 ID AAB84871 standard; Protein; 401 AA.
 XX
 AC AAB84871;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Mutant blood coagulant factor VII (FVII-39).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 235..239
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
 Asp-Arg-Lys-Thr-Leu"
 FT Misc-difference 311..317
 FT /note= "Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
 -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX
 PN JP2001061479-A.
 XX

```

PD 13-MAR-2001.
XX
XX 24-AUG-1999; 99QP-0237610.
XX
XX 24-AUG-1999; 99QP-0237610.
XX
PA (KAGA ) ZH KAGAKU & KESSHI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
XX
XX N-PSDB; AAH19464.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
XX Claim 16; Page 23-24; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-39. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX Sequence 401 AA;
SQ
Query Match 83.7%; Score 159; DB 22; Length 401;
Best Local Similarity 72.7%; Pred. No. 1.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKCKXQCSFXXAEXIFKDAKRTKLFWISY 44
Db 1 ANAFLELRGSLRCKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 7
AA35764
ID AAR35764 standard; protein; 406 AA.
XX
XX AAR35764;
XX
XX 24-SEP-1993 (first entry)
XX
XX Factor VII (VII).
XX
XX PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
XX Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
XX exosite; catalytic activity.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 1..152
XX Region /note= "Factor VII light chain"
XX FT 153..406
XX Region /note= "Factor VII heavy chain"
XX FT 374..388
XX Peptide /note= "exosite 1"
XX FT 290..310
XX Peptide /note= "exosite 2"
XX FT 290..310
XX Peptide /note= "pref. PC polypeptide; claim 2, page 136"
XX FT 374..388
XX Peptide /note= "pref. PC polypeptide; claim 2, page 136"
XX FT 289..304
XX Peptide /note= "pref. PC polypeptide; claim 4, page 137"
XX FT 290..304
XX Peptide /note= "pref. PC polypeptide; claim 4, page 137"
XX FT 245..266
XX Peptide /note= "claim 9, page 138-139 describes an antibody
XX that reacts with Factor VII; fragments
XX 289-304, 290-304, 290-310, 374-388 and
XX 400-414 but not with fragment 245-266"
XX
XX PN W09309804-A.
XX

```

```

PD 27-MAY-1993.
XX
XX 18-NOV-1992; 92WO-US10242.
XX
XX 18-NOV-1991; 91US-0793989.
XX
XX (SCRI ) SCRIPS RES INST.
XX
XX Griffin JH, Meesters RM;
XX
XX WPI; 1993-182244/22.
XX
XX Serine protease derived-polypeptide(s) and anti-peptide
XX antibodies - for inhibiting coagulation and assaying for the
XX presence of serine protease in fluid samples
XX
XX Disclosure; Page 133-135; 149pp; English.
XX
XX The PC polypeptides indicated in the Features Table inhibit
XX coagulation (they prevent binding of serine protease to natural
XX substrates), esp. when admin. to give an intravascular blood
XX concn. of 0.1-100 (pref. 0.5-10) microm.
XX
XX NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
XX in the specification but have not yet been added to the SEQUENCE
XX LISTING.
XX
XX Sequence 406 AA;
SQ
Query Match 83.7%; Score 159; DB 14; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKCKXQCSFXXAEXIFKDAKRTKLFWISY 44
Db 1 ANAFLELRGSLRCKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 8
AAW14509
ID AAW14509 standard; protein; 406 AA.
XX
XX AAW14509;
XX
XX 14-MAY-1997 (first entry)
XX
XX Modified blood coagulation Factor VII (R290S).
XX
XX Blood coagulation; factor 7; mutation; modification;
XX thrombocytopenia; von Willebrand's disease; plasma substitute.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH 6
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 7
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 14
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 16
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 19
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 20
XX Modified-site /label= OTHER
XX FT /note= "gamma-carboxylutamic acid"
XX FT 17..22
XX Disulfide-bond
XX

```

FT	Modified-site	25	//label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	26	//label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	29	//label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	32..33	/note= "proteolytic site"
FT		35	//label= OTHER
FT		/note= "gamma-carboxyglutamic acid"	
FT	Cleavage-site	38..39	/note= "proteolytic site"
FT		42..43	/note= "proteolytic site"
FT	Cleavage-site	44..45	/note= "proteolytic site"
FT		/note= "proteolytic site"	
FT	Disulfide-bond	50..61	/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	55..70	/note= "proteolytic site"
FT	Modified-site	63	//label= OTHER
FT		/note= "beta-hydroxy-aspartic acid"	
FT	Disulfide-bond	72..81	/note= "proteolytic site"
FT	Disulfide-bond	91..102	/note= "proteolytic site"
FT	Disulfide-bond	98..112	/note= "proteolytic site"
FT	Disulfide-bond	114..127	/note= "proteolytic site"
FT	Disulfide-bond	135..162	/note= "proteolytic site"
FT	Cleavage-site	143..144	/note= "proteolytic site"
FT	Modified-site	145	/note= "proteolytic site"
FT		/note= "glycosylation site"	
FT	Disulfide-bond	159..164	/note= "proteolytic site"
FT	Disulfide-bond	178..194	/note= "proteolytic site"
FT	Active-site	193	/note= "proteolytic site"
FT	Active-site	242	/note= "proteolytic site"
FT	Active-site	344	/note= "proteolytic site"
FT	Cleavage-site	290..291	/note= "proteolytic site"
FT	Misc-difference	290	/note= "proteolytic site in unmodified factor VII"
FT		/note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"	
FT	Disulfide-bond	310..329	/note= "proteolytic site"
FT	Cleavage-site	315..316	/note= "proteolytic site"
FT	Modified-site	322	/note= "glycosylation site"
FT	Disulfide-bond	340..368	/note= "proteolytic site"
FT	Cleavage-site	341..342	/note= "proteolytic site"
FT	Cleavage-site	392..393	/note= "proteolytic site"
FT	Cleavage-site	396..397	/note= "proteolytic site"
FT	Cleavage-site	402..403	/note= "proteolytic site"
FT		/note= "proteolytic site"	
PN	US5580560-A.		
PD	03-DEC-1996.		
XX			
PF	13-NOV-1989;	89US-0434149.	
XX			
PR	09-AUG-1993;	93US-0104509.	
PR	13-NOV-1989;	89US-0434149.	
PR	12-JUN-1992;	92US-0898248.	
PR	22-AUG-1994;	94US-0293778.	
XX			
PA	(NOVO) NOVO-NORDISK AS.		
XX			

PI	Bjorn SE, Nicolaissen EM, Wiberg FC, Woodbury R;	
DR	WPI, 1997-033523/03.	
XX		
PT	Mutated human factor VII or VIIa proteins - with amino acid	
PT	substitutions to improve proteolytic stability	
PS	Example 3; Page -: 28pp; English.	
XX		
CC	Modified human factor VII or VIIa proteins are stabilised against	
CC	proteolytic cleavage by substitution of one of the residues Lys32,	
CC	Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and	
CC	Lys341 by an amino acid that provides a proteolytically more stable	
CC	peptide bond, provided that Lys32 is replaced by Gln, Glu, His,	
CC	Gly, Thr, Ala or Ser. The modified proteins are useful for treating	
CC	bleeding disorders such as thrombocytopenia and von Willebrand's	
CC	disease. They are also suitable for addition to plasma substitutes.	
CC	The present sequence is a specific example of a modified factor VII	
CC	protein.	
SQ	Sequence 406 AA;	
	Query Match 83.7%; Score 159; DB 18; Length 406;	
	Best Local Similarity 72.7%; Pred. No. 1.9e-18;	
	Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0	
OY	1 ANAFPLXLRGSLRXKCKXKQCSFPXAEKIFPDARTKLFWISY 44	
Db	1 ANAFLELRPGSLRECKECCSFEARERIFDARTKLFWISY 44	
	RESULT 9	
AAWI4510	ID AAWI4510 standard; protein; 406 AA.	
XX		
AC	AAWI4510;	
XX		
DT	14-MAY-1997 (first entry)	
XX		
DE	Modified blood coagulation Factor VII (B3156).	
XX		
KW	Blood coagulation; factor 7; mutein; mutation; modification;	
KW	thrombocytopenia; von Willebrand's disease; plasma substitute.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FH	Modified-site	6
FT	/label= OTHER	
FT	/note= "gamma-carboxylutamic acid"	
FT		
FT	Modified-site	7
FT	/label= OTHER	
FT	/note= "gamma-carboxylutamic acid"	
FT		
FT	Modified-site	14
FT	/label= OTHER	
FT	/note= "gamma-carboxylutamic acid"	
FT		
FT	Modified-site	16
FT	/label= OTHER	
FT	/note= "gamma-carboxylutamic acid"	
FT		
FT	Modified-site	19
FT	/label= OTHER	
FT	/note= "gamma-carboxylutamic acid"	
FT		
FT	Modified-site	20
FT	/label= OTHER	
FT	/note= "gamma-carboxylutamic acid"	
FT		
FT	Disulfide-bond	17..22
FT	Modified-site	25
FT	/label= OTHER	
FT	/note= "gamma-carboxylutamic acid"	
FT		
FT	Modified-site	26
FT	/label= OTHER	
FT	/note= "gamma-carboxylutamic acid"	

```

FT Modified-site 29
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 32..33
FT /note= "proteolytic site"
FT Modified-site 35
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 38..39
FT /note= "proteolytic site"
FT Cleavage-site 42..43
FT /note= "proteolytic site"
FT Cleavage-site 44..45
FT /note= "proteolytic site"
FT Disulfide-bond 50..61
FT Disulfide-bond 55..70
FT Modified-site 63
FT /label= OTHER
FT /note= "beta-hydroxy-aspartic acid"
FT Disulfide-bond 72..81
FT Disulfide-bond 91..102
FT Disulfide-bond 98..112
FT Disulfide-bond 114..127
FT Disulfide-bond 135..162
FT Cleavage-site 143..144
FT /note= "proteolytic site"
FT Modified-site 145
FT /note= "glycosylation site"
FT Disulfide-bond 159..164
FT Disulfide-bond 178..194
FT Active-site 193
FT Active-site 242
FT Active-site 344
FT Cleavage-site 290..291
FT /note= "proteolytic site"
FT Disulfide-bond 310..329
FT Cleavage-site 315..316
FT /note= "proteolytic site in unmodified factor VII"
FT Misc-difference 315
FT /note= "active Arg315 has been substituted by Ser to
FT provide a proteolytically more stable peptide
FT bond"
FT Modified-site 322
FT /note= "glycosylation site"
FT Disulfide-bond 340..368
FT Cleavage-site 341..342
FT /note= "proteolytic site"
FT Cleavage-site 392..393
FT /note= "proteolytic site"
FT Cleavage-site 396..397
FT /note= "proteolytic site"
FT Cleavage-site 402..403
FT /note= "proteolytic site"
FT US560560-A.
FT PD 03-DEC-1996.
FT PF 13-NOV-1989; 89US-0434149.
FT XX 09-AUG-1993; 93US-0104509.
FT PR 13-NOV-1989; 89US-0434149.
FT PR 12-JUN-1992; 92US-0898248.
FT PR 22-AUG-1994; 94US-0293778.
FT XX (NOVO ) NOVO-NORDISK AS.
FT PA
FT XX Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
FT DR MPI; 1997-033523/03.
FT Mutated human factor VII or VIIa proteins - with amino acid
FT substitutions to improve proteolytic stability

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XX
PS Example 4; Page -; 28pp; English.
XX
CC Modified human factor VII or VIIa proteins are stabilised against
CC proteolytic cleavage by substitution of one of the residues Lys32,
CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
CC Lys341 by an amino acid that provides a proteolytically more stable
CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
CC bleeding disorders such as thrombocytopenia and von Willebrand's
CC disease. They are also suitable for addition to plasma substitutes.
CC The present sequence is a specific example of a modified factor VII
CC protein.
XX
SQ Sequence 406 AA;
XX
Query Match 83.7%; Score 159; DB 18; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
QY 1 ANAFLLXXLRGSLXRXCKXXQCSEFXAXEXIFKDXRTXLFWISY 44
DB 1 ANAFLELRPGLSRCKEKCSEFEARETFKDAERTKLFWISY 44
XX
RESULT 10
AAU77745
ID AAU77745 standard; protein; 406 AA.
XX
AC AAU77745;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human factor VIIa active site mutant.
XX
XX Factor VIIa; human; shock heat treatment; protein stability;
XX KW protein manufacture; protein conformation; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH 193
XX FT Active-site /note= "Member of the factor VIIa catalytic triad"
XX FT Active-site 242 /note= "Member of the factor VIIa catalytic triad"
XX FT Active-site 344 /note= "Member of the factor VIIa catalytic triad"
XX FT Misc-difference 344
XX FT /label= Gly, Met, Thr
XX FT /note= "Preferably Ala. Wild type Ser"
XX
XX MO200177141-A1.
XX PN
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-DK00234.
XX PR 06-APR-2000; 2000DK-0000573.
XX PR 17-APR-2000; 2000US-197650P.
XX
XX (NOVO ) NOVO NORDISK AS.
XX PA
XX Matchiesen F;
XX DR MPI; 2001-657162/75.
XX
XX Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX PT involves a shock heat treatment -
XX PS Disclosure; Page -; 22pp; English.
XX The invention describes a method of stabilising a polypeptide involving

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CC shock heat treatment of the polypeptide. The method is useful in a
 CC pharmaceutical composition, in the industrial or large scale method of
 CC manufacturing a polypeptide, also as a unit operation during preparation,
 CC purification, recovery and/or formulation of polypeptides. The shock heat
 CC treatment improves the protein stability without substantial loss of
 CC biological activity. The method can be applied to change polypeptide
 CC conformation in a very fast and non-invasive manner. The polypeptide
 CC formed is stable. The method is also useful for decreasing the
 CC association of the polypeptide. This sequence represents a modified
 CC human factor VIIa protein, mutated at the catalytic site, described
 CC in the invention.
 CC Note: This sequence does not appear in the specification but has
 CC been obtained using information given in the invention.

CC Sequence 406 AA;

Query Match 83.7%; Score 159; DB 22; Length 406;
 Best Local Similarity 72.7%; Pred. No. 1.9e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRGSLRXCKXQCSFXXAEXIFPDAXRTKLFWISY 44
 |||||
 Db 1 ANAFLXLRPGSLRXCKXQCSFEEAREIFDAXRTKLFWISY 44

RESULT 11

AAM52171 AAM52171 standard; Protein; 406 AA.

XX AC AAM52171;

XX DT 07-FEB-2002 (first entry)

XX DE Human FVII SEQ ID NO 1.

XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KW cardiatic; hepatocytic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.
 XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 6 /label= Glu, OTHER

FT Misc-difference 7 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 14 /label= Glu, OTHER

FT Misc-difference 16 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 19 /label= Glu, OTHER

FT Misc-difference 20 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 25 /label= Glu, OTHER

FT Misc-difference 26 /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 29 /label= Glu, OTHER

FT Misc-difference 35 /label= Glu, OTHER

FT Misc-difference 35 /note= "OTHER = gamma carboxyglutamic acid"

FT Modified-site 52 /note= "OTHER = gamma carboxyglutamic acid"

FT

FT /note= "O-glycosylated"
 FT Modified-site 60 /note= "O-glycosylated"
 FT Modified-site 145 /note= "N-glycosylated"
 FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
 FT to an activated form, comprising two chains
 FT linked by a single disulphide bridge"

FT Modified-site 322 /note= "N-glycosylated"

FT WO200158935-A2.

FT 16-AUG-2001.

FT 12-FEB-2001; 2001WO-DK00094.

FT 11-FEB-2000; 2000DK-0000218.

FT 18-OCT-2000; 2000DK-0001558.

FT (MAXY-) MAXYGEN APS.

FT Andersen KV, Pedersen AH, Bornaes C;
 DR WPI; 2001-581807/65.
 DR N-PSDB; AA199982.

PT New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -

XX Claim 1; Page 81-83; 89pp; English.

XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, cardiatic, hepatocytic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections.

XX Sequence 406 AA;

Query Match 83.7%; Score 159; DB 22; Length 406;
 Best Local Similarity 95.5%; Pred. No. 1.9e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLXLRGSLRXCKXQCSFXXAEXIFPDAXRTKLFWISY 44
 |||||
 Db 1 ANAFLXLRPGSLRXCKXQCSFXXAEXIFPDAXRTKLFWISY 44

RESULT 12

AAM52172 AAM52172 standard; Protein; 406 AA.

XX AC AAM52172;

XX DT 07-FEB-2002 (first entry)

XX Mammalian expressed human FVII SEQ ID NO 3.

XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;

KW

```

KW cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Modified-site 52
FT /note= "O-glycosylated"
FT Modified-site 60
FT /note= "O-glycosylated"
FT Modified-site 145
FT /note= "N-glycosylated"
FT Cleavage-site 152..153
FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322
FT /note= "N-glycosylated"
XX
XX MO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-DK00094.
XX
XX 11-FEB-2000; 2000DK-0000218.
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX
XX WPI; 2001-581807/65.
XX N-PSDB; AA199983.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently
XX attached to polypeptide group -
XX
XX
XX Disclosure; Page 85-86; 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX polypeptide conjugates, comprising at least one non-polypeptide group
XX covalently attached to a polypeptide, where the amino acid sequence of
XX polypeptide differs from that of the wildtype FVIIa (AAM52181) in that at
XX least one amino acid residue containing an attachment group for the
XX non-polypeptide group has been introduced or removed. The FVIIa
XX conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and
XX cerebroprotective activity and are useful for treating FVIIa/TF-related
XX diseases or disorders such as haemophilia, liver disease, myocardial
XX infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
XX have increased functional in vivo half life and/or increased plasma half
XX life, increased bioavailability and/or reduced sensitivity to proteolytic
XX degradation. Consequently medical treatment using the conjugates has a
XX number of advantages over currently available such as longer duration
XX between injections.
XX
XX
XX SQ Sequence 406 AA;
XX
XX Query Match 83.7%; Score 159; DB 22; Length 406;
XX Best Local Similarity 72.7%; Pred. No. 1.9e-18;
XX Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX QY 1 ANAFLLXXLRGSLRKCKXXQCSFXAXE1FKDAXRTKLFWISY 44
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 1 ANAFLELRPGSLRECKEGCSFEARER1FKDAERTKLFWISY 44
XX
XX RESULT 13
XX AAM52181
XX ID AAM52181 standard; Protein; 406 AA.
XX

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AC AAM52181;
XX
XX 07-FEB-2002 (first entry)
XX
XX Human FVII mutant T106N.
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KM cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 6
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 7
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 14
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 16
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 19
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 20
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 25
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 26
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 29
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 35
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Modified-site 52
FT /note= "OTHER = gamma carboxylutamic acid"
FT Modified-site 60
FT /note= "O-glycosylated"
FT Misc-difference 106
FT /note= "O-glycosylated"
FT Modified-site 145
FT /note= "Wild-type Thr substituted by Asn"
FT Cleavage-site 152..153
FT /note= "N-glycosylated"
FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322
FT /note= "N-glycosylated"
XX
XX MO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-DK00094.
XX
XX 11-FEB-2000; 2000DK-0000218.
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX

```

DR	WP1; 2001-581807/65.
XX	New conjugate, useful for treating Factor VIIA related diseases or
PT	disorders such as haemophilia, liver disease, myocardial infarction and
PR	deep-vein thrombosis, comprises non-polypeptide group covalently
PT	attached to polypeptide group -
XX	
PS	Example 3; Page -, 89pp; English.
XX	
CC	The invention relates to novel Factor VII (FVII) or Factor VIIA (FVIIA)
CC	polypeptide conjugates, comprising at least one non-polypeptide group
CC	covalently attached to a polypeptide, where the amino acid sequence of
CC	polypeptide differs from that of the wildtype FVIIA (AAM52171) in that at
CC	least one amino acid residue containing an attachment group for the
CC	non-polypeptide group has been introduced or removed. The FVIIA
CC	conjugates have haemostatic, thrombolytic, cardant, hepatotropic and
CC	cerebroprotective activity and are useful for treating FVIIA/TF-related
CC	diseases or disorders such as haemophilia, liver disease, myocardial
CC	infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC	have increased functional in vivo half life and/or increased plasma half
CC	life, increased bioavailability and/or reduced sensitivity to proteolytic
CC	degradation. Consequently medical treatment using the conjugates has a
CC	number of advantages over currently available such as longer duration
CC	between injections. The present sequence is that of a human FVII mutant,
CC	having an addition in vivo glycosylation site and tested for its
CC	amidolytic activity.
CC	Note: The present sequence is not shown in the specification but is
CC	derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC	(AAM52171).
XX	
SQ	Sequence 406 AA:
	Query Match 83.7%; Score 159; DB 22; Length 406;
	Best Local Similarity 95.5%; Pred. No. 1.9e-18;
	Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0
OY	1 ANAFLLXREGSLRXCKKXXCSEFXAXEIPDAXRTKLFWISY 44 1 ANAFLLXRLRPGSLRXCKKXCSEFXAXRIPDAXRTKLFWISY 44
D6	
RESULT 14	
AAM52182	ID AAM52182 standard; Protein; 406 AA.
XX	
AC	AAM52182;
XX	
DT	07-FEB-2002 (first entry)
XX	
DE	Human FVII mutant K143N/N145T.
KM	Factor VII; FVII: Factor VIIA; FVIIa; haemostatic; thrombolytic; cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease; myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant; mutin.
OS	Homo sapiens.
XX	Synthetic.
FT	
Key	Location/Qualifiers
FT	Misc-difference 6
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference 7
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference 14
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference 16
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	
FT	Misc-difference 19
FT	/note= "OTHER = gamma carboxyglutamic acid"

FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	20
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	25
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	26
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	29
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	35
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Modified-site
FT	52
FT	/note= "O-glycosylated"
FT	Modified-site
FT	60
FT	/note= "O-glycosylated"
FT	Misc-difference
FT	143
FT	/note= "Wild-type Lys substituted by Asn"
FT	Misc-difference
FT	145
FT	/note= "Wild-type Asn substituted by Thr"
FT	Cleavage-site
FT	152..153
FT	/note= "Proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
FT	Modified-site
FT	322
FT	/note= "N-glycosylated"
PV	
PN	WO200158935-A2.
XX	
PD	16-AUG-2001.
PF	12-FEB-2001; 2001WO-DK00094.
PR	11-FEB-2000; 2000DK-0000218.
PR	18-OCT-2000; 2000DK-0001558.
PA	(MAXY-) MAXYGEN ABS.
PI	Andersen KV, Pedersen AH, Bornaes C;
DR	WPI; 2001-581807/65.
XX	
PT	New conjugate, useful for treating Factor VIIa related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -
PS	Example 3; Page --; 89pp; English.
CC	The invention relates to novel Factor VII (FVIII) or Factor VIIA (FVIIA) polypeptide conjugates, comprising at least one non-polypeptide group covalently attached to a polypeptide, where the amino acid sequence of polypeptide differs from that of the wildtype FVIIA (AAWS2171) in that at least one amino acid residue containing an attachment group for the non-polypeptide group has been introduced or removed. The FVIIA conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and cerebroprotective activity and are useful for treating FVIIA/rf-related diseases or disorders such as haemophilia, liver disease, myocardial infarction, thrombotic stroke and deep-vein thrombosis. The conjugates have increased functional <i>in vivo</i> half life and/or increased plasma half life, increased bioavailability and or reduced sensitivity to proteolytic degradation. Consequently medical treatment using the conjugates has a number of advantages over currently available such as longer duration between injections. The present sequence is that of a human FVII mutant, having an addition <i>in vitro</i> glycosylation site and tested for its amidolytic activity.
CC	Note: The present sequence is not shown in the specification but is derived from the human wild-type FVII sequence shown in SEQ ID NO 1

```

CC      (AAMS2171).
XX      Sequence      406 AA;
SQ      Query Match
          Best Local Similarity 83.7%; Score 159; DB 22; Length 406;
          Matches 42; Conservative 95.5%; Pred. No. 1.9e-18;
          Mismatches 2; Indels 0; Gaps 0;

QY      1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44
          |||
          1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44

Db      1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44

RESULT 15
AAMS2183 standard; Protein; 406 AA.
XX      AAMS2183;
AC      AAMS2183;
XX      07-FEB-2002 (first entry)
XX      Human FVII mutant V253N.
XX      Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KM      cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
KM      myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
XX      mutain.
XX      Homo sapiens.
OS      Synthetic.
XX      Key
FH      Location/Qualifiers
FT      Misc-difference 6 /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 7 /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 14 /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 16 /note="OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 19 /note="OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 20 /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 25 /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 26 /note="OTHER = gamma carboxyglutamic acid"
FT      /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 29 /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 35 /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 35 /label= Glu, OTHER
FT      /note="OTHER = gamma carboxyglutamic acid"
FT      Modified-site 52 /note="O-glycosylated"
FT      Modified-site 60 /note="O-glycosylated"
FT      Modified-site 145 /note="O-glycosylated"
FT      Cleavage-site 152..153 /note="N-glycosylated"
FT      /note="proteolytic cleavage site converting FVII zymogen
FT      to an activated form, comprising two chains
FT      linked by a single disulphide bridge"
FT      Misc-difference 253

```

```

FT      /note="Wild-type Val substituted by Asn"
FT      Modified-site 322 /note="N-glycosylated"
FT      WO200158935-A2.
XX      16-AUG-2001.
XX      12-FEB-2001; 2001WO-DK00094.
XX      11-FEB-2000; 2000DK-0000218.
XX      18-OCT-2000; 2000DK-0001558.
XX      (MAXY-) MAXYGEN APS.
XX      Andersen KV, Pedersen AH, Bornaes C;
XX      WPI; 2001-581807/65.
XX      New conjugate, useful for treating Factor VIIa related diseases or
PT      disorders such as haemophilia, liver disease, myocardial infarction and
PT      deep-vein thrombosis, comprises non-polypeptide group covalently
PT      attached to polypeptide group -
XX      Example 3; Page -: 89pp; English.
XX      The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX      CC polypeptide conjugates, comprising at least one non-polypeptide group
XX      CC covalently attached to a polypeptide, where the amino acid sequence of
XX      CC polypeptide differs from that of the wildtype FVIIa (AAMS2171) in that at
XX      CC least one amino acid residue containing an attachment group for the
XX      CC non-polypeptide group has been introduced or removed. The FVIIa
XX      CC conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and
XX      CC cerebroprotective activity and are useful for treating FVIIa/TF-related
XX      CC diseases or disorders such as haemophilia, liver disease, myocardial
XX      CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
XX      CC have increased functional in vivo half life and/or increased plasma half
XX      CC life, increased bioavailability and/or reduced sensitivity to proteolytic
XX      CC degradation. Consequently medical treatment using the conjugates has a
XX      CC number of advantages over currently available such as longer duration
XX      CC between injections. The present sequence is that of a human FVII mutant,
XX      CC having an addition in vivo glycosylation site and tested for its
XX      CC amidolytic activity.
XX      CC Note: The present sequence is not shown in the specification but is
XX      CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
XX      CC (AAMS2171).
SQ      Sequence 406 AA;
XX      Query Match
          Best Local Similarity 83.7%; Score 159; DB 22; Length 406;
          Matches 42; Conservative 95.5%; Pred. No. 1.9e-18;
          Mismatches 2; Indels 0; Gaps 0;

QY      1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44
          |||
          1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44

Db      1 ANAFLLXXLRGSLXRXCKXXQCSFXXAEXIFKDAKRTKLFWISY 44

Search completed: March 19, 2003, 14:51:07
Job time : 32.4375 secs

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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10GLU28GLU
Perfect score: 190
Sequence: 1 ANAFLLXDLREGSLXRXCKX.....XXAEXIFXDAXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	83.7	466	1 KFHU7	coagulation factor
2	125	65.8	443	2 I46932	coagulation factor
3	115	60.5	407	1 KFB07	coagulation factor
4	102	53.7	461	1 JX0210	protein C (activat
5	101	53.2	461	1 S18994	protein C (activat
6	99	52.1	488	1 EXHU	coagulation factor
7	99	52.1	492	1 EXBO	coagulation factor
8	93	48.9	482	1 EXRT	coagulation factor
9	91	47.9	456	1 KXBO	coagulation factor
10	89	46.8	475	1 EXCH	coagulation factor
11	85	44.7	461	1 KXHU	protein C (activat
12	85	44.7	622	1 TBHU	thrombin (EC 3.4.2
13	81	42.6	416	1 KFB0	coagulation factor
14	81	42.6	617	2 S10511	thrombin (EC 3.4.2
15	81	42.6	618	2 A35827	thrombin (EC 3.4.2
16	80	41.1	461	1 KFHU	coagulation factor
17	73	38.4	452	1 A30351	coagulation factor
18	73	38.4	459	2 J00419	coagulation factor
19	67	35.3	642	2 S53433	coagulation factor
20	65	34.2	625	1 TBBO	plasma protein S p
21	64	33.7	396	1 KXB02	plasma protein Z -
22	63	33.2	675	1 KXB05	plasma protein S p
23	62	32.6	642	2 S53434	plasma protein S p
24	62	32.1	676	1 KXHU5	plasma protein S p
25	61	32.1	646	2 S38819	plasma protein S -
26	60	31.6	675	1 KXRTS	plasma protein S p
27	59	31.1	422	1 KXHU2	plasma protein Z p
28	58.5	30.8	576	2 G96763	probable MAP kinase
29	53	27.9	673	2 A48089	growth arrest-spec

30	53	27.9	675	1 KXMS	plasma protein S p
31	52.5	27.6	594	2 D84859	probable MAP kinase
32	52.5	27.6	603	2 C96575	probable MAP kinase
33	51	26.8	674	2 I55476	growth potentialin
34	51	26.8	678	2 B8089	growth potentialin
35	48.5	25.5	455	2 C83494	growth arrest-spec
36	48	25.3	211	2 D96996	uncharacterized lo
37	45	23.7	879	2 S55864	uncharacterized prote
38	44	23.2	413	1 VHVNIH	neuropeptide - in
39	44	23.2	447	2 B95185	mur ligase family
40	44	23.2	447	2 B8052	conserved hypotet
41	43.5	22.9	322	2 T20272	hypothetical prote
42	42.5	22.4	161	2 F82637	conserved hypotet
43	42.5	22.4	319	2 T5137	hypothetical prote
44	42.5	22.4	410	2 T25574	hypothetical prote
45	42.5	22.4	907	2 T15792	hypothetical prote

ALIGNMENTS

RESULT 1
KFHU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000
C:Accession: A28322; A23819; A31186; B31186; S63524
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.V.; Hagen, F.S.; Murr
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A>Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OH>
A:Cross-references: GB:J02933; NID:G180333; PIDN:AAA51883.1; PID:G180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A>Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; MUID:86205965; PMID:3466420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M3232; NID:G182799; PIDN:AAA8040.1; PID:G182801
R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A>Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A:Reference number: A90539; MUID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <THI>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TH2>
R:Bjorn, S.; Foster, D.C.; Thim, L.; Wilberg, F.C.; Christensen, M.; Komiyama, Y.; Peder
J. Biol. Chem. 266, 11051-11057, 1991
A>Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A:Reference number: A40529; MUID:91250411; PMID:1904059
R:Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A>Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A:Reference number: S63524; MUID:96096752; PMID:8529655
A:Accession: S63524
A:Molecule type: protein
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
coagulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-60/Domain: propeptide #status predicted <PRO>
F:45-104/Domain: Gla domain homology <Gla>
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F:610-141/Domain: EGF homology <EG1>
F:151-187/Domain: EGF homology <EG2>
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:213-447/Domain: trypsin homology <TRY>
F:66: 67,74,76,79,80,85,86,89,96/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:77-82,110-121,115-130,133-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
F:112,120/Binding site: carboxylate (Ser) (covalent) #status experimental
F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F:205,382/Binding site: carboxylate (Asn) (covalent) #status experimental
F:212-213/Cleavage site: Arg-116 (coagulation factor XIIIa) #status experimental
F:253,302,409/Active site: His, Asp, Ser #status predicted
F:350-351/Cleavage site: Arg-Gly (coagulation factor XIa) #status predicted

Query Match 83.7%; Score 159; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 1,9e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXKXCSFYXAXEIPKDAKRTKLFWISY 44
Db 61 ANAFLEELRPGSLRECKEKEQCSFEAREIFPDARTKLFWISY 104
|||||
A:Accession: 146932
R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A>Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A:Reference number: 146932; MUID:91190306; PMID:8383365
A:Accession: 146932
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-443 <PRO>
A:Cross-references: GB:S56300; NID:G266294; PID:G266295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F:24-83/Domain: Gla domain homology <Gla>
F:89-120/Domain: EGF homology <EG1>
F:130-166/Domain: EGF homology <EG2>
F:192-425/Domain: trypsin homology <TRY>

Query Match 65.8%; Score 125; DB 2; Length 443;
Best Local Similarity 54.5%; Pred. No. 1.4e-13;
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXKXCSFYXAXEIPKDAKRTKLFWISY 44
Db 40 ANAFLEELRPGSLRECKEKEQCSFEAREVFGSTERTKQFWITY 83
|||||
RESULT 3
KRB07
coagulation factor VIIa (EC 3.4.21.21) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-May-1990 #sequence_rev15ion 23-Mar-1995 #text_change 16-Jul-1999
C:Accession: A31979; C20274
R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A>Title: Bovine factor VII. Its purification and complete amino acid sequence.
A:Reference number: A31979; MUID:89008362; PMID:3049594
A:Accession: A31979
A:Molecule type: protein
A:Residues: 1-407 <TK>
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX in the presence of calcium and tissue factor

A'Reference number: A20274; PMID:83308813; PMID:6688526

A'Accession: C20274

A'Molecule type: protein

A'Residues: 58-62, 'X', 64-68 <MCM>

A'Note: The residue designated 'X' was determined to be hydroxyaspartic acid

J. Biochem. 104, 867-868, 1988

A>Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor VIIa light chain #status experimental <MA1>

A'Reference number: A44556; PMID:89213999; PMID:3149667

A'Contents: annotation

A'Note: Structure and location of covalently bound carbohydrate

C'Function:

A'Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor

A'Pathway: blood coagulation extrinsic pathway

C'Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid

F.1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>

F.1-44/Domain: Gla domain homology (fragment) <GLA>

F.50-81/Domain: EGF homology <EG1>

F.91-127/Domain: EGF homology <EG2>

F.153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F.153-387/Domain: trypsin homology <TRY>

F.16, '14, 16, 19, 20, 25, 26, 29, 34, 35/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental

F.17-22, 50-51, 55-70, 72-81, 91-102, 98-112, 114-127, 135-262, 159-164, 178-194, 310-323, 340-368/

F.552/Binding site: carboxylate (Ser) (covalent) #status experimental

F.563/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental

F.145, 203/Binding site: carboxylate (Asn) (covalent) #status experimental

F.152-153/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental

F.193, 242, 334/Active site: His, Asp, Ser #status predicted

F.290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match

Best Local Similarity 50.0%; Score 115; DB 1; Length 407;

Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

1 ANAFLLXLRGSLRXCKXQCSFXXAXEIKFKAXRTKLEWISY 44

1 ANGFLLELLPGSLRECRBELCSPEAHAEIFRNEERTQFVWSY 44

Db

1 ANGFLLELLPGSLRECRBELCSPEAHAEIFRNEERTQFVWSY 44

RESULT 4

protein C (activated) (EC 3.4.21.69) precursor - mouse

N.Alternate names: vitamin K-dependent serine proteinase

C.Species: Mus musculus (house mouse)

C.Date: 10-Sep-1999 #sequence_revastion 10-Sep-1999 #text_change 16-Jun-2000

C'Accession: JX0210

R.Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Haehimoto-Gotoh, T.

J. Biochem. 111, 491-495, 1992

A>Title: Isolation and characterization of a mouse protein C cDNA.

A'Reference number: JX0210; PMID:92316897; PMID:1618739

A'Accession: JX0210

A'Molecule type: mRNA

A'Residues: 1-461 <TAD>

A'Cross-references: GB:DI0445; NID:g220385; PIDN:BA401235.1; PID:g220386

A'Experimental source: liver

C'Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that rc

C'Family: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C'Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid

F.1-33/Domain: signal sequence #status predicted <IG>

F.27-85/Domain: Gla domain homology <GLA>

F.34-41/Domain: propeptide #status predicted <PRO>

F.42-196, 199-461/Product: protein C #status predicted <PC>

F.91-130/Domain: EGF homology <EG1>

F.139-174/Domain: EGF homology <EG2>

F.199-461/Domain: heavy chain #status predicted <PCH>

F.199-211/Domain: activation peptide #status predicted <ACT>

F.212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

J. Mol. Biol. 237, 947-966, 1993

A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.

A/Reference number: A49458; PMID:93360277; PMID:8355279

A/Content: annotation; X-ray crystallography, 2.2 angstroms

C/Comment: The two chains held together by one disulfide bond are formed from a single-c

C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or

C/Genetics: GDB:PI0

A/Genes: GDB:PI0

A/Cross-references: GDB:119890; OMIM:227600

A/Map position: 13q34-13q34

A/Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1

A/Note: efficiency of this factor causes Stuart disease

C/Function:

A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr

A/Pathway: blood coagulation

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-40/Domain: propeptide #status predicted <PRO>

F/25-84/Domain: Gla domain homology <Gla>

F/41-179/Product: coagulation factor X light chain #status experimental <LCH>

F/90-121/Domain: EGF homology <EGF>

F/129-164/Domain: EGF homology <EG2>

F/183-488/Product: coagulation factor X heavy chain #status experimental <HCH>

F/235-234/Domain: activation peptide #status experimental <APT>

F/235-488/Product: coagulation factor X heavy chain #status experimental <ACT>

F/235-462/Domain: trypsin homology <TRY>

F/46-47/54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F/57-62/Diulfide bonds: #status predicted

F/80-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/

F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F/129,211/Binding site: carboxylate (Thr) (covalent) #status experimental

F/221,231/Binding site: carboxylate (Asn) (covalent) #status experimental

F/234-235/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stat

F/276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 52.1%; Score 99; DB 1; Length 488;

Best Local Similarity 38.6%; Pred. NO. 4.8e-09;

Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFXXLRGSLRXCKXXCSEFXAXEXIFKDXKRTKLFWISY 44

41 ANSLFEMKKGHLEKCEMEETCSYBARREVEDSDKTNEFNKKY 84

Db

RESULT 7

EXBO

coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N/Alternate names: Stuart factor

C/Species: Bos primigenius taurus (cattle)

C/Date: 24-Apr-1984 #sequence, revision 17-Mar-1987 #text change 16-Jul-1999

C/Accession: A22867; A14997; A12030; A34412; S39414; A00925

R/Pung: M.R.; Campbell, R.M.; MacGillivray, T.A.

Nucleic Acids Res. 12, 4481-4492, 1984

A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a

A/Reference number: A22867; PMID:84247315; PMID:6330671

A/Accession: A22867

A/Molecule type: mRNA

A/Residues: 1-487 <FN>

A/Cross-references: GB:X00673; NID:q192; PIDN:CA28286.1; PID:q193

R/Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.

Biochemistry 19, 659-667, 1980

A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).

A/Reference number: A14997; PMID:80130563; PMID:6766735

A/Accession: A14997

A/Molecule type: protein

A/Residues: 41-102 'N', 104-180 <ENP>

R/McMullen, B.A.; Fujikawa, K.; Kiesel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A/Reference number: A20274; PMID:83308813; PMID:6688526

A/Contents: annotation; revision to residue 103

R/Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.

Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975

A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.

A/Reference number: A12030; PMID:76053069; PMID:1059993

A/Accession: A12030

A/Molecule type: protein

A/Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <T

A/Note: carbohydrate binding sites and disulfide bonds were determined

R/Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.

J. Biol. Chem. 264, 16897-16994, 1989

A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal

A/Reference number: A34412; PMID:89380326; PMID:2789221

A/Accession: A34412

A/Molecule type: protein

A/Residues: 85-126 <PER>

R/Imoue, K.; Morita, T.

Eur. J. Biochem. 216, 153-163, 1993

A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of

A/Reference number: S39414; PMID:94062825; PMID:8243461

A/Accession: S39414

A/Molecule type: protein

A/Residues: 183-196,199-209,216-233 <IND>

A/Note: carbohydrate binding sites

R/Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D

Biochemistry 11, 4899-4903, 1972

A>Title: Bovine factor X-1a (activated Stuart factor): Evidence of homology with mammali

A/Reference number: A12453; PMID:73053314; PMID:4264286

A/Contents: annotation; active site

R/Fujikawa, K.; Titani, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975

A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to

A/Reference number: A13504; PMID:76053321; PMID:1059122

A/Contents: annotation; activation

R/Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.

J. Biol. Chem. 259, 5705-5710, 1984

A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic

A/Reference number: A38024; PMID:84185716; PMID:6546930

A/Contents: annotation; calcium binding

R/Morita, T.; Jackson, C.M.

J. Biol. Chem. 261, 4008-4014, 1986

A/Reference number: A38025; PMID:86140210; PMID:3949800

A/Contents: annotation; sulfide binding

C/Comment: Factor Xa converts prothrombin to thrombin during blood clotting.

C/Comment: The two chains are formed from a single-chain precursor by the excision of tw

C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), o

activation.

C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro

C/Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C/Genetics:

A/Genes: PI0

A/Map position: 13q34

C/Function:

A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr

A/Pathway: blood coagulation

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F/1-15/Domain: signal sequence #status predicted <SIG>

F/16-40/Domain: propeptide #status predicted <PRO>

F/41-180/Product: coagulation factor X light chain #status experimental <LCH>

F/90-121/Domain: EGF homology <EG1>

F/129-164/Domain: EGF homology <EG2>

F/183-492/Product: coagulation factor X heavy chain #status experimental <HCH>

F/183-333/Domain: activation peptide #status experimental <APT>

F/234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>

F/234-461/Domain: trypsin homology <TRY>

F/46-47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s

F/57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Diulfide bonds: #status p

F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F/200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental

F/208,485/Binding site: carboxylate (Thr) (covalent) #status experimental

F/218/Binding site: carboxylate (Asn) (covalent) #status experimental

F/233-234/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stat


```
F:98-128/Domain: EGF homology <EG1>
F:137-172/Domain: EGF homology <EG2>
F:197-456/Product: protein C heavy chain #status experimental <HCH>
F:197-210/Domain: activation peptide #status experimental <APT>
F:211-440/Domain: trypsin homology <TRY>
F:45-46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Distal disulfide bonds: #stat
F:136,289,350/Binding site: carbonyl group (Asn) (covalent) #status predicted
F:252,298,397/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carbonyl group (Asn) (covalent) #status predicted

Query Match      47.9%; Score 91; DB 1; Length 456;
Best Local Similarity 40.9%; Pred. No. 1.1e-07;
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
```

1 ANAFLLXLRGSLKRXCKXXQCFXAXEYIFKDAKRTKLFMISY 44

40 ANSFLELRPGNVERECSEVCEFEAREIFQNTEDTMATFSFY 83

RESULT 10

EXCH

coagulation factor Xa (BC 3.4.21.6) precursor - chicken

N/Alternate names: virus-activating proteinase

C/Species: Gallus gallus (chicken)

C/Date: 12-Feb-1993 #sequence, revision 07-Feb-1997 #text_change 16-Jul-1999

C/Accession: S15838; S20380; S20381

R: Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotch, B.; Ogasawara, T.; Na

FEBS Lett. 283, 281-285, 1991

A/Title: Primary structure of the virus activating proteinase from chick embryo. Its ident

A/Reference number: S15838; MUID:91257322; PMID:2044767

A/Accession: S15838

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-475 <SUZ>

A/Cross-references: DDBJ: D00844; NID: G222869; PID: BAA00724.1; PID: G222870

R: Gotch, B.; Yamuchi, F.; Ogasawara, T.; Nagai, Y.

FEBS Lett. 296, 274-278, 1992

A/Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib

A/Reference number: S20380; MUID:92164779; PMID:1537403

A/Accession: S20380

A/Molecule type: protein

A/Residues: 41-55 <G02>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246, 'X', 248-251, 'X', 253-261 <G0T>

C/Function:

A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr

A/Pathway: blood coagulation

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keyword: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-40/Domain: propeptide #status predicted <PRO>

F:45-84/Domain: Gla domain homology <GLA>

F:91-185/Product: coagulation factor X light chain #status experimental <LCH>

F:90-121/Domain: EGF homology <EG1>

F:129-167/Domain: EGF homology <EG2>

F:186-175/Product: coagulation factor X heavy chain #status predicted <HCH>

F:186-240/Domain: activation peptide #status predicted <APT>

F:241-475/Product: coagulation factor Xa heavy chain #status experimental <HCH>

F:241-468/Domain: trypsin homology <TRY>

F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s

F:57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,42

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:196,207,228,285/Binding site: carbonyl group (Asn) (covalent) #status predicted

F:282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 46.8%; Score 89; DB 1; Length 475;

Best Local Similarity 36.4%; Pred. No. 2.5e-07;

Matches 16; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

1 ANAFLLXLRGSLKRXCKXXQCFXAXEYIFKDAKRTKLFMISY 44

```
DB 41 ANSFLEMRKGNIERECNERGCKEAREFAFEDNKEEFEMWNY 84

RESULT 11
KXHU
protein C (activated) (EC 3.4.21.69) precursor - human
N/Alternate names: autoprothrombin IIA; plasma protein C
C/Species: Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence, revision 17-Mar-1987 #text_change 16-Jul-1999
C/Accession: A22331; A25426; A21781; A23789; A00927
R: Foster, D.C.; Yoshitake, S.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
A/Title: The nucleotide sequence of the gene for human protein C.
A/Reference number: A22331; MUID:85270390; PMID:2991887
A/Accession: A22331
A/Molecule type: DNA
A/Residues: 1-461 <FOS2>
A/Cross-references: GB:M11228; NID:G190333; PID:AAA60164.1; PID:G190334
R: Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
A/Title: Evolution and organization of the human protein C gene.
A/Reference number: A25426; MUID:86120978; PMID:3511471
A/Accession: A25426
A/Molecule type: DNA
A/Residues: 1-445, 'L', 446-461 <PLU>
A/Cross-references: GB:M12712; NID:G190330; PID:AAA60165.1; PID:G190332
R: Foster, D.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
A/Title: Characterization of a cDNA coding for human protein C.
A/Reference number: A21781; MUID:84272714; PMID:6589623
A/Accession: A21781
A/Molecule type: mRNA
A/Residues: 1-107, 461 <FOS2>
A/Cross-references: GB:K02059; NID:G190322; PID:AAA60164.1; PID:G190323
R: Beckmann, R.J.; Schmidt, R.J.; Santre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
Nucleic Acids Res. 13, 5233-5247, 1985
A/Title: The structure and evolution of a 461 amino acid human protein C precursor and 1
A/Reference number: A23789; MUID:85269659; PMID:2991859
A/Accession: A23789
A/Molecule type: mRNA
A/Residues: 1-461 <BEC>
A/Cross-references: GB:X02750; NID:G35689; PID:CAA26528.1; PID:G763120
R: Mierlich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 265, 11397-11404, 1990
A/Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation f
A/Reference number: A44605; MUID:90293094; PMID:1694179
A/Contents: annotation; carbonyl group binding sites; activation peptide
A/Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
R: Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A/Title: O-linked fucose is present in the first epidermal growth factor domain of facc
A/Reference number: A44606; MUID:92184750; PMID:1544894
A/Contents: annotation; beta-hydroxyaspartic acid
A/Comment: protein C is the zymogen of the vitamin K-dependent serine proteinase that ir
A/Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
C/Genetics:
A/Gene: GDB:PROC
A/Cross-references: GDB:120317; OMIM:176860
A/Map position: 2q13-2q21
A/Intons: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keyword: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F:1-32/Domain: signal sequence #status predicted <SIG>
F:37-86/Domain: Gla domain homology <GLA>
F:93-42/Domain: propeptide #status predicted <PRO>
F:43-157/Product: protein C light chain #status predicted <LCH>
F:92-131/Domain: EGF homology <EG1>
F:140-175/Domain: EGF homology <EG2>
F:200-461/Product: protein C heavy chain #status predicted <HCH>
F:200-211/Domain: activation peptide #status experimental <APT>
```

F.212-445/Domain: trypsin homology <TRY>
 F.48-49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
 F.59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D
 F.106-111/Disulfide bonds: #status predicted
 F.110/Binding site: carboxylate (Thr) (covalent) #status absent
 F.113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F.139,290,335/Binding site: carboxylate (Asn) (covalent) #status experimental
 F.211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
 F.253,299,402/Active site: His, Asp, Ser #status predicted
 F.371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 44.7%; Score 85; DB 1; Length 461;
 Best Local Similarity 43.9%; Pred. No. 1.2e-06;
 Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRBGSIXRCKXQCSFXAXEIPFDAXTKLFW 41
 DB 43 ANSFLELRHSSLERECIEBICDFEAKEIFQVNDTLAFW 83

RESULT 12

Thrombin (EC 3.4.21.5) precursor [validated] - human
 N:Alternate names: coagulation factor II
 N:Contains: prothrombin
 C:Species: Homo sapiens (man)
 C>Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000
 C:Accession: A29351; A00914; B00914; A37549; A37550; I51952
 R:Degeen, S.J.F.; Davie, E.W.
 Biochemistry 26, 6165-6177, 1987
 A>Title: Nucleotide sequence of the gene for human prothrombin.
 A:Reference number: A29351; PMID:8807877; PMID:2825773
 A:Accession: A29351

A:Molecule type: DNA
 A:Residues: 1-622 <DEG>
 A:Cross-references: GB:M17262; GB:M33691; NID:9558069; PIDN:AC63054.1; PID:G3339641
 R:Degeen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.
 Biochemistry 22, 2087-2097, 1983
 A>Title: Characterization of the complementary deoxyribonucleic acid and gene coding for
 A:Reference number: A00914; PMID:8321469; PMID:6305407
 A:Accession: A00914

A:Molecule type: mRNA
 A:Residues: 8-163, 'N', 165-622 <DE2>
 A:Cross-references: GB:V00595; GB:J00307; NID:G37128; PIDN:CAA23842.1; PID:G1335344
 A:Accession: B00914

A:Molecule type: DNA
 A:Residues: 188-311 <DE3>
 R:Walt, D.A.; Hewett-Emllett, D.; Seegers, W.H.
 Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
 A:Reference number: A37549; PMID:77193964; PMID:266717
 A:Accession: A37549

A:Molecule type: protein
 A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-308,
 R:Butkowski, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.
 J. Biol. Chem. 252, 4942-4957, 1977
 A>Title: Primary structure of human prothrombin 2 and alpha-thrombin.
 A:Reference number: A37550; PMID:77207112; PMID:873923
 A:Accession: A37550

A:Molecule type: protein
 A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
 J:Rabiet, M.J.; Blachill, A.; Furie, B.; Furie, B.C.
 J. Biol. Chem. 261, 13310-13315, 1986
 A:Reference number: A37551; PMID:87008532; PMID:3759958
 A:Contents: annotation; activation cleavages
 R:MacGillivray, R.T.; Irwin, D.M.; Guinno, E.R.; Stone, J.C.
 Ann. N.Y. Acad. Sci. 485, 73-79, 1986
 A>Title: Recombinant genetic approaches to functional mapping of thrombin.
 A:Reference number: I51952; PMID:87182874; PMID:3471151
 A:Accession: I51952

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2, 'RI', 5-100 <RES>
 A:Cross-references: GB:M33031; NID:G190723; PIDN:AAA60220.1; PID:G190724

C/Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
 C/Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
) can be removed either by factor Xa or thrombin: the cleavage into light and heavy chain
 ter 314-Arg, are released in natural blood clotting.
 C/Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
 C/Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
 ent interaction with the negatively charged phospholipid membrane surface.
 C/Comment: The prothrombin precursor is synthesized in the liver.
 C:GeneticS:
 A:Gene: GDB:P2
 A:Cross-references: GDB:119894; OMIM:176930
 A:Map position: 11p11-11q12
 A:Features: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C:Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli
 F.1-24/Domain: signal sequence #status predicted <SIG>
 F.25-43/Domain: propeptide #status predicted <PRO>
 F.28-87/Domain: Gla domain homology <Gla>
 F.44-622/Product: prothrombin #status experimental <MAT>
 F.44-327/Domain: activation peptide #status experimental <APT>
 F.108-186/Domain: kringle homology <KR1>
 F.213-291/Domain: kringle homology <KR2>
 F.328-363/Product: thrombin light chain #status experimental <LCH>
 F.364-622/Product: thrombin heavy chain #status experimental <HCH>
 F.364-613/Domain: trypsin homology <TRY>
 F.49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F.60-65,90-103,108-186,129-159,157-181,213-291,234-274,262-286/Disulfide bonds: #status
 F.221,143/Binding site: carboxylate (Asn) (covalent) #status predicted
 F.336-482,536-550,564-594/Disulfide bonds: #status predicted
 F.391-407/Disulfide bonds: #status experimental
 F.406,462/Active site: His, Asp #status predicted
 F.416/Binding site: carboxylate (Asn) (covalent) #status experimental
 F.568/Active site: Ser #status experimental

Query Match 44.7%; Score 85; DB 1; Length 622;
 Best Local Similarity 36.4%; Pred. No. 1.6e-06;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRBGSIXRCKXQCSFXAXEIPFDAXTKLFWISY 44
 DB 44 ANTFLEVRKGNLRECEVETCSYEAPFALBSTATDFWAKY 87

RESULT 13

KEBO
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine
 N:Alternate names: Christmas factor
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text change 16-Jul-1999
 C:Accession: A14757; B20274; I45891; A00923
 R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Ti
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
 A>Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa
 A:Reference number: A14757; PMID:80056619; PMID:291916
 A:Accession: A14757

A:Molecule type: protein
 A:Residues: 1-63, 'T', 65-416 <KAT>
 R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
 Blochm. Biophys. Res. Commun. 115, 8-14, 1983
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; PMID:83308813; PMID:6688526
 A:Accession: B20274

A:Molecule type: protein
 A:Residues: 59-63, 'X', 65-69 <MCW>
 R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
 Nature 299, 178-180, 1982
 A>Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
 A:Reference number: I45891; PMID:82272386; PMID:6287289
 A:Accession: I45891

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 52-139 <CHO>
 A:Cross-references: GB:J00007; NID:G163053; PIDN:AAA30520.1; PID:G163054

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10GLU28GLU
Perfect score: 190
Sequence: 1 ANAFIXXIREGSLRXCKXX.....XXAEXIFMDAXTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	83.7	466	FA7_HUMAN	P08709 homo sapien
2	125	65.8	444	FA7_RABIT	P98139 oryctolagus
3	115	60.5	407	FA7_BOVIN	P22457 bos taurus
4	114	60.0	446	FA7_MOUSE	P70375 mus musculus
5	102	53.7	461	PRTC_MOUSE	P33587 mus musculus
6	101	53.2	459	PRTC_PIG	O991P2 sus scrofa
7	101	53.2	461	PRTC_RAT	P31394 rattus norv
8	99	52.1	488	FA10_HUMAN	P00742 homo sapien
9	99	52.1	490	FA10_RABIT	O19045 oryctolagus
10	99	52.1	492	FA10_BOVIN	P00743 bos taurus
11	97	51.1	218	TMG1_HUMAN	O14668 homo sapien
12	91	47.9	456	PRTC_BOVIN	P00745 bos taurus
13	90	47.4	231	TMG3_HUMAN	P092d7 homo sapien
14	89	46.8	475	FA10_CHICK	P25155 gallus gall
15	85	44.7	458	PRTC_RABIT	O28661 oryctolagus
16	85	44.7	461	PRTC_HUMAN	P04070 homo sapien
17	85	44.7	622	THRB_HUMAN	P00734 homo sapien
18	81	42.6	416	FA9_BOVIN	P00741 bos taurus
19	81	42.6	617	THRB_RAT	P18292 rattus norv
20	81	42.6	618	THRB_MOUSE	P19221 mus musculus
21	80	42.1	461	FA9_HUMAN	P00740 homo sapien
22	79	41.6	376	FA10_TROCA	P81428 tropidichth
23	76	40.0	202	TMG2_HUMAN	O14669 homo sapien
24	73	38.4	452	FA9_CANFA	P15540 canis famli
25	73	38.4	459	FA9_MOUSE	P16294 mus musculus
26	69.5	36.6	226	TMG4_HUMAN	O992d6 homo sapien
27	65	34.2	625	THRB_BOVIN	P00735 bos taurus
28	64	33.7	396	PRTC_BOVIN	P00733 bos taurus
29	63	33.2	675	PRTS_BOVIN	P07224 bos taurus
30	62	32.6	649	PRTS_MACMU	O28520 macaca mula
31	62	32.6	646	PRTS_HUMAN	P98118 oryctolagus
32	61	32.1	675	PRTS_RABIT	P53813 rattus norv
33	60	31.6	675	PRTS_RAT	

34	59	31.1	400	1	PRTZ_HUMAN	P22891 homo sapien
35	53	27.9	675	1	PRTS_MOUSE	O08761 mus musculus
36	45	23.7	879	1	YN65_YEAST	P42837 saccharomyc
37	44	23.2	413	1	NCAP_IHNV	P19691 infectious
38	43.5	22.9	322	1	YOL3_CAEEL	O09292 caenorhabdi
39	43	22.6	343	1	HMD_METVO	O50840 methanococc
40	43	22.6	353	1	HMD_METTL	O50759 m coenzyme
41	42	22.1	185	1	HEX1_MOUSE	O61658 mus musculus
42	42	22.1	263	1	PELA_STRMU	O68575 streptococc
43	41.5	21.8	356	1	MURB_BUCAI	P57153 buchnera ap
44	41.5	21.8	1290	1	BXB_CLOBO	P10844 clostridium
45	41	21.6	584	1	DML1_AQUAE	O67398 aquifex aeo

ALIGNMENTS

RESULT 1
ID FA7_HUMAN STANDARD; PRT; 466 AA.
AC P08709; O14339;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Eptacog alfa).
CN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
[3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Armei T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
[4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjørn S., Christensen W., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
[5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjørn S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.";
RL J. Biol. Chem. 266:11051-11057(1991).
[6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;

RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
 RA Shionouchi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [17]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [110]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950;
 RA Wutanyu A., Finn B.E., Gippert G.P., Forssen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [111]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [112]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patraccchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Gasnaco A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [113]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patraccchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [114]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Kemali E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [115]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE=94264305; PubMed=8204879;
 RA Chaining S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [116]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodighiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [117]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohira M., Hayashi T., Wada H., Minamikawa K., Shirekawa S.,
 RA Suzuki K.;
 RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [118]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arhini A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [119]
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodighiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [120]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaitov R., Seligsohn U.;
 RT "A1244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [121]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Gaidies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN [122]
 RP FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIa BY FACTOR Xa, FACTOR XIIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -1- PHARMACEUTICAL: Available under the names Nitease or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match 83.7%; Score 159; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 1.4e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRREGSLRXCKXQCSFXAXEXIFPDAXRTKLFMTSY 44
Db 61 ANAFLXLRREGSLRXCKXQCSFXAXEXIFPDAXRTKLFMTSY 104

RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";
RL Thromb. Res. Suppl. 69:231-238(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RL - FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).
CC - CARALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
CC - SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).
CC - TISSUE SPECIFICITY: PLASMA.
CC - PM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC - SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77477; AAB37326.1; -;
DR HSSP; P08709; 1FAK.
DR MEROPS; S01.215; -;
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin_1.
DR Pfam; PF00594; gla_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.
KM EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
FT DISULFID 198 203
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CMC64;

Query Match 65.8%; Score 125; DB 1; Length 444;
Best Local Similarity 54.5%; Pred. No. 1.5e-14;
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLXLRREGSLRXCKXQCSFXAXEXIFPDAXRTKLFMTSY 44
Db 40 ANAFLXLRREGSLRXCKXQCSFXAXEXIFPDAXRTKLFMTSY 83

RESULT 3

FA7_BOVIN
ID FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008362; PubMed=3049594;
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,
RA Iwanaga S.,
RT "Bovine factor VII. Its purification and complete amino acid
RT sequence."
RT J. Biol. Chem. 263:14868-14877(1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine
RT blood coagulation factors VII and IX."
RT J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Klsiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z."
RT Adv. Exp. Med. Biol. 281:121-131(1990).
RN [4]
RP FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGN FORM. FACTOR VII IS
RP CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
RP THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
RP AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
RP BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
RP FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC PIR: A31979; A31979.
DR HSSP: P08709; 1BF9.
DR MEROPS: S01.215; .
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR001438; EGF-IT.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease TRY.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 1.

DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYD_SPE; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
FT CHAIN 153 407 FACTOR VII HEAVY CHAIN.
FT DOMAIN 6 35 GLA-RICH.
FT DOMAIN 46 82 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 87 128 EGF-LIKE 2.
FT DOMAIN 153 407 SERINE PROTEASE.
FT SITE 152 153 CLEAVAGE (BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR THROMBIN).
FT ACT_SITE 193 193 BY SIMILARITY.
FT ACT_SITE 242 242 BY SIMILARITY.
FT ACT_SITE 344 344 BY SIMILARITY.
FT BINDING 338 338 SUBSTRATE (BY SIMILARITY).
FT DISULFID 17 22 BY SIMILARITY.
FT DISULFID 50 61 BY SIMILARITY.
FT DISULFID 55 70 BY SIMILARITY.
FT DISULFID 72 81 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 98 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 135 152 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 178 194 BY SIMILARITY.
FT DISULFID 310 329 BY SIMILARITY.
FT DISULFID 340 368 BY SIMILARITY.
FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 52 52 O-LINKED (GLCNAC. . .).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 407 AA; 44431 MM; 703B1FE0636F7F10 CRC64;

Query Match 60.5%; Score 115; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 8; 4e-13;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

CY 1 ANAFLLXLRGSLXRYCKXXQCSFXXAEXIFKDAXTKLFWISY 44
DB 1 ANGFLELLPGSLERCREBLCSFEBAHEIFRNEERTROFWISY 44

RESULT 4
ID FA7_MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97127167; PubMed=8972017;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood
 RT coagulation factor VII gene."
 RL Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U66079; AAC3796.1; -.
 DR HSSP; P08709; I8F9.
 DR MEROPS; S01.215; -.
 DR MGD; MGI:109325; F7.
 DR InterPro; IPR000152; Aex_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Set_protease_TRY.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Glaf; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL; 1 24
 FT PROPEP; 25 41
 FT CHAIN; 42 193
 FT CHAIN; 194 446
 FT DOMAIN; 47 76
 FT DOMAIN; 87 123

FT DOMAIN; 128 169
 FT DOMAIN; 194 446
 FT SITE; 193 194
 FT ACT SITE; 234 234
 FT ACT SITE; 283 283
 FT ACT SITE; 385 385
 FT BINDING; 379 379
 FT DISULFID; 58 63
 FT DISULFID; 91 102
 FT DISULFID; 96 111
 FT DISULFID; 113 122
 FT DISULFID; 132 143
 FT DISULFID; 139 153
 FT DISULFID; 155 168
 FT DISULFID; 176 203
 FT DISULFID; 200 205
 FT DISULFID; 219 235
 FT DISULFID; 351 370
 FT DISULFID; 381 409
 FT MOD_RES; 47 47
 FT MOD_RES; 48 48
 FT MOD_RES; 55 55
 FT MOD_RES; 57 57
 FT MOD_RES; 60 60
 FT MOD_RES; 61 61
 FT MOD_RES; 66 66
 FT MOD_RES; 67 67
 FT MOD_RES; 70 70
 FT MOD_RES; 76 76
 FT MOD_RES; 104 104
 FT CARBOHYD; 186 186
 FT CARBOHYD; 244 244
 SQ SEQUENCE 446 AA; 50276 MW; 2512B44A45CB966 CRC64;
 Query Match 60.0%; Score 114; DB 1; Length 446;
 Best Local Similarity 54.5%; Pred. No. 1.4e-12;
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFPLXLRREGSLXKCKKXQCSFYKAXEIPKDMRTLFWISY 44
 Db 42 ANSLLEELWPGSLERECNEBQCSFEAREIFKSPRTQFWILVY 85

RESULT 5

PTC_MOUSE STANDARD; PRT; 461 AA.
 AC P33587; O35498;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Antiproteohembin IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92316897; PubMed=1618739;
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
 RT "Isolation and characterization of a mouse protein C cDNA."
 RL J. Biochem. 111:491-495(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=96152576; PubMed=9493582;
 RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine gene encoding

RT anticoagulant protein C.";
 RL Thromb. Haemost. 79:310-316(1998).
 RN [3]
 RP SEQUENCE OF 274-434 FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=94318474; PubMed=8043441;
 RA Murkawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
 RT "A comparative study of partial primary structures of the catalytic
 region of mammalian protein C.";
 RL Br. J. Haematol. 86:590-600(1994).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 and VIIIA.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
 REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 SITE IS NECESSARY FOR THE RECOGNITION OF THE
 THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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 CC EMBL; D10445; BAA01235.1; -.
 DR EMBL; AF034569; AAC3795.1; -.
 DR EMBL; D43755; BAA07812.1; -.
 DR PIR; JX0210; JX0210.
 DR HSSP; P04070; JPCU.
 DR MEROPS; S01.218; -.
 DR MGD; MGI:97771; PFCO.
 DR InterPro; IPR000152; Aex_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF Ca..
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Glycoprotein; Serine protease;
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.

FT	SIGNAL	1	33	BY SIMILARITY.
FT	PROPER	34	41	BY SIMILARITY.
FT	CHAIN	42	196	PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT	CHAIN	199	461	PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT	PEPTIDE	199	212	ACTIVATION PEPTIDE (BY SIMILARITY).
FT	SITE	212	213	CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT	DOMAIN	96	131	EGF-LIKE 1.
FT	DOMAIN	135	175	EGF-LIKE 2.
FT	DOMAIN	213	461	SERINE PROTEASE.
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	48	48	(BY SIMILARITY).
FT	MOD_RES	48	48	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	55	55	(BY SIMILARITY).
FT	MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	57	57	(BY SIMILARITY).
FT	MOD_RES	57	57	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	60	60	(BY SIMILARITY).
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	61	61	(BY SIMILARITY).
FT	MOD_RES	61	61	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	66	66	(BY SIMILARITY).
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	67	67	(BY SIMILARITY).
FT	MOD_RES	67	67	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	70	70	(BY SIMILARITY).
FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	112	112	(BY SIMILARITY).
FT	MOD_RES	112	112	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	253	253	CHARGE RELAY SYSTEM.
FT	ACT_SITE	299	299	CHARGE RELAY SYSTEM.
FT	ACT_SITE	402	402	CHARGE RELAY SYSTEM.
FT	DISULFID	58	63	BY SIMILARITY.
FT	DISULFID	91	110	BY SIMILARITY.
FT	DISULFID	100	105	BY SIMILARITY.
FT	DISULFID	104	119	BY SIMILARITY.
FT	DISULFID	121	130	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	146	159	BY SIMILARITY.
FT	DISULFID	161	174	BY SIMILARITY.
FT	DISULFID	182	319	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	238	254	BY SIMILARITY.
FT	DISULFID	373	387	BY SIMILARITY.
FT	DISULFID	398	426	BY SIMILARITY.
FT	CARBOHYD	214	214	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	328	328	MISSING (IN REF. 2).
FT	CONFLICT	393	393	N -> D (IN REF. 2).
FT	SEQUENCE	461 AA;	51945 MW;	53FA0D85B194D6E CRC64;

Query Match 53.7%; Score 102; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 2e-10;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFXXLRGSLRXCKXQCSFXXAEXIFPDAXTKLFWISY 44
 DB 42 ANSFLEMRPGSLERECMBETCFEPAQELFQVVEDTLAIFWIKY 85

RESULT 6
 PRIC_PIG STANDARD; PRT; 459 AA.
 AC 09GLP2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Suidae.

OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21121490; PubMed=11229814;
 RA Grimm D.R., Colter W.B., Braunschweig M., Alexander L.J., Neame P.J.,
 RA Kim H.K.W.;
 RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
 RT protein modeling of membrane binding sites and comparative anatomy of
 RT domains";
 RL Cell. Mol. Life Sci. 58:148-159(2001).
 CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
 CC regulates blood coagulation by inactivating factors Va and VIIIa
 CC in the presence of calcium ions and phospholipids.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIa.
 CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
 CC into a light chain and a heavy chain held together by a disulfide
 CC bond. The enzyme is then activated by thrombin, which cleaves a
 CC tetradecapeptide from the amino end of the heavy chain; this
 CC reaction, which occurs at the surface of endothelial cells, is
 CC strongly promoted by thrombomodulin.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some glu
 CC residues allows the modified protein to bind calcium.
 CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the
 CC thrombin-thrombomodulin complex.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: AF191307; AACU28380.1; -;
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218; -;
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR002383; GLA blood.
 DR InterPro: IPR001254; Ser protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin_1.
 DR Pfam: PF00594; gla_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00001; EGF_like_2.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; TRYP_SPC_1.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1_1.
 DR PROSITE: PS01186; EGF_2_2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS00240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS_1.
 DR PROSITE: PS00135; TRYPSIN_SER_1.
 KW Blood coagulation: Glycoprotein; Serine protease;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 41 BY SIMILARITY.
 FT CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.

FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY
 FT SIMILARITY).
 FT CHAIN 199 459 PROTEIN C HEAVY CHAIN (BY
 FT SIMILARITY).
 FT PEPTIDE 199 213 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT SITE 213 214 CLEAVAGE (BY THROMBIN) (BY
 FT SIMILARITY).
 FT DOMAIN 96 131 EGF-LIKE 1.
 FT DOMAIN 135 175 EGF-LIKE 2.
 FT DOMAIN 214 459 SERINE PROTEASE.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
 FT ACT_SITE 255 255 CHARGE RELAY SYSTEM.
 FT ACT_SITE 301 301 CHARGE RELAY SYSTEM.
 FT ACT_SITE 400 400 CHARGE RELAY SYSTEM.
 FT DISULFID 58 63 BY SIMILARITY.
 FT DISULFID 91 110 BY SIMILARITY.
 FT DISULFID 100 105 BY SIMILARITY.
 FT DISULFID 104 119 BY SIMILARITY.
 FT DISULFID 121 130 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 146 159 BY SIMILARITY.
 FT DISULFID 161 174 BY SIMILARITY.
 FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 240 256 BY SIMILARITY.
 FT DISULFID 371 385 BY SIMILARITY.
 FT DISULFID 396 424 BY SIMILARITY.
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CCL6D09 CRC64;
 Query Match 53.2%; Score 101; DB 1; Length 459;
 Best Local Similarity 45.5%; Pred. No. 3e-10; 21; Indels 0; Gaps 0;
 Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRKESLXRXCKXKCSFYXAEYIFDAXRTKLFWSY 44
 DB 42 ANSFLELRPSLRKCEKFTCDFEAREIFONTENTMAFWKSY 85
 RESULT 7
 PRTC RAT STANDARD; PRT; 461 AA.
 AC P31354;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic IIR) (Anticoagulant protein C) (blood coagulation
 DE factor XIV).
 GN PROC.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Metcar; TISSUE=Liver;
RX MEDLINE=92329550; PubMed=1627650;
RA Okatsuji T., Maekawa K., Nawa K., Marumoto Y.;
RT "The cDNA cloning and mRNA expression of rat protein C.;"
RL Biochim. Biophys. Acta 1131:329-332(1992).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADCAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; X64336; CAA45617.1; -
DR PIR; S18994; S18994.
DR PIR; S24312; S24312.
DR HSP; P04070; IPCU.
DR MEROPS; S01.218; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Blood coagulation: Glycoprotein; Serine protease;
KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL 1 32
FT PROPEP 33 41 BY SIMILARITY.
FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT CHAIN 199 461 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT PEPTIDE 199 212 ACTIVATION PEPTIDE (BY SIMILARITY).

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FT SITE 212 213 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT DOMAIN 96 131 EGF-LIKE 1.
FT DOMAIN 135 175 EGF-LIKE 2.
FT DOMAIN 213 461 SERINE PROTEASE.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 48 48 (BY SIMILARITY).
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 55 55 (BY SIMILARITY).
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 57 57 (BY SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 60 60 (BY SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 61 61 (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 (BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 67 67 (BY SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 70 70 (BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 112 112 (BY SIMILARITY).
FT ACT_SITE 254 254 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT ACT_SITE 58 63 CHARGE RELAY SYSTEM.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 255 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT DISULFID 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 8A4CF9364EDACD5 CRC64;

Query Match 53.2%; Score 101; DB 1; Length 461;
Best Local Similarity 45.5%; Pred No. 36-10;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXXQCSFXXAEXIFKDXRTKLFWISY 44
DB 42 ANGFLEVRAGSLERECMEICDFEENQEIFQVEDTLAFWIKY 85

RESULT 8
FA10 HUMAN STANDARD; PRT; 488 AA.
ID FA10 HUMAN 014340:
AC P00742; O14340:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
ON (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=91216473; PubMed=1902434;
RA Messler T.L., Filtman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RL human coagulation factor X.;"
Gene 99:291-294 (1991).
RN [2]

```

RP SEQUENCE FROM N.A.
 RX MEDLINE=87026600; PubMed=3768335;
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RT protein C.";
 RL Biochemistry 25:5098-5102(1986).
 RN (3)
 RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RT blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN (4)
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";
 RL Gene 41:311-314(1986).
 RN (5)
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kistel W., Saeagawa T., Howald W.N.,
 RA Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884(1983).
 RN (6)
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kistel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 RN (7)
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN (8)
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusnam K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519(1989).
 RN (9)
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
 RA Huber R., Blumenship D.T., Caroin A.D., Kistel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966(1993).
 RN (10)
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kamata K., Kawamoto H., Homma T., Iwana T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXa (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIa (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; K03194; AAA52490.1; -
 DR EMBL; M57285; AAA52421.1; -
 DR EMBL; L29433; AAA52764.1; -
 DR EMBL; L00390; AAA52764.1; JOINED.
 DR EMBL; L00391; AAA52764.1; JOINED.
 DR EMBL; L00392; AAA52764.1; JOINED.
 DR EMBL; L00393; AAA52764.1; JOINED.
 DR EMBL; L00394; AAA52764.1; JOINED.
 DR EMBL; L00395; AAA52764.1; JOINED.
 DR EMBL; L00396; AAA52764.1; JOINED.
 DR EMBL; M22613; AAA51984.1; -
 DR EMBL; K01886; AAA52486.1; -
 DR EMBL; M33297; AAA52636.1; -
 DR PIR; A00924; EXHU
 DR PIR; A05853; A25853.
 DR PIR; A24478; A24478.
 DR PDB; 1HCG; 08-MAY-95.
 DR PDB; 1FAX; 29-OCT-97.
 DR PDB; 1EXY; 17-JUN-98.
 DR PDB; 1XKA; 23-MAR-99.
 DR PDB; 1XKB; 23-MAR-99.
 DR MEROPS; S01.216; -
 DR GlycoSuiteDB; P00742; -
 DR GeneW; HGNC:3528; F10.
 DR MIM; 134530; -
 DR MIM; 227600; -
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF-2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRY_P; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS00186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00340; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR GlycoProtein; Hydroxylase; Serine protease; Plasma; Blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;


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FT  MOD_RES      66      66      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      69      69      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      72      72      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      75      75      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      79      79      GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES      103     103     HYDROXYLATION (BY SIMILARITY).
FT  ACT_SITE     274     274     CHARGE RELAY SYSTEM.
FT  ACT_SITE     320     320     CHARGE RELAY SYSTEM.
FT  ACT_SITE     417     417     CHARGE RELAY SYSTEM.
FT  DISULFID     90      101     BY SIMILARITY.
FT  DISULFID     95      110     BY SIMILARITY.
FT  DISULFID     112     121     BY SIMILARITY.
FT  DISULFID     129     140     BY SIMILARITY.
FT  DISULFID     136     149     BY SIMILARITY.
FT  DISULFID     151     164     BY SIMILARITY.
FT  DISULFID     172     240     INTERCHAIN (BY SIMILARITY).
FT  DISULFID     239     244     BY SIMILARITY.
FT  DISULFID     259     275     BY SIMILARITY.
FT  DISULFID     388     402     BY SIMILARITY.
FT  DISULFID     413     441     BY SIMILARITY.
FT  CARBOHYD     61      61      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD     187     187     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD     205     205     N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE      490 AA; 53965 MM; 3A39FA85AF2AD6D1 CR664;

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Query Match      52.1%; Score 99; DB 1; Length 490;
Best Local Similarity 40.9%; Pred. No. 7,2e-10;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

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Oy  1 ANAFLXLRGSLRXKXKXQCSFXAXEXIFDQAKRTKLFWISY 44
Db  41 ANSFLEELKGNLRECEMNCSEYFALVFEDEKRETNFWMXY 84

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RESULT 10
ID  FA10_BOVIN  STANDARD; PRT; 492 AA.
AC  P00743;
DT  21-JUL-1986 (Rel. 01, Created)
DT  13-AUG-1987 (Rel. 05, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
GN  F10.
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  1
RP  SEQUENCE OF 1-487 FROM N.A.
RX  MEDLINE=84247315; PubMed=6330671;
RA  "Pung M.R., Campbell R.M., McGillivray R.T.A.;
RT  "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT  containing a prepro leader sequence.";
RL  Nucleic Acids Res. 12:4481-4492(1984).
RN  2
RP  SEQUENCE OF 41-180.
RX  MEDLINE=80130563; PubMed=6766735;
RA  Entfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA  Titani K.;
RT  "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT  factor).";
RL  Biochemistry 19:659-667(1980).
RN  3
RP  REVISION TO 103.
RX  MEDLINE=83308813; PubMed=6688526;
RA  McMullen B.A., Fujikawa K., Kistel W.;
RT  "The occurrence of beta-hydroxyaspartic acid in the vitamin

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RT  K-dependent blood coagulation zymogens.";
RL  Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN  4
RP  SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX  MEDLINE=76053069; PubMed=1059093;
RA  Titani K., Fujikawa K., Entfield D.L., Ericsson L.H., Walsh K.A.,
RA  Neurath H.;
RT  "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT  chain.";
RL  Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN  5
RP  SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX  MEDLINE=94062825; PubMed=8243461;
RA  Inoue K., Morita T.;
RT  "Identification of O-linked oligosaccharide chains in the activation
RT  peptides of blood coagulation factor X. The role of the carbohydrate
RT  moieties in the activation of factor X.";
RL  Eur. J. Biochem. 218:153-163(1993).
RN  6
RP  ACTIVE SITE.
RX  MEDLINE=73053114; PubMed=4264286;
RA  Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA  Neurath H., Davie E.W.;
RT  "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT  with mammalian serine proteases.";
RL  Biochemistry 11:4899-4903(1972).
RN  7
RP  PROCESSING.
RX  MEDLINE=76053121; PubMed=1059122;
RA  Fujikawa K., Titani K., Davie E.W.;
RT  "Activation of bovine factor X (Stuart factor): conversion of factor
RT  Xa-alpha to factor Xa-beta.";
RL  Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN  8
RP  CALCIUM-BINDING DATA.
RX  MEDLINE=84185716; PubMed=6546930;
RA  Sugo T., Bjorker I., Holmgren A., Stenflo J.;
RT  "Calcium-binding properties of bovine factor X lacking the gamma-
RT  carboxyglutamic acid-containing region.";
RL  J. Biol. Chem. 259:5705-5710(1984).
RN  9
RP  SULFATION.
RX  MEDLINE=86140210; PubMed=3949800;
RA  Morita T., Jackson C.M.;
RT  "Localization of the structural difference between bovine blood
RT  coagulation factors XI and X2 to tyrosine 18 in the activation
RT  peptide.";
RL  J. Biol. Chem. 261:4008-4014(1986).
RN  10
RP  STRUCTURE BY NMR OF 85-126.
RX  MEDLINE=91084483; PubMed=2261466;
RA  Selander M., Persson E., Stenflo J., Drakenberg T.;
RT  "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT  the amino-terminal epidermal growth factor like domain in coagulation
RT  factor X.";
RL  Biochemistry 29:8111-8118(1990).
RN  11
RP  STRUCTURE BY NMR OF 85-126.
RX  MEDLINE=92329412; PubMed=1627540;
RA  Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA  Telemann O.;
RT  "Three-dimensional structure of the apo form of the N-terminal
RT  EGF-like module of blood coagulation factor X as determined by NMR
RT  spectroscopy and simulated folding.";
RL  Biochemistry 31:5974-5983(1992).
RN  12
RP  STRUCTURE BY NMR OF 85-126.
RX  MEDLINE=92406922; PubMed=1527084;
RA  Selander-Sunnerhagen M., Ullner M., Persson E., Telemann O.,
RA  Stenflo J., Drakenberg T.;
RT  "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT  resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT  like domain in coagulation factor X.";

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DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1. Transmembrane.
KM Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROSEP 1 20
FT CHAIN 21 218
FT DOMAIN 21 83 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT TRAMSEM 84 106 POTENTIAL.
FT DOMAIN 107 218 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 24 61 POTENTIAL.
FT DOMAIN 131 135 CYTOSOLIC (POTENTIAL).
FT DOMAIN 131 135 GLA-RICH.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

Query Match 51.1%; Score 97; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 7.2e-10;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXKCKXQCSFXAXEKFQDAXRTKLFWSY 44
DB 21 ANGFPEIRQGNIERCKEPECTFEARARAFENNEKTEFWSY 64

RESULT 12
ID PRTC_BOVIN STANDARD; PRT; 456 AA.
AC P00745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
GN PROC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=85014826; PubMed=6091100;
RA Long G.L., Balagata R.M., McGillivray R.T.A.;
RT "Cloning and sequencing of liver cDNA coding for bovine protein C";
RT Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656 (1984).
RN (2)
RP SEQUENCE OF 40-194.
RX MEDLINE=83007325; PubMed=6896876;
RA Fernlund P., Stenflo J.;
RT "Amino acid sequence of the light chain of bovine protein C";
RT J. Biol. Chem. 257:12170-12179 (1982).
RN (3)
RP REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Drekenberg T., Fernlund P., Roepstorff P., Stenflo J.;
RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";
RT Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806 (1983).
RN (4)
RP SEQUENCE OF 197-456.
RX MEDLINE=83007326; PubMed=6896877;
RA Stenflo J., Fernlund P.;
RT "Amino acid sequence of the heavy chain of bovine protein C";
RT J. Biol. Chem. 257:12180-12190 (1982).
RN (5)
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Esmon N.L., Debault L.E., Esmon C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
RT domainless protein C.";
RT J. Biol. Chem. 258:5548-5553 (1983).
RN (6)
RP PROCESSING, AND CALCIUM-BINDING DATA.

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RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmon N.L., Lave T.M., Esmon C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid.";
RL J. Biol. Chem. 258:5554-5560 (1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K02435; AAA0685.1; -.
DR PIR; A00928; KXBO.
DR HSSP; P04070; LPCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01187; EGF_2; 2.
DR PROSITE; PS01186; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT NON TER 1 1
FT SIGNAL 1 29
FT PROSEP 30 39
FT CHAIN 40 194
FT CHAIN 197 456
FT PEPTIDE 197 210
FT DOMAIN 94 129
FT DOMAIN 133 173
FT DOMAIN 211 456
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53

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PROTEIN C LIGHT CHAIN.
PROTEIN C HEAVY CHAIN.
ACTIVATION PEPTIDE.
EGF-LIKE 1.
EGF-LIKE 2.
SERINE PROTEASE.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.

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FT  MOD_RES      55      55      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD_RES      58      58      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD_RES      59      59      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD_RES      62      62      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD_RES      64      64      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD_RES      65      65      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD_RES      68      68      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD_RES      74      74      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD_RES      110     110     HYDROXYLATION.
FT  ACT_SITE     252     252     CHARGE RELAY SYSTEM.
FT  ACT_SITE     298     298     CHARGE RELAY SYSTEM.
FT  ACT_SITE     397     397     CHARGE RELAY SYSTEM.
FT  DISULFID     56      61      BY SIMILARITY.
FT  DISULFID     89      108     BY SIMILARITY.
FT  DISULFID     98      103     BY SIMILARITY.
FT  DISULFID     102     117     BY SIMILARITY.
FT  DISULFID     119     128     BY SIMILARITY.
FT  DISULFID     137     148     BY SIMILARITY.
FT  DISULFID     144     157     BY SIMILARITY.
FT  DISULFID     159     172     BY SIMILARITY.
FT  DISULFID     180     318     INTERCHAIN.
FT  DISULFID     237     253     N-LINKED (GLCNAC. . .)
FT  DISULFID     368     382     N-LINKED (GLCNAC. . .)
FT  DISULFID     393     421     N-LINKED (GLCNAC. . .)
FT  CARBOHYD     136     136     N-LINKED (GLCNAC. . .)
FT  CARBOHYD     289     289     N-LINKED (GLCNAC. . .)
FT  CARBOHYD     350     350     N-LINKED (GLCNAC. . .)
FT  CARBOHYD     366     366     N-LINKED (GLCNAC. . .)
FT  VARIANT      82      82      F -> K.
FT  CONFLICT     455     456     VP -> PV (IN REF. 4).
SQ  SEQUENCE     456 AA; 51407 MW; CAPE683F894C209 CRC64;

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Query Match      47.9%; Score 91; DB 1; Length 456;
Best Local Similarity 40.9%; Pred. No. 1.8e-08;
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

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QY 1 ANAFXXLRGSLXRXCKXXQCSFXAXEIPKDXRTKLFWISY 44
Db 40 ANSELELRPGNVERECSEVECFEAREIFQNTEDTMAFWSFY 83

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RESULT 13
TMG3_HUMAN      STANDARD;      PRT;      231 AA.
AC 09BZD7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=2117044; PubMed=1171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues."
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Glu residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF326350; AAK00955.1; -.
DR HSSP; P00740; 1CFH.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP      1      19      POTENTIAL.
FT CHAIN       20      231     TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT FT          20      78      EXTRACELLULAR (POTENTIAL).
FT FT          79      101     POTENTIAL.
FT FT          102     231     CYTOPLASMIC (POTENTIAL).
FT FT          23      60      GLA-RICH.
SQ  SEQUENCE     231 AA; 25848 MW; 8A373E4848490D81 CRC64;

```

```

Query Match      47.4%; Score 90; DB 1; Length 231;
Best Local Similarity 36.4%; Pred. No. 1.4e-08;
Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

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```

QY 1 ANAFXXLRGSLXRXCKXXQCSFXAXEIPKDXRTKLFWISY 44
Db 20 ANSELELRPGNVERECSEVECFEAREIFQNTEDTMAFWSFY 63

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RESULT 14
FA10_CHICK      STANDARD;      PRT;      475 AA.
AC P25155;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
DE (Virus activating protease) (VAP).
GN FX.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Chorioallantoic membrane;
RX MEDLINE=91257322; PubMed=2044767;
RA Suzuki H., Harada A., Hayashi Y., Wada K., Asaka J.-I., Gotoh B.,
RA Ogasawara T., Nagai Y.;
RT "Primary structure of the virus activating protease from chick
RT embryo. Its identity with the blood clotting factor Xa."
RL FEBS Lett. 283:281-285(1991).
RN [2]
RP SEQUENCE OF 41-55 AND 241-261.
RC TISSUE=Allantoic fluid;
RX MEDLINE=91065352; PubMed=2174359;
RA Gotoh B., Ogasawara T., Toyoda T., Innocencio N.M., Hameguchi M.,
RA Nagai Y.;
RT "An endoprotease homologous to the blood clotting factor X as a
RT determinant of viral tropism in chick embryo."
RL EMBO J. 9:4189-4195(1990).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,
CC AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING
CC SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
CC SAC.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

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CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, D00844; BAA00724.1; -
 CC PIR, S15838; S15838.
 CC HSP, P00742; S15838.
 CC MEROPS, S01.216; -
 CC InterPro, IPR000152; Asx_hydroxyl.
 CC InterPro, IPR001314; Chymotrypsin.
 CC InterPro, IPR000561; EGF-1-like.
 CC InterPro, IPR000742; EGF 2.
 CC InterPro, IPR001881; EGF_Ca.
 CC InterPro, IPR001438; EGF_11.
 CC InterPro, IPR002383; GLA_blood.
 CC InterPro, IPR001254; Ser_protease_Try.
 CC InterPro, IPR000294; Vitr_dep_GLA.
 CC Pfam, PF00008; EGF_2.
 CC Pfam, PF00594; trypsin; 1.
 CC PRINTS, PR00722; CHYMOTRYPSIN.
 CC PRINTS, PR00010; EGFblood.
 CC PRINTS, PR00001; GLABLOOD.
 CC SMART, SM00179; EGF_CA; 1.
 CC SMART, SM00063; GLA; 1.
 CC SMART, SM00020; TRYP_Spec; 1.
 CC PROSITE, PS00010; ASX_HYDROXYL; 1.
 CC PROSITE, PS00022; EGF_1; 1.
 CC PROSITE, PS01186; EGF_2; 2.
 CC PROSITE, PS01187; EGF_CA; 1.
 CC PROSITE, PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE, PS50240; TRYPSIN_DOM; 1.
 CC PROSITE, PS00134; TRYPSIN_HIS; 1.
 CC PROSITE, PS00135; TRYPSIN_SER; 1.
 CC GlycoProfile; Hydrolase; Serine protease; Plasma; blood coagulation;
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat.
 CC SIGNAL 1 20 OR 30, OR 31 (POTENTIAL).
 CC PROPEP 21 40
 CC CHAIN 41 180 FACTOR X LIGHT CHAIN.
 CC CHAIN 186 475 FACTOR X HEAVY CHAIN.
 CC PROPEP 186 241 ACTIVATION PEPTIDE.
 CC CHAIN 242 475 ACTIVATED FACTOR XA, HEAVY CHAIN.
 CC DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 CC DOMAIN 125 168 EGF-LIKE 2.
 CC DOMAIN 241 475 SERINE PROTEASE.
 CC MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).

FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID
 FT (BY SIMILARITY).
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
 FT (BY SIMILARITY).
 FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID
 FT (BY SIMILARITY).
 FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID
 FT (BY SIMILARITY).
 FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID
 FT (BY SIMILARITY).
 FT MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
 FT ACT_SITE 282 282 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 328 328 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 425 425 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 90 101 BY SIMILARITY.
 FT DISULFID 95 110 BY SIMILARITY.
 FT DISULFID 112 121 BY SIMILARITY.
 FT DISULFID 129 140 BY SIMILARITY.
 FT DISULFID 136 152 BY SIMILARITY.
 FT DISULFID 154 167 BY SIMILARITY.
 FT DISULFID 175 348 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 247 252 BY SIMILARITY.
 FT DISULFID 267 283 BY SIMILARITY.
 FT DISULFID 396 410 BY SIMILARITY.
 FT DISULFID 421 449 BY SIMILARITY.
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 475 AA; 53142 MW; 570BF84956C5C74D CRC64;

Query Match 46.8%; Score 89; DB 1; Length 475;
 Best Local Similarity 36.4%; Pred. No. 4.2e-08;
 Matches 16; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXQCSFXXAEXIFDAXRTKLWISY 44
 DB 41 ANSFLKMKQGNIBRECNERSCKEAREAFEDNKEEFNFIY 84

RESULT 15
 ID PRIC RABIT STANDARD; PRT; 458 AA.
 AC 028661;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic cleavage) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV) (Fragment).
 GN PROC.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Shen L., He X., Dahlback B.;
 RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIa.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME

CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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CC EMBL; U49933; AAA92956.1; -
CC HSSP; P04070; 1PCU.
DR MEROPS; S01.218: -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_deg_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00020; TRYP_SPE; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT PROPEP 28 36
FT CHAIN 37 458
FT CHAIN 37 192
FT CHAIN 195 458
FT PEPTIDE 195 209
FT SITE 209 210
FT DOMAIN 91 126
FT DOMAIN 130 170
FT DOMAIN 210 458
FT MOD_RES 42 42
FT MOD_RES 43 43
FT MOD_RES 50 50
FT MOD_RES 52 52
FT MOD_RES 55 55
FT MOD_RES 56 56
FT MOD_RES 61 61
FT MOD_RES 62 62
FT MOD_RES 65 65
FT MOD_RES 107 107
FT ACT_SITE 250 250
FT ACT_SITE 296 296

FT ACT_SITE 399 399 CHARGE RELAY SYSTEM.
FT DISULFID 53 58 BY SIMILARITY.
FT DISULFID 86 105 BY SIMILARITY.
FT DISULFID 95 100 BY SIMILARITY.
FT DISULFID 99 114 BY SIMILARITY.
FT DISULFID 116 125 BY SIMILARITY.
FT DISULFID 134 145 BY SIMILARITY.
FT DISULFID 141 154 BY SIMILARITY.
FT DISULFID 156 169 BY SIMILARITY.
FT DISULFID 177 316 INTERCHAIN (BY SIMILARITY).
FT DISULFID 235 251 BY SIMILARITY.
FT DISULFID 370 384 BY SIMILARITY.
FT DISULFID 395 423 BY SIMILARITY.
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 458 AA; 51087 MW; D75A5F990C8F29D7 CRC64;

Query Match 44.7%; Score 85; DB 1; Length 458;
Best Local Similarity 40.9%; Pred. No. 2.1e-07;
Matches 18; Conservative 3; Mismatches 23; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSFYXAEXIPKDAKTKLFWISY 44
Db 37 ANSFLELRPSLRECVCEVCDLEBAKEIFQGVDDTLAFWYKY 80

Search completed: March 19, 2003, 14:52:46
Job time : 6.625 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10GLU28GLU
Perfect score: 190
Sequence: 1 ANAFIXLREGSLKRXCKXK.....XXAEXIFDXARKLFWISY 44

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 21:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp virus:*
16: sp bacteriap:*
17: sp archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	83.7	701	4 Q96P08	Q96P08 homo sapien
2	114	60.0	446	11 Q61I09	Q61I09 mus musculu
3	102	53.7	460	11 Q91MN8	Q91MN8 mus musculu
4	96	50.5	460	11 Q99PC6	Q99PC6 mus musculu
5	93	48.9	482	11 Q63207	Q63207 rattus norv
6	92	48.4	456	6 Q9TTR0	Q9TTR0 canis faml
7	91	47.9	469	6 Q9GMD9	Q9GMD9 ornithorhyn
8	91	47.9	481	11 Q54740	Q54740 mus musculu
9	91	47.9	481	11 Q99L32	Q99L32 mus musculu
10	91	47.9	481	11 Q88947	Q88947 mus musculu
11	85	44.7	100	4 Q15253	Q15253 homo sapien
12	81	42.6	49	6 Q95ME8	Q95ME8 bos taurus
13	80	42.1	456	4 Q14316	Q14316 homo sapien
14	80	42.1	461	6 Q95ND7	Q95ND7 pan troglod
15	80	42.1	461	6 Q95ND6	Q95ND6 pan troglod
16	76	40.0	179	4 Q87AS3	Q87AS3 homo sapien

17	76	40.0	198	11 Q8R182	Q8R182 mus musculu
18	74	38.9	138	6 Q28994	Q28994 sus scrofa
19	70	36.8	433	13 Q90YK1	Q90YK1 brachydanio
20	67	35.3	648	6 Q29094	Q29094 sus scrofa
21	65	34.2	98	13 P82807	P82807 notechis sc
22	64	33.7	399	11 Q9COW3	Q9COW3 mus musculu
23	63	33.2	608	13 Q9PTW7	Q9PTW7 struthio ca
24	62	32.6	650	4 Q9NSD0	Q9NSD0 homo sapien
25	62	32.6	650	4 Q16519	Q16519 homo sapien
26	60	31.6	607	13 Q91001	Q91001 gallus gall
27	58.5	30.8	431	10 Q94EY5	Q94EY5 arabidopsis
28	58.5	30.8	492	10 Q9SM07	Q9SM07 cicer ariet
29	58.5	30.8	543	10 Q9MB23	Q9MB23 arabidopsis
30	58.5	30.8	576	10 Q9C9U4	Q9C9U4 arabidopsis
31	58.5	30.8	589	10 Q9LMS2	Q9LMS2 arabidopsis
32	57.5	30.3	196	10 Q04284	Q04284 selaginella
33	57.5	30.3	542	5 Q8T613	Q8T613 halocynthia
34	56.5	29.7	459	10 Q9SE22	Q9SE22 oryza sativ
35	55.5	29.2	506	10 Q9SPF0	Q9SPF0 oryza sativ
36	55.5	29.2	506	10 Q9SE23	Q9SE23 oryza sativ
37	55.5	29.2	567	10 Q8M4J2	Q8M4J2 arabidopsis
38	55	28.9	25	11 Q9QVH6	Q9QVH6 rattus sp.
39	54.5	28.7	510	10 Q9MB22	Q9MB22 arabidopsis
40	54.5	28.7	619	10 Q9LV37	Q9LV37 arabidopsis
41	53	27.9	673	11 Q61592	Q61592 mus musculu
42	53	27.9	674	11 Q99K57	Q99K57 mus musculu
43	52.5	27.6	588	10 Q9LM33	Q9LM33 arabidopsis
44	52.5	27.6	603	10 Q9LEP7	Q9LEP7 arabidopsis
45	52.5	27.6	606	10 Q9SUG9	Q9SUG9 arabidopsis

ALIGNMENTS

RESULT 1
Q96P08 PRELIMINARY: PRT; 701 AA.
ID Q96P08
AC Q96P08
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AAK58686.1; -.
DR InterPro; IPR000152; Asx hydrolase.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SMO0181; EGF; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CB42C992F CRC64;

Query Match 83.7%; Score 159; DB 4; Length 701;
 Best Local Similarity 72.7%; Pred. No. 8e-21;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRREGSLRXKCKXQCSFXXAEXIFKDAKRTKLFWISY 44
 DB 61 ANAFLELRPGSLRECKECCSFEEAREIFKDAERTKLFWISY 104

RESULT 2
 O61109 PRELIMINARY; PRT; 446 AA.

ID O61109;
 AC O61109;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Coagulation factor VII.
 GN F7 OR FVII.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96276538; PubMed=8701412;
 RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Characterization of a cDNA encoding murine coagulation factor VII.",
 RT Thromb. Haemost. 75:481-487(1996).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY
 DR EMBL: U44795; AAC52570.1; -.
 DR HSSP: P08709; 1FAK.
 DR MEROPS: S01.215; -.
 DR MGD: MGI:109325; F7.
 DR InterPro: IPR002086; Aldehyde dehydr.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001064; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; Tryp_SPC; 1.
 DR PROSITE: PS00070; ALDEHYDE DEHYDR. CYS; UNKNOWN_1.
 DR PROSITE: PS00025; ASX HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00025; CRYSTALLIN BETAGANMA; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
 KM Serine protease.
 SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 60.0%; Score 114; DB 11; Length 446;

Best Local Similarity 54.5%; Pred. No. 1.3e-12;
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRREGSLRXKCKXQCSFXXAEXIFKDAKRTKLFWISY 44
 DB 42 ANSLEELWPGSLRECKECCSFEEAREIFKSPERTKQFWIVY 85

RESULT 3

ID Q91WN8 PRELIMINARY; PRT; 460 AA.

AC Q91WN8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC018896; AH18896.1; -.
 DR MGD: MGI:97771; Proc.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PROSITE: PS00010; ASX HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE: PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; UNKNOWN_1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 460 AA; 51818 MW; 0117F2E686FCC274 CRC64;

Query Match 53.7%; Score 102; DB 11; Length 460;
 Best Local Similarity 45.5%; Pred. No. 2.2e-10;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRREGSLRXKCKXQCSFXXAEXIFKDAKRTKLFWISY 44
 DB 42 ANSLEELWPGSLRECKECCSFEEAREIFQVVEDTLAWIKY 85

RESULT 4

ID Q99PC6 PRELIMINARY; PRT; 460 AA.

AC Q99PC6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Anticoagulant protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Korf I.;

RT "Complete sequence of UC72A01."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
DR EMBL: AF318182; AKK07918.1; -.
DR HSSP: P04070; 1PCU.
DR MGD: MG1:97771; Proc.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00001; EGF_like_2.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

Query Match 50.5%; Score 96; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 3e-09;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFDKAXRTKLFWISY 44
DB 42 ANSFLEMRPGSLERECMEICOLEEAQEIFQVEDTLAFWIKY 85

RESULT 5
Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
for intracellular processing by the vitamin K-dependent gamma-
carboxylase.";
RT Thromb. Res. 80:63-73 (1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
CC EMBL: X79807; CAA56202.1; -.
DR HSSP: P00742; IXKA.
DR MEROPS: S01.216; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_like_1.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 48.9%; Score 93; DB 11; Length 482;
Best Local Similarity 38.6%; Pred. No. 1.1e-08;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFDKAXRTKLFWISY 44
DB 41 ANSFPEIKGNLRECVETICSFEBAREVFDNKTTEFMWY 84

RESULT 6
Q9TTR0 PRELIMINARY; PRT; 456 AA.
AC Q9TTR0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Protein C precursor.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Flesipedida; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matlis U., Brunberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene.";
RT Mamm. Genome 10:135-139 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms.";
RL Anim. Genet. 30:237-238 (1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
CC EMBL: AJ001979; CAA05126.1; -.
DR HSSP: P04070; 1PCU.
DR MEROPS: S01.218; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR001254; Ser_protease_Try.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
 KM Repeat; Serine protease; Signal.
 FT SIGNAL 1 40 POTENTIAL.
 FT CHAIN 41 481 COAGULATION FACTOR X.
 SQ SEQUENCE 481 AA; 53986 MW; CF702DSEFP9D7AE CRC64;

Query Match 47.9%; Score 91; DB 11; Length 481;
 Best Local Similarity 36.4%; Pred. No. 2.7e-08;
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLXLRGSLRXCKXQCSFXXAEXIFKDAKTKLFWISY 44
 Db 41 ANSFEEFKGNLERECMEICSYEEVREIFEDDEKTKYWKY 84

RESULT 9
 ID Q99L32 PRELIMINARY; PRT; 481 AA.
 AC Q99L32;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Coagulation factor X.
 GN F10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL; BC003877; AAH03877.1; -.
 DR HSSP; P00742; 1XKA.
 DR MEROPS; S01.216; -.
 DR MGD; MGI:103107; F10.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_11.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGFLOOD.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00001; EGF-like; 2.
 DR SMART; SM00063; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
 KW Serine protease; Signal.
 SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 47.9%; Score 91; DB 11; Length 481;
 Best Local Similarity 36.4%; Pred. No. 2.7e-08;

Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 ANAFLXLRGSLRXCKXQCSFXXAEXIFKDAKTKLFWISY 44
 Db 41 ANSFEEFKGNLERECMEICSYEEVREIFEDDEKTKYWKY 84

RESULT 10
 ID O88947 PRELIMINARY; PRT; 481 AA.
 AC O88947;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update).
 DE Coagulation factor X precursor.
 GN F10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
 RX MEDLINE=98347933; PubMed=9684791;
 RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
 RA Castellino F.J., Rosen E.D.;
 RT "Cloning and characterization of a cDNA encoding murine coagulation
 RT factor X.";
 RL Thromb. Haemost. 80:87-91(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129Sj;
 RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
 RT "Cloning and characterization of the murine Factor X Gene.";
 RT Thromb. Haemost. 0:0-0(2000).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL; AF087644; AAC6345.1; -.
 DR EMBL; AF211347; AAF22980.1; -.
 DR HSSP; P00742; 1XKA.
 DR MEROPS; S01.216; -.
 DR MGD; MGI:103107; F10.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_Ca; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR SMART; SM00063; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
 KW Serine protease; Signal.
 FT SIGNAL 1 40 POTENTIAL.
 FT CHAIN 41 481 COAGULATION FACTOR X.
 SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5EFP9D271E CRC64;

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10GLU28GLU

Perfect score: 190

Sequence: 1 ANAFLXLRREGSLXRCCKX.....XXAEXIFKDAKRTLFWISY 44

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	165	86.8	44	3	US-08-955-636-26
2	162	85.3	44	3	US-08-955-636-27
3	159	83.7	44	3	US-08-955-636-3
4	159	83.7	406	1	US-08-293-778-24
5	159	83.7	406	1	US-08-295-411-5
6	159	83.7	406	2	US-08-955-471-5
7	159	83.7	406	5	PCT-US92-10242-5
8	159	83.7	444	1	US-08-475-845-2
9	159	83.7	444	2	US-08-327-690-2
10	159	83.7	444	2	US-08-660-289-2
11	159	83.7	444	2	US-08-537-807-2
12	159	83.7	444	2	US-08-871-003-2
13	159	83.7	444	2	US-08-464-233-2
14	159	83.7	444	4	US-09-189-607-2
15	159	83.7	444	4	US-09-378-907-2
16	159	83.7	444	5	PCT-US94-05779-2
17	159	83.7	466	1	US-07-882-202A-4
18	159	83.7	466	1	US-08-021-615A-4
19	159	83.7	466	1	US-08-321-777-4
20	159	83.7	466	4	US-09-009-217-14
21	159	83.7	466	4	US-09-009-655-14
22	159	83.7	466	5	PCT-US93-04493-4
23	158	83.2	44	3	US-08-955-636-30
24	156	82.1	44	3	US-08-955-636-28
25	153	80.5	44	3	US-08-955-636-29
26	144	75.8	41	1	US-08-229-280-4
27	123	64.7	44	3	US-08-955-636-4

28	108	56.8	139	1	US-08-330-978-2	Sequence 2, Appli
29	108	56.8	139	1	US-08-474-042-2	Sequence 2, Appli
30	108	56.8	139	1	US-08-484-558-2	Sequence 2, Appli
31	108	56.8	139	1	US-08-774-592-2	Sequence 2, Appli
32	108	56.8	437	1	US-08-487-037-2	Sequence 2, Appli
33	108	56.8	437	1	US-08-487-037-3	Sequence 3, Appli
34	108	56.8	488	1	US-08-487-037-1	Sequence 3, Appli
35	101	53.2	44	3	US-08-955-636-35	Sequence 35, Appli
36	99	52.1	44	3	US-08-955-636-18	Sequence 3, Appli
37	99	52.1	448	1	US-08-295-411-3	Sequence 3, Appli
38	99	52.1	448	2	US-08-955-471-3	Sequence 3, Appli
39	99	52.1	448	5	PCT-US92-10068-1	Sequence 1, Appli
40	99	52.1	448	5	PCT-US92-10242-3	Sequence 3, Appli
41	99	52.1	487	1	US-08-469-486-53	Sequence 53, Appli
42	99	52.1	487	2	US-08-469-658-53	Sequence 2, Appli
43	99	52.1	492	1	US-08-469-486-2	Sequence 2, Appli
44	99	52.1	492	2	US-08-469-658-2	Sequence 2, Appli
45	98	51.6	44	3	US-08-955-636-24	Sequence 24, Appli

ALIGNMENTS

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RESULT 1
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match      86.8%; Score 165; DB 3; Length 44;
Best Local Similarity 97.7%; Pred.No. 1.2e-20;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXLRREGSLXRCCKXCSFYXAXEIPKDAKRTLFWISY 44
Db 1 ANAFLXLRREGSLXRCCKXCSFYXAXEIPKDAKRTLFWISY 44

RESULT 2
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27
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Query Match
Best Local Similarity 85.3%; Score 162; DB 3; Length 44;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 ANAFLLXLRGSLRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
Db 1 ANAFLLXLRGSLRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
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RESULT 3
US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3
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Query Match
Best Local Similarity 83.7%; Score 159; DB 3; Length 44;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 ANAFLLXLRGSLRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
Db 1 ANAFLLXLRGSLRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
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RESULT 4
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
; GENERAL INFORMATION:
; APPLICANT: Nicolaisen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wiberg, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560ch America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,778
; FILING DATE:
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,509
; FILING DATE:
; APPLICATION NUMBER: DK 3235/87
; FILING DATE: 25-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/434,149
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK88/00103
; FILING DATE: 24-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,248
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agrie, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3129,224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-293-778-24
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Query Match
Best Local Similarity 83.7%; Score 159; DB 1; Length 406;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY 1 ANAFLLXLRGSLRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
Db 1 ANAFLLYLRGSLYRXCKYYQCSFYVARYIFPDAYRTKLFWISY 44
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RESULT 5
US-08-295-411-5
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Meesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
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;   REGISTRATION NUMBER: 34,163
;   REFERENCE/DOCKET NUMBER: TSR1263.0C1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 619-554-2937
;   TELEFAX: 619-554-6312
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 406 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 1..152
;   OTHER INFORMATION: /note= "Factor VII Light Chain"
;
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 153..406
;   OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
US-08-295-411-5

Query Match      83.7%; Score 159; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Cy 1 ANAFIXLRGSLRXCKXKOCSPXAXEIPFDARTKLFWISY 44
Db 1 ANAFLELRPGSLRCKEBCQCFEAREIFPDARTKLFWISY 44

RESULT 6
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Meesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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;
;   LENGTH: 406 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 1..152
;   OTHER INFORMATION: /note= "Factor VII Light Chain"
;
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 153..406
;   OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
US-08-955-471-5

Query Match      83.7%; Score 159; DB 2; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Cy 1 ANAFIXLRGSLRXCKXKOCSPXAXEIPFDARTKLFWISY 44
Db 1 ANAFLELRPGSLRCKEBCQCFEAREIFPDARTKLFWISY 44

RESULT 7
PCT-US92-10242-5
; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Meesters, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10242
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR0472P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
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OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match      83.7%; Score 159; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44
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DB 1 ANAFLELRPGSLRCKEKCQCSFEAREIFKDAERTKLFWISY 44

RESULT 8
US-08-475-845-2
; Sequence 2, Application US/08475845
; Patent No. 5788965
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,845
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-845-2

Query Match      83.7%; Score 159; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
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Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44
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DB 39 ANAFLELRPGSLRCKEKCQCSFEAREIFKDAERTKLFWISY 82

RESULT 9
US-08-327-690-2
; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-690-2

Query Match      83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 39 ANAFLELRPGSLRCKEKCQCSFEAREIFKDAERTKLFWISY 82

RESULT 10
US-08-660-289-2
; Sequence 2, Application US/08660289
; Patent No. 5833982
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
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; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,269
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-269-2

Query Match      83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKXCKXQCSFXXAEXIFKDAARTKLFWISY 44
DB 39 ANAFLELRPGSLRCKEKCQCSFEARERIFKDAERTKLFWISY 82

RESULT 11
US-08-537-807-2
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-537-807-2

Query Match      83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKXCKXQCSFXXAEXIFKDAARTKLFWISY 44
DB 39 ANAFLELRPGSLRCKEKCQCSFEARERIFKDAERTKLFWISY 82

RESULT 12
US-08-871-003-2
; Sequence 2, Application US/08871003
; Patent No. 5997864
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,003
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07c7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXKXQCSFXAXEXIFKDAKRTKLFWISY 44
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 13
US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match 83.7%; Score 159; DB 3; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXKXQCSFXAXEXIFKDAKRTKLFWISY 44
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14
US-09-189-607-2
Sequence 2, Application US/09189607
Patent No. 6168789
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,607
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,289
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-189-607-2

Query Match 83.7%; Score 159; DB 4; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXKXQCSFXAXEXIFKDAKRTKLFWISY 44
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15
US-09-378-907-2
Sequence 2, Application US/09378907
Patent No. 6183743

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; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,907
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/871,003
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-378-907-2

Query Match      83.7%; Score 159; DB 4; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRSGSLRXRCXKXCSFXKXAEKIFKDAKTKLFWISY 44
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Db 39 ANAFLELRPGSLRRCRCKEQCSFEAREIFKDAERTKLFWISY 82
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Job time : 10.75 secs

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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10GLU28GLU
Perfect score: 190
Sequence: 1 ANAFLXXLRGSLXRCCKX.....XXAEXIFDXARTKLFWISY 44

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Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	83.7	406	US-10-109-498-1	Sequence 1, Appli
2	98	51.6	419	US-10-182-263-6	Sequence 6, Appli
3	96	50.5	419	US-10-182-263-3	Sequence 3, Appli
4	96	50.5	419	US-10-182-263-4	Sequence 4, Appli
5	96	50.5	419	US-10-182-263-5	Sequence 5, Appli
6	85	44.7	419	US-10-182-263-1	Sequence 1, Appli
7	85	44.7	419	US-09-978-917A-4	Sequence 4, Appli
8	85	44.7	461	US-10-182-263-2	Sequence 2, Appli
9	85	44.7	461	US-09-978-917A-2	Sequence 2, Appli
10	80	42.1	415	US-09-118-748-2	Sequence 2, Appli
11	80	42.1	461	US-10-132-829-5	Sequence 5, Appli
12	80	42.1	461	US-09-884-901-3	Sequence 3, Appli
13	69.5	36.6	96	US-09-759-1308-113	Sequence 313, App
14	69.5	36.6	209	US-09-759-1308-112	Sequence 312, App
15	69.5	36.6	226	US-09-759-1308-110	Sequence 310, App
16	54.5	28.7	908	US-09-759-1308-355	Sequence 355, App
17	54.5	28.7	208	US-09-759-1308-356	Sequence 356, App
18	54.5	28.7	225	US-09-759-1308-353	Sequence 353, App
19	45	23.7	273	US-09-764-868-966	Sequence 966, App

20	44	23.2	447	10	US-09-815-242-13490	Sequence 13490, A
21	44	23.2	447	10	US-09-815-242-13612	Sequence 13612, A
22	44	23.2	447	10	US-09-735-564-2	Sequence 2, Appli
23	43	22.6	88	10	US-09-811-284-194	Sequence 194, App
24	43	22.6	1266	9	US-09-931-969A-2	Sequence 2, Appli
25	43	22.6	1266	9	US-10-079-699-2	Sequence 2, Appli
26	43	22.6	1266	10	US-09-757-781-63	Sequence 63, Appli
27	43	22.6	1356	10	US-09-757-781-2	Sequence 2, Appli
28	42	22.1	608	10	US-09-908-664-5	Sequence 5, Appli
29	42	22.1	729	9	US-10-145-396-11	Sequence 11, Appli
30	42	22.1	1258	10	US-09-922-943-1	Sequence 1, Appli
31	42	22.1	1274	10	US-09-746-491-12	Sequence 8, Appli
32	41.5	21.8	440	9	US-09-910-186A-8	Sequence 1, Appli
33	40.5	21.3	1149	10	US-09-969-528-5	Sequence 5, Appli
34	40	21.1	744	10	US-09-862-179A-1	Sequence 1, Appli
35	40	21.1	924	12	US-10-028-056-5	Sequence 5, Appli
36	40	21.1	1337	10	US-09-757-781-62	Sequence 62, Appli
37	39	20.5	347	10	US-09-780-053-4	Sequence 4, Appli
38	39	20.5	730	9	US-10-145-396-12	Sequence 12, Appli
39	39	20.5	730	10	US-09-780-053-2	Sequence 2, Appli
40	39	20.5	873	9	US-10-200-154-2	Sequence 2, Appli
41	39	20.5	873	10	US-09-954-043-2	Sequence 2, Appli
42	38.5	20.3	49	10	US-09-764-864-1054	Sequence 1054, App
43	38.5	20.3	1348	10	US-09-982-510-18	Sequence 18, Appli
44	38.5	20.3	1298	10	US-09-982-510-33	Sequence 33, Appli
45	38.5	20.3	1363	9	US-09-375-248-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      83.7% ; Score 159 ; DB 9 ; Length 406 ;
Best Local Similarity 95.5% ; Pred. No. 1.2e-20 ;
Matches 42 ; Conservative 0 ; Mismatches 2 ; Indels 0 ; Gaps 0 ;

QY 1 ANAFLXXLRGSLXRCCKXQCSFXAEXIFDXARTKLFWISY 44
Db 1 ANAFLXXLRGSLXRCCKXQCSFXAEXIFDXARTKLFWISY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022154A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

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Best Local Similarity 48.8%; Pred. No. 1.2e-09;
Matches 20; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDFEBAKEIFEDVDTLAFW 41

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          50.5%; Score 96; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.9e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDFEBAKEIFEDVDTLAFW 41

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          50.5%; Score 96; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.9e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDFEBAKEIFEDVDTLAFW 41

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          50.5%; Score 96; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.9e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDFEBAKEIFEDVDTLAFW 41

RESULT 6
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          42.1%; Score 80; DB 9; Length 461;
Best Local Similarity 40.0%; Pred. No. 2.4e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy      10 EGSIXRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
Db      57 QGNLRECMCKSCSFEEAREVFENTERTERTEFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOPW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: HomoSapien
US-09-884-901-3

Query Match          42.1%; Score 80; DB 10; Length 461;
Best Local Similarity 40.0%; Pred. No. 2.4e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy      10 EGSIXRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
Db      57 QGNLRECMCKSCSFEEAREVFENTERTERTEFWKQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
```

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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match          36.6%; Score 69.5; DB 9; Length 96;
Best Local Similarity 36.4%; Pred. No. 3.5e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

Qy      2 NAF-LXXLRGSLRXCKXXQCSFXXAEXIFKDXARTKLFWISY 44
Db      36 NRPDLLEFTPGNLERCBNEELCNVEAREIFVDEDXTIAFWQCY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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```
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-312

Query Match          36.6%; Score 69.5; DB 9; Length 209;
Best Local Similarity 36.4%; Pred. No. 8.1e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2 NAF-LXXLRGSLXRXCKXQCSFXXAEXIFKDXARTKLFWISY 44
Db      36 NRPDLFLTPGNLRECNELCNVEEARLIFVDEDKTIAFWQRY 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtel, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPIO0-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-759-130B-310

Query Match          36.6%; Score 69.5; DB 9; Length 226;
Best Local Similarity 36.4%; Pred. No. 8.8e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2 NAF-LXXLRGSLXRXCKXQCSFXXAEXIFKDXARTKLFWISY 44
Db      53 NRPDLFLTPGNLRECNELCNVEEARLIFVDEDKTIAFWQRY 96

Search completed: March 20, 2003, 13:30:09
Job time : 9.375 secs
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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds
(without alignments)
186.865 Million cell updates/sec

Title: 10GLU28PHE
Perfect score: 191
Sequence: 1 ANAFLXLRREGSLXRXCKX.....XXAFYFKDAXRKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	86.4	44	20	AAV18312
2	162	84.8	44	20	AAV18310
3	159	83.2	44	20	AAV18311
4	156	81.7	44	20	AAV18305
5	156	81.7	44	22	AAV18395
6	156	81.7	401	22	AAV184870
7	156	81.7	401	22	AAV184871
8	156	81.7	406	14	AAV185764
9	156	81.7	406	18	AAV14509
10	156	81.7	406	18	AAV14510

11	156	81.7	406	22	AAV77745	Human factor VIIa
12	156	81.7	406	22	AAV52171	Human FVII SEQ ID
13	156	81.7	406	22	AAV52172	Mammalian expresse
14	156	81.7	406	22	AAV52181	Human FVII mutant
15	156	81.7	406	22	AAV52182	Human FVII mutant
16	156	81.7	406	22	AAV52183	Human FVII mutant
17	156	81.7	406	22	AAV52184	Human FVII mutant
18	156	81.7	406	22	AAV52185	Human FVII mutant
19	156	81.7	406	22	AAV52186	Human FVII mutant
20	156	81.7	406	22	AAV52187	Human FVII mutant
21	156	81.7	406	22	AAV52188	Human FVII mutant
22	156	81.7	406	22	AAV52189	Human FVII mutant
23	156	81.7	406	22	AAV52190	Human FVII mutant
24	156	81.7	406	22	AAV52191	Human FVII mutant
25	156	81.7	406	22	AAV52192	Human FVII mutant
26	156	81.7	406	22	AAV52193	Human FVII mutant
27	156	81.7	406	22	AAV52194	Human FVII mutant
28	156	81.7	406	22	AAV52195	Human FVII mutant
29	156	81.7	406	22	AAV52196	Human FVII mutant
30	156	81.7	406	22	AAV52197	Human FVII mutant
31	156	81.7	406	22	AAV52198	Human FVII mutant
32	156	81.7	406	22	AAV52199	Human FVII mutant
33	156	81.7	406	22	AAV52200	Human FVII mutant
34	156	81.7	406	22	AAV52201	Human FVII mutant
35	156	81.7	406	22	AAV52202	Human FVII mutant
36	156	81.7	406	22	AAV52203	Human FVII mutant
37	156	81.7	406	22	AAV52204	Human FVII mutant
38	156	81.7	406	22	AAV52205	Human FVII mutant
39	156	81.7	406	22	AAV52206	Human FVII mutant
40	156	81.7	406	22	AAV52207	Human FVII mutant
41	156	81.7	406	22	AAV52208	Human FVII mutant
42	156	81.7	406	22	AAV52209	Human FVII mutant
43	156	81.7	406	22	AAV52210	Human FVII mutant
44	156	81.7	406	22	AAV52211	Human FVII mutant
45	156	81.7	406	22	AAV52212	Human FVII mutant

ALIGNMENTS

RESULT 1	AAV18312	standard; peptide; 44 AA.
ID	AAV18312	
AC	AAV18312;	
DT	17-AUG-1999	(first entry)
DE	Modified GLA domain of vitamin K-dependent protein.	
KW	GLA domain; muten; vitamin K-dependent protein; clotting disorder; therapy.	
OS	Homo sapiens.	
FT	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 1..44	
FT	FT	note="Xaa=gamma-carboxyglutamic acid, or glutamic acid"
PN	MO9920767-A1.	
PD	29-APR-1999.	
PF	20-OCT-1998;	98WO-US22152.
PR	23-OCT-1997;	9TUS-0955636.
PA	(MINU) UNIV MINNESOTA.	
PI	Nelstuen GL;	
XX		

DR WPI; 1999-288309/24.
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain; useful for treating clotting disorders
 XX
 XX
 PS Disclosure; Page 80; 86pp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 XX
 SQ Sequence 44 AA;
 Query Match 86.4%; Score 165; DB 20; Length 44;
 Best Local Similarity 97.7%; Pred. No. 3e-20; 1; Indels 0; Gaps 0;
 Matches 43; Conservative 0; Mismatches 1;
 QY 1 ANAFLXXLRGSLXRCCKXXQCSFXAXFIKDXARTLFWISY 44
 Db 1 ANAFLXXLRGSLXRCCKXXQCSFXAXFIKDXARTLFWISY 44
 RESULT 2
 AAY18310
 ID AAY18310 standard; peptide; 44 AA.
 XX
 XX AAY18310;
 DT 17-AUG-1999 (first entry)
 XX
 XX Modified GLA domain of vitamin K-dependent protein.
 DE
 XX
 KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 KM
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX
 XX
 XX W09920767-A1.
 XX
 XX
 PD 29-APR-1999.
 XX
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 PA
 XX
 PI Nelaeetuen GL;
 PI
 XX
 DR WPI; 1999-288309/24.
 XX
 XX
 PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain; useful for treating clotting disorders
 XX
 XX
 PS Disclosure; Page 80; 86pp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 XX
 SQ Sequence 44 AA;
 Query Match 86.4%; Score 165; DB 20; Length 44;
 Best Local Similarity 97.7%; Pred. No. 3e-20; 1; Indels 0; Gaps 0;
 Matches 43; Conservative 0; Mismatches 1;
 QY 1 ANAFLXXLRGSLXRCCKXXQCSFXAXFIKDXARTLFWISY 44
 Db 1 ANAFLXXLRGSLXRCCKXXQCSFXAXFIKDXARTLFWISY 44

CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 XX
 XX
 SQ Sequence 44 AA;
 Query Match 84.8%; Score 162; DB 20; Length 44;
 Best Local Similarity 97.7%; Pred. No. 9.6e-20;
 Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANAFLXXLRGSLXRCCKXXQCSFXAXFIKDXARTLFWISY 44
 Db 1 ANAFLXXLRGSLXRCCKXXQCSFXAXFIKDXARTLFWISY 44
 RESULT 3
 AAY18311
 ID AAY18311 standard; peptide; 44 AA.
 XX
 XX
 AC AAY18311;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 XX Modified GLA domain of vitamin K-dependent protein.
 DE
 XX
 KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 KM
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX
 XX
 XX W09920767-A1.
 XX
 XX
 PD 29-APR-1999.
 XX
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 XX
 PA (MINU) UNIV MINNESOTA.
 PA
 XX
 PI Nelaeetuen GL;
 PI
 XX
 DR WPI; 1999-288309/24.
 XX
 XX
 PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain; useful for treating clotting disorders
 XX
 XX
 PS Disclosure; Page 80; 86pp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 XX
 SQ Sequence 44 AA;
 Query Match 83.2%; Score 159; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 3.1e-19;
 Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ANAFLXXLRGSLXRCCKXXQCSFXAXFIKDXARTLFWISY 44
 Db 1 ANAFLXXLRGSLXRCCKXXQCSFXAXFIKDXARTLFWISY 44

```

RESULT 4
AAV18305
ID AAV18305 standard; peptide; 44 AA.
XX
XX
AC AAV18305;
XX
XX
DT 17-AUG-1999 (first entry)
XX
XX
DE Human factor VII GLA domain.
XX
XX
KW GLA domain; vitamin K-dependent protein; clotting disorder;
therapy.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT /note= "Xaa=gamma-carboxyglutamic acid, or glutamic
FT acid"
FT
XX
XX
PM WO920767-A1.
XX
XX
PD 29-APR-1999.
XX
XX
PF 20-OCT-1998; 98WO-US22152.
XX
XX
PR 23-OCT-1997; 97US-0955636.
XX
XX
PA (MINU ) UNIV MINNESOTA.
XX
XX
PI Nelstuen GL;
XX
XX
DR WPI, 1999-288309/24.
XX
XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
XX
PS Disclosure; Page 15; 86pp; English.
XX
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
XX
SQ Sequence 44 AA;
XX
XX
Query Match 81.7%; Score 156; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 9.7e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ANAFLLXLRGSLRXRCXKXQCSFXXAFXIFDAXRTKLFWISY 44
Db 1 ANAFLLXLRGSLRXRCXKXQCSFXXAFXIFDAXRTKLFWISY 44
XX
XX
RESULT 5
AAB36395
ID AAB36395 standard; peptide; 44 AA.
XX
XX
AC AAB36395;
XX
XX
DT 27-FEB-2001 (first entry)
XX
XX
DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX
XX
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW factor X; prothrombin; enhanced membrane binding affinity;
XX

```

```

KW clot formation; thrombolytic; haemostatic; bleeding disorder;
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
KW liver disease.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200066753-A2.
XX
XX
PD 09-NOV-2000.
XX
XX
PF 28-APR-2000; 2000WO-US11416.
XX
XX
PR 29-APR-1999; 99US-0302239.
XX
XX
PA (MINU ) UNIV MINNESOTA.
XX
XX
PI Nelstuen GL;
XX
XX
DR WPI, 2001-007226/01.
XX
XX
PT Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity
XX
XX
PS Disclosure; Page 12; 81pp; English.
XX
XX
CC The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
XX
SQ Sequence 44 AA;
XX
XX
Query Match 81.7%; Score 156; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 9.7e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ANAFLLXLRGSLRXRCXKXQCSFXXAFXIFDAXRTKLFWISY 44
Db 1 ANAFLLXLRGSLRXRCXKXQCSFXXAFXIFDAXRTKLFWISY 44
XX
XX
RESULT 6
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX
XX
AC AAB84870;
XX
XX
DT 31-JUL-2001 (first entry)
XX
XX
DE Mutant blood coagulant factor VII (FVII-31).
XX
XX
KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutein.
XX
XX
OS Homo sapiens.
XX
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 311..317
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
FT
XX

```

```

PN JP2001061479-A.
XX
XX 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
XX
XX N-PSDB; AAH19463.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
XX Claim 14; Page 20-21; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-31. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX Sequence 401 AA;
XX
XX Query Match 81.7%; Score 156; DB 22; Length 401;
XX Best Local Similarity 72.7%; Pred. No. 9, 2e-18;
XX Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0.
XX
XX 1 ANAFLXLREGSLRXKCKXXCSFFXXAFYIFDXAKRTKLEWISY 44
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 AANFLBELRPGSLERCKECCSFEERAREIFDXAERTKLFWISY 44
XX
XX Db
XX
XX RESULT 7
XX AAB84871
XX ID AAB84871 standard; Protein; 401 AA.
XX
XX AAB84871;
XX
XX 31-JUL-2001 (first entry)
XX
XX Mutant blood coagulant factor VII (FVII-39).
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutuin.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH Misc-difference 235..239 /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
XX FT Misc-difference 311..317 Asp-Arg-Lys-Thr-Leu"
XX FT Misc-difference 311..317 /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
XX FT /note= "Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX PN JP2001061479-A.
XX
XX 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
XX
XX N-PSDB; AAH19464.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
XX

```

xx	Claim 16; Page 23-24; 29pp; Japanese.
ps	
cc	The present invention relates to mutants of blood coagulant factor VII
cc	(FVII) or activated blood coagulant factor VII (FVIIa). The present
cc	sequence is one such mutant FVII: VII-39. The mutants can be used as an
cc	agent for the substitution therapy of haemophilia inhibitor patients.
xx	
sq	Sequence 401 AA;
	Query Match 81.7%; Score 156; DB 22; Length 401;
	Best Local Similarity 72.7%; Pred. No. 9.2e-18;
	Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Oy	1 ANAFIXLREGSLKRXCKXOCSEFXAFXIFKDXARTKLFWISY 44
Dd	1 ANAFLEELRPGSLERECKECCSFEEAREIRFDARTKLFWISY 44
	RESULT 8
	AAR35764
ID	AAR35764 standard; protein; 406 AA.
xx	
AC	AAR35764;
DT	24-SEP-1993 (first entry)
xx	
DE	Factor VII (VII).
xx	
KW	PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII; Factor VII; CT; chymotrypsinogen; SP; serine protease; binding; exosite; catalytic activity.
KM	
xx	Homo sapiens.
OS	
xx	
FH	Key Location/Qualifiers
FT	Region 1..152
FT	/note= "Factor VII light chain"
FT	Region 153..406
FT	/note= "Factor VII heavy chain"
FT	Peptide 374..388
FT	/note= "exosite 1"
FT	Peptide 290..310
FT	/note= "exosite 2"
FT	Peptide 290..310
FT	/note= "pref. PC polypeptide; claim 2, page 136"
FT	Peptide 374..388
FT	/note= "pref. PC polypeptide; claim 2, page 136"
FT	Peptide 289..304
FT	/note= "pref. PC polypeptide; claim 4, page 137"
FT	Peptide 290..304
FT	/note= "pref. PC polypeptide; claim 4, page 137"
FT	Peptide 245..266
FT	/note= "claim 9, page 138-139 describes an antibody that reacts with Factor VII; fragments 289-304, 290-304, 290-310, 374-388 and 400-414 but not with fragment 245-266"
xx	
PN	WO9309804-A.
xx	
PD	27-MAY-1993.
xx	
PF	18-NOV-1992; 92MO-US10242.
xx	
PR	18-NOV-1991; 91US-0793989.
xx	
PA	(SCRI) SCRIPPS RES INST.
xx	
PI	Griffin JH, Masters RM;
xx	
DR	WPI, 1993-182244/22.
xx	
PT	Serine protease derived-polypeptide(s) and anti-peptide

PT	antibodies - for inhibiting coagulation and assaying for the
PT	presence of serine protease in fluid samples
XX	
PS	Disclosure; Page 133-135; 149p; English.
XX	
CC	The PC polypeptides indicated in the Features Table inhibit
CC	coagulation (they prevent binding of serine protease to natural
CC	substrates), esp. when admin. to give an intravascular blood
CC	concn. of 0.1-100 (pref. 0.5-10) microm.
CC	NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
CC	in the specification but have not yet been added to the SEQUENCE
CC	LISTING.
XX	
XX	
SQ	Sequence 406 AA:
Query Match	81.7%; Score 156; DB 14; Length 406;
Best Local Similarity	72.7%; Pred. NO. 9.3e-18;
Matches 32; Conservative	0; Mismatches 14; Indels 0; Gaps 0.
Oy	
1	ANAFPLXLRGSLRXKCKXCCSFFXAFIFPDAXRTKLFWISY 44
1	ANAFLELRPGSLRECKECCSFEARARIFPDARTKLFWISY 44
Db	
RESULT 9	
AAW14509	
ID	AAW14509 standard; protein; 406 AA.
XX	
XX	AAW14509;
XX	
DT	14-MAY-1997 (first entry)
XX	
DE	Modified blood coagulation Factor VII (R290S).
XX	
KW	Blood coagulation; factor 7; mutein; mutation; modification;
KM	thrombocytopenia; von Willebrand's disease; plasma substitute.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PH	
FT	Key
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	7
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	14
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	16
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	19
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	20
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	17..22
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	26
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	29
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	32..33
FT	/note= "proteolytic site"
FT	35
FT	/label= OTHER

FT		/note= "gamma-carboxyglutamic acid"
FT	Cleavage-site	38..39
FT		/note= "proteolytic site"
FT	Cleavage-site	42..43
FT		/note= "proteolytic site"
FT	Cleavage-site	44..45
FT		/note= "proteolytic site"
FT	Disulfide-bond	50..61
FT	Disulfide-bond	55..70
FT	Modified-site	63
FT		/label= OTHER
FT		/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	72..81
FT	Disulfide-bond	91..102
FT	Disulfide-bond	98..112
FT	Disulfide-bond	114..127
FT	Disulfide-bond	135..162
FT	Cleavage-site	143..144
FT		/note= "proteolytic site"
FT	Modified-site	145
FT		/note= "glycosylation site"
FT	Disulfide-bond	159..164
FT	Disulfide-bond	178..194
FT	Active-site	193
FT	Active-site	242
FT	Active-site	344
FT	Cleavage-site	290..291
FT		/note= "proteolytic site in unmodified factor VII"
FT	Misc-difference	290
FT		/note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"
FT	Disulfide-bond	310..329
FT	Cleavage-site	315..316
FT		/note= "proteolytic site"
FT	Modified-site	322
FT		/note= "glycosylation site"
FT	Disulfide-bond	340..368
FT	Cleavage-site	341..342
FT		/note= "proteolytic site"
FT	Cleavage-site	392..393
FT		/note= "proteolytic site"
FT	Cleavage-site	396..397
FT		/note= "proteolytic site"
FT	Cleavage-site	402..403
FT		/note= "proteolytic site"
XX		
PN	USS580560-A.	
XX		
PD	03-DEC-1996.	
XX		
PF	13-NOV-1989;	89US-0434149.
XX		
XX	09-AUG-1993;	93US-0104509.
PR	13-NOV-1989;	89US-0434149.
PR	12-JUN-1992;	92US-0898248.
PR	22-AUG-1994;	94US-0293778.
XX		
PA	(NOVO) NOVO-NORDISK AS.	
XX		
XX	Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;	
PI	WPI; 1997-033523/03.	
DR		
XX		
PT	Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability	
XX		
PS	Example 3; Page -; 28pp; English.	
XX		
CC	Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an amino acid that provides a proteolytically more stable	
CC		

CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
 CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
 CC bleeding disorders such as thrombocytopenia and von Willebrand's
 CC disease. They are also suitable for addition to plasma substitutes.
 CC The present sequence is a specific example of a modified factor VII
 CC protein.

XX Sequence 406 AA;

Query Match 81.7%; Score 156; DB 18; Length 406;
 Best Local Similarity 72.7%; Pred. No. 9.3e-18;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AANFLXXLRGSLKRXCKXQCSFXAIFKDXAKRTKLFWISY 44
 1 AANFLBELRPGSLERCKECSFEAREIFKDXAKRTKLFWISY 44
 Db

RESULT 10

AAW14510
 ID AAW14510 standard; protein; 406 AA.

XX AAW14510;

DT 14-MAY-1997 (first entry)

XX Modified blood coagulation Factor VII (R315S).

KW Blood coagulation; factor 7; mutacin; mutation; modification;
 KM thrombocytopenia; von Willebrand's disease; plasma substitute.

XX Homo sapiens.

OS Synthetic.

XX Location/Qualifiers

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

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FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Disulfide-bond /note= "proteolytic site"
 FT Disulfide-bond 50..61
 FT Disulfide-bond 55..70
 FT Modified-site
 FT Disulfide-bond /label= OTHER
 FT Disulfide-bond /note= "beta-hydroxy-aspartic acid"
 FT Disulfide-bond 72..81
 FT Disulfide-bond 91..102
 FT Disulfide-bond 98..112
 FT Disulfide-bond 114..127
 FT Disulfide-bond 135..162
 FT Disulfide-bond 143..144
 FT Disulfide-bond /note= "proteolytic site"
 FT Disulfide-bond 145
 FT Disulfide-bond /note= "glycosylation site"
 FT Disulfide-bond 159..164
 FT Disulfide-bond 178..194
 FT Active-site 193
 FT Active-site 242
 FT Active-site 344
 FT Active-site 290..291
 FT Disulfide-bond /note= "proteolytic site"
 FT Disulfide-bond 310..329
 FT Disulfide-bond 315..316
 FT Disulfide-bond /note= "proteolytic site in unmodified factor VII"
 FT Disulfide-bond /note= "native Arg315 has been substituted by Ser to provide a proteolytically more stable peptide bond"
 FT Disulfide-bond 322
 FT Disulfide-bond /note= "glycosylation site"
 FT Disulfide-bond 340..368
 FT Disulfide-bond 341..342
 FT Disulfide-bond /note= "proteolytic site"
 FT Disulfide-bond 392..393
 FT Disulfide-bond /note= "proteolytic site"
 FT Disulfide-bond 396..397
 FT Disulfide-bond /note= "proteolytic site"
 FT Disulfide-bond 402..403
 FT Disulfide-bond /note= "proteolytic site"

US5580560-A.

PD 03-DEC-1996.

XX 13-NOV-1989; 89US-0434149.

XX 09-AUG-1993; 93US-0104509.

PR 13-NOV-1989; 89US-0434149.

PR 12-JUN-1992; 92US-0898248.

PR 22-AUG-1994; 94US-0293778.

XX (NOVO) NOVO-NORDISK AS.

XX Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;

XX WPI; 1997-033523/03.

XX Mutated human factor VII or VIIa proteins - with amino acid

XX substitutions to improve proteolytic stability

XX Example 4; Page -; 28pp; English.

XX Modified human factor VII or VIIa proteins are stabilised against
 CC proteolytic cleavage by substitution of one of the residues Lys32,
 CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
 CC Lys341 by an amino acid that provides a proteolytically more stable
 CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
 CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
 CC bleeding disorders such as thrombocytopenia and von Willebrand's
 CC disease. They are also suitable for addition to plasma substitutes.
 CC The present sequence is a specific example of a modified factor VII
 CC protein.


```
XX SQ Sequence 406 AA;
Query Match 81.7%; Score 156; DB 18; Length 406;
Best Local Similarity 72.7%; Pred. No. 9.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXKCKXQCSFXXAFKIFKDAKRTKLFMISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ANAFLEELRPGSLRCKECCSFEARREIFKDAERTKLFMISY 44

RESULT 11
AAU77745
ID AAU77745 standard; protein; 406 AA.
XX AAU77745;
AC AAU77745;
DT 05-JUN-2002 (first entry)
XX
DE Human factor VIIa active site mutant.
XX
KW Factor VIIa; human; shock heat treatment; protein stability;
KW protein manufacture; protein conformation; mutant; mutein.
XX
OS Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Active-site 193
FT /note= "Member of the factor VIIa catalytic triad"
FT Active-site 242
FT /note= "Member of the factor VIIa catalytic triad"
FT Active-site 344
FT /note= "Member of the factor VIIa catalytic triad"
FT Misc-difference 344
FT /label= Gly, Met, Thr
FT /note= "Preferably Ala. Wild type Ser"
XX
PN WO200177141-A1.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-DK00234.
XX
PR 06-APR-2000; 2000DK-0000573.
XX
PR 17-APR-2000; 2000US-197650P.
XX
PA (NOVO ) NOVO NORDISK AS.
XX
PI Mathiesen F;
XX
PI WPI; 2001-657162/75.
XX
PT Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX involves a shock heat treatment -
XX
PS Disclosure; Page -; 22pp; English.
XX
XX The invention describes a method of stabilising a polypeptide involving
XX shock heat treatment of the polypeptide. The method is useful in a
XX pharmaceutical composition, in the industrial or large scale method of
XX manufacturing a polypeptide, also as a unit operation during preparation,
XX purification, recovery and/or formulation of polypeptides. The shock heat
XX treatment improves the protein stability without substantial loss of
XX biological activity. The method can be applied to change polypeptide
XX conformation in a very fast and non-invasive manner. The polypeptide
XX formed is stable. The method is also useful for decreasing the
XX association of the polypeptide. This sequence represents a modified
XX human factor VIIa protein, mutated at the catalytic site, described
XX in the invention.
XX Note: This sequence does not appear in the specification but has
XX been obtained using information given in the invention.
```

```
XX SQ Sequence 406 AA;
Query Match 81.7%; Score 156; DB 22; Length 406;
Best Local Similarity 72.7%; Pred. No. 9.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXKCKXQCSFXXAFKIFKDAKRTKLFMISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ANAFLEELRPGSLRCKECCSFEARREIFKDAERTKLFMISY 44

RESULT 12
AAM52171
ID AAM52171 standard; Protein; 406 AA.
XX AAM52171;
AC AAM52171;
DT 07-FEB-2002 (first entry)
XX
DE Human FVII SEQ ID NO 1.
XX
KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW cardiant; hepatocrophic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 6
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 7
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 14
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 16
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 19
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 20
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 25
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 26
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 29
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Misc-difference 35
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxylutamic acid"
FT Modified-site 52
FT /note= "O-glycosylated"
FT Modified-site 60
FT /note= "O-glycosylated"
FT Modified-site 145
FT /note= "N-glycosylated"
FT Cleavage-site 152..153
FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322
FT /note= "N-glycosylated"
XX
PN WO200158935-A2.
```

```

XX 16-AUG-2001.
PD
XX
XX
XX 12-FEB-2001; 2001WO-DK00094.
PF
XX
XX 11-FEB-2000; 2000DK-0000218.
PR
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX
XX MPI: 2001-581807/65.
XX
XX N-PSDB; AAI99982.
XX
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX Claim 1; Page 81-83; 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections.
XX
XX Sequence 406 AA;
SQ
XX
XX Query Match 81.7%; Score 156; DB 22; Length 406;
XX Best Local Similarity 95.5%; Pred. No. 9.3e-18;
XX Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ANAFLXXLRBGSILRXCKXKXQCSFXAXFXFKDAXRTKLFWISY 44
QY
XX
XX 1 ANAFLXXLRPGSLRXCKXCKXQCSFXAXXIFKDXAKRTKLFWISY 44
Db
XX
XX RESULT 13
XX ID AAM52172 standard; Protein; 406 AA.
XX
XX AAM52172;
XX
XX 07-FEB-2002 (first entry)
XX
XX Mammalian expressed human FVII SEQ ID NO 3.
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KM cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Modified-site 52 /note= "O-glycosylated"
XX Modified-site 60 /note= "O-glycosylated"
XX Modified-site 145 /note= "N-glycosylated"
XX Cleavage-site 152..153
FT

```

```

FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322 /note= "N-glycosylated"
XX
XX MO200158935-A2.
XX
XX 16-AUG-2001.
PD
XX
XX 12-FEB-2001; 2001WO-DK00094.
PF
XX
XX 11-FEB-2000; 2000DK-0000218.
PR
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX
XX MPI: 2001-581807/65.
XX
XX N-PSDB; AAI99983.
XX
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX Disclosure; Page 85-86; 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections.
XX
XX Sequence 406 AA;
SQ
XX
XX Query Match 81.7%; Score 156; DB 22; Length 406;
XX Best Local Similarity 72.7%; Pred. No. 9.3e-18;
XX Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX 1 ANAFLXXLRBGSILRXCKXKXQCSFXAXFXFKDAXRTKLFWISY 44
QY
XX
XX 1 ANAFLXELRPGLERBECKECSFEERARLIFKDAERTKLFWISY 44
Db
XX
XX RESULT 14
XX ID AAM52181 standard; Protein; 406 AA.
XX
XX AAM52181;
XX
XX 07-FEB-2002 (first entry)
XX
XX Human FVII mutant T106N.
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KM cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
XX muteln.
XX
XX Homo sapiens.
XX
XX Synthetic.
OS

```

```
XX Key Location/Qualifiers
FH Misc-difference 6 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 7 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 14 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 16 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 19 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 20 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 25 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 26 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 29 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 35 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Modified-site 52 /note="O-glycosylated"
FT
FT Modified-site 60 /note="O-glycosylated"
FT
FT Misc-difference 106 /note="Wild-type Thr substituted by Asn"
FT
FT Modified-site 145 /note="N-glycosylated"
FT
FT Cleavage-site 152..153 /note="proteolytic cleavage site converting FVII zymogen
to an activated form, comprising two chains
linked by a single disulphide bridge"
FT
FT Modified-site 322 /note="N-glycosylated"
FT
XX WO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-DK00094.
XX
XX 11-FEB-2000; 2000DK-0000218.
XX
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX
XX MPI; 2001-581807/65.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently
XX attached to polypeptide group -
XX
XX Example 3; Page -: 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX polypeptide conjugates, comprising at least one non-polypeptide group
XX covalently attached to a polypeptide, where the amino acid sequence of
XX polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
```

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CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardant, hepatotropic and
CC cerebroprotective activity and are useful for treating FVIIa/FV-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a human FVII mutant,
CC having an addition in vivo glycosylation site and tested for its
CC amidolytic activity.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC (AAM52171).
XX
XX SQ Sequence 406 AA;
XX
XX Query Match 81.7%; Score 156; DB 22; Length 406;
XX Best Local Similarity 95.5%; Pred. No. 9.3e-18;
XX Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 ANAFLXXLRGSLRXCKXXQCSFXXAFYIFPDAXRTKLFWISY 44
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 ANAFLXXLRGSLRXCKXXQCSFXXARXIFPDAXRTKLFWISY 44
XX
XX RESULT 15
XX AAM52182
XX ID AAM52182 standard; Protein; 406 AA.
XX
XX AC AAM52182;
XX
XX DT 07-FEB-2002 (first entry)
XX
XX DE Human FVII mutant K143N/N145T.
XX
XX KW Factor VII; FVII; Factor VIIa; haemostatic; thrombolytic;
XX cardant; hepatotropic; cerebroprotective; haemophilia; liver disease;
XX myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
XX mutcin.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FH Misc-difference 6 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 7 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 14 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 16 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 19 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 20 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 25 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 26 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 29 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT
```


GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10GLU28PHE

Perfect score: 191

Sequence: 1 ANAFLLXLRREGSLRXKCKX.....XXAFXFKDAXRKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	466	1 KFHU7	coagulation factor
2	122	63.9	443	2 I46932	coagulation factor
3	114	59.7	407	1 KFB07	coagulation factor
4	97	50.8	461	1 JX0210	protein C (activat
5	96	50.3	461	1 S18994	protein C (activat
6	96	50.3	488	1 EXHU	coagulation factor
7	96	50.3	492	1 EXBO	coagulation factor
8	94	49.2	622	1 TBHU	thrombin (BC 3.4.2
9	90	47.1	482	1 EXRT	coagulation factor
10	90	47.1	617	2 S10511	thrombin (BC 3.4.2
11	90	47.1	618	2 A35827	thrombin (BC 3.4.2
12	88	46.1	458	1 KXBO	protein C (activat
13	86	45.0	475	1 EXCH	coagulation factor
14	81	42.4	461	1 KXHU	protein C (activat
15	78	40.8	416	1 KFB0	coagulation factor
16	77	40.3	461	1 KFHU	coagulation factor
17	74	38.7	625	1 TBBO	thrombin (BC 3.4.2
18	70	36.6	452	1 A30351	coagulation factor
19	70	36.6	452	2 JQ0419	coagulation factor
20	64	33.5	642	2 S53433	plasma protein S p
21	61	31.9	675	1 KXBO5	plasma protein Z -
22	60	31.4	675	1 KXBO5	plasma protein S p
23	59	30.9	642	2 S53434	plasma protein S p
24	59	30.9	642	1 KXHU5	plasma protein S p
25	58	30.4	646	2 S38819	plasma protein S p
26	57	29.8	675	1 KXRT5	plasma protein S p
27	56	29.3	422	1 KXHUZ	plasma protein Z p
28	55.5	29.1	576	2 G96763	probable MAP kinase
29	50	26.2	673	2 A48089	growth arrest-spec

30	50	26.2	675	1 KXMS5	plasma protein S p
31	49.5	25.9	594	2 D84859	probable MAP kinase
32	49.5	25.9	603	2 C96575	probable MAP kinase
33	48	25.1	674	2 I55476	growth potentialin
34	48	25.1	678	2 B48089	growth arrest-spec
35	45.5	23.8	83	2 T17839	hypothetical prote
36	45	23.6	271	2 S66691	hypothetical prote
37	45	23.6	879	2 S55864	hypothetical prote
38	45	23.6	907	2 T15792	hypothetical prote
39	44	22.8	306	2 I49068	protein kinase SRY
40	43.5	22.8	455	2 C83494	probable 2-isoprop
41	43	22.5	394	1 S30286	tetracycline resis
42	43	22.5	440	2 C70198	conserved hypothet
43	43	22.5	447	2 B95185	Mur ligase family
44	43	22.5	447	2 B98052	conserved hypothet
45	42.5	22.3	180	2 H90450	hypothetical prote

ALIGNMENTS

RESULT 1
KFHU7
coagulation factor VIIa (BC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000
C:Accession: A28322; A23819; A31186; B31186; S63524
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murr
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII.
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OH>
A:Cross-references: GB:J02933; NID:9180333; PID:AAA51963.1; PID:9180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saarl, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; MUID:86205965; PMID:3466420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M1323; NID:9182799; PID:AAA8040.1; PID:9182801
R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A:Reference number: A90539; MUID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <TH>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TH>
R:Bjorn, S.; Foster, D.C.; Thim, L.; Wiber, F.C.; Christensen, M.; Komiyama, Y.; Peder
J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A:Reference number: A40529; MUID:91250411; PMID:1904059
A:Contents: annotation; carbohydrate binding sites
R:Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A:Reference number: S63524; MUID:96096752; PMID:8529655
A:Accession: S63524
A:Molecule type: Protein
A:Residues: 61-65/99-103; 105-109/213-217/308-312 <PER>
C:Genetics:
A:Gene: GDB:E7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
coagulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-60/Domain: propeptide #status predicted <PRO>
 F:45-104/Domain: Gla domain homology <GLA>
 F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
 F:110-141/Domain: EGF homology <EG1>
 F:151-187/Domain: EGF homology <EG2>
 F:213-447/Domain: trypsin homology <TRY>
 F:213-447/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F:66-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:17-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
 F:112,120/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
 F:205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:212-213/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental
 F:253,302,404/Active site: His, Asp, Ser #status predicted
 F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 81.7%; Score 156; DB 1; Length 466;
 Best Local Similarity 72.7%; Pred. No. 6,2e-19;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLXRXCKXXCSFXXAFXFKDAXRTKLFWISY 44
 61 ANAFLEELRPGSLERCKEELCSFEERAEIPEKDEKRTKLFWISY 104

RESULT 2
 146932
 Coagulation factor VII - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
 C:Accession: I46932
 R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
 Thromb. Res. 69, 231-238, 1993
 A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
 A:Reference number: I46932; MUID:93190306; PMID:8333365
 A:Accession: I46932
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-443 <BRO>
 A:Cross-references: GB:S56300; NID:g266294; PID:g266295
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 F:24-83/Domain: Gla domain homology <GLA>
 F:89-120/Domain: EGF homology <EG1>
 F:130-166/Domain: EGF homology <EG2>
 F:192-425/Domain: trypsin homology <TRY>

Query Match 63.9%; Score 122; DB 2; Length 443;
 Best Local Similarity 54.5%; Pred. No. 4,5e-13;
 Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLXRXCKXXCSFXXAFXFKDAXRTKLFWISY 44
 40 ANSFLLELRPGSLERCKEELCSFEERAEVQSTERTKQFWITY 83

RESULT 3
 KPB07
 Coagulation factor VIIa (EC 3.4.21.21) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
 C:Accession: A31979; C20274
 R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
 J. Biol. Chem. 263, 14868-14877, 1988
 A:Title: Bovine factor VII. Its purification and complete amino acid sequence.
 A:Reference number: A31979; MUID:8908362; PMID:3049594
 A:Accession: A31979
 A:Molecule type: protein
 A:Residues: 1-407 <TAK>
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; MUID:83308813; PMID:6688526
 A:Accession: C20274
 A:Molecule type: protein
 A:Residues: 58-62,"X",64-68 <MCM>
 A>Note: the residue designated 'X' was determined to be hydroxyaspartic acid
 R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,
 J. Biochem. 104, 867-868, 1988
 A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
 A:Reference number: A44556; MUID:89213999; PMID:3149637
 A:Content: annotation
 A>Note: structure and location of covalently bound carbohydrate
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
 gulation factor IX in the presence of calcium and tissue factor
 A:Pathway: blood coagulation extrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>
 F:1-44/Domain: Gla domain homology (fragment) <GLA>
 F:50-81/Domain: EGF homology <EG1>
 F:91-127/Domain: EGF homology <EG2>
 F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F:153-407/Domain: trypsin homology <TRY>
 F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/
 F:52/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experiment
 F:145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:152-153/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental
 F:193,242,344/Active site: His, Asp, Ser #status predicted
 F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 59.7%; Score 114; DB 1; Length 407;
 Best Local Similarity 50.0%; Pred. No. 1e-11;
 Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLXRXCKXXCSFXXAFXFKDAXRTKLFWISY 44
 1 ANSFLLELRPGSLERCKEELCSFEERAEIPEKDEKRTKLFWISY 44

RESULT 4
 JX0210
 protein C (activated) (EC 3.4.21.69) precursor - mouse
 N:Alternate names: vitamin K-dependent serine proteinase
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: JX0210
 R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
 J. Biochem. 111, 491-495, 1992
 A:Title: Isolation and characterization of a mouse protein C cDNA.
 A:Reference number: JX0210; MUID:92316897; PMID:1618739
 A:Accession: JX0210
 A:Molecule type: mRNA
 A:Residues: 1-461 <TAD>
 A:Cross-references: GB:D10445; NID:g220385; PIDN:BA01235.1; PID:g220386
 A:Experimental source: liver
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that r
 B.
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:27-85/Domain: Gla domain homology <GLA>
 F:34-41/Domain: propeptide #status predicted <PRO>
 F:42-196,199-461/Product: protein C #status predicted <PCH>
 F:42-196/Domain: light chain #status predicted <PCL>
 F:91-130/Domain: EGF homology <EG1>
 F:139-174/Domain: EGF homology <EG2>
 F:199-461/Domain: heavy chain #status predicted <PCH>
 F:199-211/Domain: activation peptide #status predicted <ACT>
 F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

U. Mol. Biol. 222, 947-966, 1993
 A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
 A:Reference number: A49458; PMID:93360277; PMID:8355279
 A:Accession: A12030
 A:Molecule type: protein
 A:Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <T
 A:Note: The two chains held together by one disulfide bond are formed from a single-c
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) of
 C:GeneSet:
 A:Gene: GDB:F10
 A:Cross-references: GDB:119890; OMIM:227600
 A:Map position: 13q34-13q34
 A:Insertion: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
 A:Note: deficiency of this factor causes Stuart disease
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:85-179/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:233-488/Domain: activation peptide #status experimental <APT>
 F:235-462/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat
 F:57-62/Disulfide bonds: #status predicted
 F:80-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (asp) #status experimental
 F:199,211/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:234-235/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #stat
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 50.3%; Score 96; DB 1; Length 488;
 Best Local Similarity 38.6%; Pred. No. 1.5e-08;
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLREGSLRXCCKXCCSPKXAFKPKDARTLFTMSY 44
 41 ANSFLBEMKXGHLRRECMETCTSEARAREVEDSKTPEFNKY 84

RESULT 7
 EXBO
 coagulation factor Xa (BC 3.4.21.6) precursor - bovine
 N:Alternate names: Stuart factor (cattle)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999
 C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
 C:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 N:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
 Biochemistry 19, 659-667, 1980
 A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A:Reference number: A14997; PMID:80130563; PMID:6766735
 A:Accession: A14997
 A:Molecule type: protein
 A:Residues: 41-102, 'N', 104-180 <EN>
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; PMID:83308813; PMID:6688526
 A:Contents: annotation; revision to residue 103
 R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.

Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
 A:Reference number: A12030; PMID:76053069; PMID:1059093
 A:Accession: A12030
 A:Molecule type: protein
 A:Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <T
 A:Note: carboxylate binding sites and disulfide bonds were determined
 R:Person, E.; Selander, M.; Line, S.; Drakenberg, T.; Oehlén, A.K.; Stenflo, J.
 U. Biol. Chem. 264, 16897-16944, 1989
 A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
 A:Reference number: A34412; PMID:89380326; PMID:2789221
 A:Accession: A34412
 A:Molecule type: protein
 A:Residues: 65-126 <PER>
 A:Note: beta-hydroxyaspartic acid site
 R:Imoue, K.; Morita, T.
 Eur. J. Biochem. 210, 153-163, 1993
 A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A:Reference number: S39414; PMID:94062825; PMID:8243461
 A:Accession: S39414
 A:Molecule type: protein
 A:Residues: 183-196;199-209;216-233 <INO>
 A:Note: carbohydrate binding sites
 R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
 Biochemistry 11, 4899-4903, 1972
 A:Title: Bovine factor X-1a (activated Stuart factor): Evidence of homology with mammali
 A:Reference number: A12453; PMID:73053314; PMID:4664286
 A:Contents: annotation; active site
 R:Fujikawa, K.; Titani, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
 A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to
 A:Reference number: A13504; PMID:76053121; PMID:1059122
 A:Contents: annotation; activation
 R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
 J. Biol. Chem. 259, 5705-5710, 1984
 A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxylglutamic
 A:Reference number: A38024; PMID:84185716; PMID:6546930
 A:Contents: annotation; calcium binding
 J:Morita, T.; Jackson, C.W.
 J. Biol. Chem. 261, 4008-4014, 1986
 A:Reference number: A38025; PMID:86140210; PMID:3949800
 A:Contents: annotation; sulfate binding
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C:Comment: The two chains are formed from a single-chain precursor for the excision of tw
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
 activation.
 C:Comment: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with str
 C:Comment: The gamma-carboxylglutamic acid residues arise by a posttranslational, vitamir
 C:GeneSet:
 A:Gene: F10
 A:Map position: 13q34
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:85-180/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:233-492/Domain: activation peptide #status experimental <APT>
 F:234-461/Product: coagulation factor Xa heavy chain #status experimental <AMC>
 F:234-461/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #
 F:57,62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (asp) #status experimental
 F:200/Binding site: sulfate (Tyr) (covalent) #status experimental
 F:208,495/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:218/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:233-234/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #stat

C:Accession: A26250; A18385; A18386; A00928
R:Long, G.L.; Balgaje, R.M.; Macgillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A:Reference number: A26250; MUID:85014826; PMID:6091100
A:Accession: A26250
A:Molecule type: mRNA
A:Residues: 1-456 <LON>
R:Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982
A:Title: Amino acid sequence of the light chain of bovine protein C.
A:Reference number: A18385; MUID:83007325; PMID:6896876
A:Accession: A18385
A:Molecule type: Protein
A:Residues: 40-194 <PER>
A:Note: 82-Lys was also found
R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
A:Reference number: A19316; MUID:83169769; PMID:6572939
A:Contents: annotation; revision to residue 110
R:Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A:Title: Amino acid sequence of the heavy chain of bovine protein C.
A:Reference number: A18386; MUID:83007326; PMID:6896877
A:Accession: A18386
A:Molecule type: Protein
A:Residues: 197-454, 'PV' <STE>
R:Esmon, N.L.; Debault, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F
A:Reference number: A57541; MUID:83213513; PMID:6304092
A:Contents: annotation; activation; calcium binding
R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A:Title: Structural changes required for activation of protein C are induced by Ca2+ binding
A:Reference number: A57542; MUID:83213514; PMID:6406503
A:Contents: annotation; activation; calcium binding
C:Comment: protein C is the zymogen of the vitamin K-dependent serine proteinase that re
s.
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this react
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str
cognition of the thrombin-thrombomodulin complex.
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitam
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin hom
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium bind
E:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
E:24-83/Domain: Gla domain homology <Gla>
F:30-39/Domain: propeptide #status predicted <PRO>
F:40-194/Product: protein C light chain #status experimental <LCH>
F:98-128/Domain: EGF homology <EG1>
E:137-172/Domain: EGF homology <EG2>
E:197-456/Product: protein C heavy chain #status experimental <HCH>
F:197-210/Domain: activation peptide #status experimental <APr>
F:211-440/Domain: trypsin homology <TR>
F:45-53, 55, 58, 59, 62, 65, 68, 74/Modified site: gamma-carboxyglutamic acid (Glu) #sta
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
E:119-128, 137-148, 144-157, 159-172, 180-318, 237-253, 368-382, 393-421/Disulfide bonds: #sta
F:136, 289, 350/Binding site: carboxylate (Asn) (covalent) #status predicted
F:252, 298, 397/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.1%; Score 88; DB 1; Length 456;
Best Local Similarity 40.9%; Pred. NO. 3.5e-07;
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

1 ANAFLXLRREGSLRXCKXQCSFYXAFYIFRDARTKLFWSY 44
|||::|::|::|::|::|::|::|::|::|::|::|::|::|
Db ANSFLELRPGNVERECSEVCFEAEARIEFQNTEDTNAFMF 83

RESULT 13

EXCH
coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N|Alternate names: virus-activating proteinase
C|Species: Gallus gallus (chicken)
C|Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 16-Jul-1999
A|Accession: S15838; S20380; S20381
R|Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na
RBS Lett. 283, 281-285, 1991
A|Title: Primary structure of the virus activating protease from chick embryo. Its ident
A|Reference number: S15838; MUID:91257322; PMID:2044767
A|Accession: S15838
A|Status: not compared with conceptual translation
A|Molecule type: mRNA
A|Residues: 1-475 <SUZ>
A|Cross-references: DDBJ:D00844; NID:g222869; PID:BAA00724.1; PID:g222870
R|Gotoh, B.; Yamachi, F.; Ogasawara, T.; Nagai, Y.
FBS Lett. 296, 274-278, 1992
A|Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
A|Reference number: S20380; MUID:92164779; PMID:1537403
A|Accession: S20380
A|Molecule type: protein
A|Residues: 241-246,'X',248-251,'X',253-261 <GOT>
C|Function:
A|Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A|Pathway: blood coagulation
C|Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C|Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F|21-40/Domain: signal sequence #status predicted <SIG>
F|21-40/Domain: tripeptide #status predicted <PRO>
F|25-84/Domain: Gla domain homology <GLA>
F|41-185/Product: coagulation factor X light chain #status experimental <LGH>
F|90-121/Domain: EGF homology <EG1>
F|129-167/Domain: EGF homology <EG2>
F|186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F|186-240/Domain: activation peptide #status predicted <APr>
F|241-475/Product: coagulation factor Xa heavy chain #status experimental <AMC>
F|241-468/Domain: trypsin homology <TRY>
F|46-47.54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F|57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,422
F|103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F|196,207,228,285/Binding site: carbohydrate (asn) (covalent) #status predicted
P|282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 45.0%; Score 86; DB 1; Length 475;
Best Local Similarity 36.4%; Pred. No. 8e-07; Mismatches 18; Indels 0; Gaps 0;
Matches 16; Conservative 10;

Oy 1 ANAFLLRLREGSLRRCKKXCSPFXAXFIPIKDXARKLFWISY 44
|||:::|||||:::|||||
Db 41 ANSFLEMKQGNIERECNERCKSEARAEFDNEKRIFENITY 84
|||:::|||||:::|||||

RESULT 14
KKHU
protein C (activated) (EC 3.4.21.69) precursor - human
N|Alternate names: autoprothrombin IIA; plasma protein C
C|Species: Homo sapiens (man)
C|Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
A|Accession: A22331; A25426; A21781; A23789; A00927
R|Foster, D.C.; Yoshitake, S.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
A|Title: The nucleotide sequence of the gene for human protein C.
A|Reference number: A22331; MUID:85270390; PMID:2991887
A|Accession: A22331
A|Molecule type: DNA
A|Residues: 1-461 <FOSI>
A|Cross-references: GB:M11228; NID:g190333; PION:AAA60166.1; PID:g190334
R|Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
A|Title: Evolution and organization of the human protein C gene.

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10GLU28PNE
Perfect score: 191
Sequence: 1 ANAFLLXHLREGSLXRXCKX.....XXAFXIFDXARTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	81.7	466	FA7_HUMAN	P08709 homo sapien
2	122	63.9	444	FA7_RABIT	P98139 oryctolagus
3	114	59.7	407	FA7_BOVIN	P22457 bos taurus
4	111	58.1	446	FA7_MOUSE	P10735 mus musculu
5	102	53.4	490	FA10_RABIT	O19045 oryctolagus
6	98	51.3	459	PRTC_PIG	O991p2 sus scrofa
7	97	50.8	461	PRTC_MOUSE	P33587 mus musculu
8	96	50.3	488	PRTC_RAT	P00742 homo sapien
9	96	50.3	492	FA10_HUMAN	P00743 bos taurus
10	96	50.3	492	FA10_HUMAN	O14668 homo sapien
11	94	49.2	218	THRB_HUMAN	P00734 homo sapien
12	94	49.2	622	THRB_HUMAN	P18292 rattus norv
13	90	47.1	617	THRB_RAT	P19221 mus musculu
14	90	47.1	618	THRB_MOUSE	P00745 bos taurus
15	88	46.1	456	PRTC_BOVIN	O9bnd7 homo sapien
16	86	45.0	231	TMG3_HUMAN	P25155 gallus gall
17	86	45.0	475	FA10_CHICK	Q28661 oryctolagus
18	81	42.4	458	PRTC_RABIT	P04070 homo sapien
19	81	42.4	461	PRTC_HUMAN	P00741 bos taurus
20	78	40.8	416	FA9_BOVIN	P00740 homo sapien
21	77	40.3	461	FA9_HUMAN	P81428 tropidochis
22	76	39.8	376	FA10_TROCA	P00735 bos taurus
23	74	38.7	625	THRB_BOVIN	O14669 homo sapien
24	73	38.2	202	TMG2_HUMAN	P19540 canis famli
25	70	36.6	452	FA9_MOUSE	P16294 mus musculu
26	70	36.6	459	FA9_MOUSE	O9bnd6 homo sapien
27	66.5	34.8	226	TMG4_HUMAN	P00744 bos taurus
28	61	31.9	396	PRTC_HUMAN	P07224 bos taurus
29	60	31.4	675	PRTC_BOVIN	Q28520 macaca mula
30	59	30.9	649	PRTC_MACMO	P98118 oryctolagus
31	59	30.9	646	PRTC_HUMAN	P53813 rattus norv
32	58	30.4	646	PRTC_RABIT	
33	57	29.8	675	PRTC_RAT	

34 56 29.3 400 1 PRTC_HUMAN P22891 homo sapien
35 50 26.2 675 1 PRTC_MOUSE Q08761 mus musculu
36 45 23.6 271 1 MD12_YEAST Q92328 saccharomyc
37 45 23.6 879 1 YN65_YEAST P42871 saccharomyc
38 43 22.5 343 1 HMD_METVO Q50840 methanococc
39 43 22.5 353 1 HMD_METTL Q50759 m coenzym
40 43 22.5 394 1 TCR4_SALOR P33733 salmoneila
41 43 22.5 440 1 Y788_BORBU O51728 borreilia bu
42 42 22.0 185 1 HEX1_MOUSE O61658 mus musculu
43 41 21.5 263 1 PRLA_STRMU O68575 streptococc
44 41 21.5 393 1 DRS5_PINSY Q02323 pinus sylve
45 41 21.5 616 1 JEN1_YEAST P36035 saccharomyc

ALIGNMENTS

RESULT 1
FA7_HUMAN STANDARD; PRT; 466 AA.
AC P08709: Q14339;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Eptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kissel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.",
RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.",
RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.U., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725.
RA Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.",
RT Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Thim L., Wildberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kissel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.",
RT J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;

RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN
 RP STRUCTURE BY NMR OF 105-145
 RX MEDLINE=98367502; PubMed=9692950;
 RA Muranyi A., Finn B.E., Gelpert G.P., Forsen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN
 RP VARIANTS GLN-132-140(1991).
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral polymorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kembell-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lunley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94264305; PubMed=8204879;
 RA Chang S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohlwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Abidin A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr39Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalom L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaitov R., Seligsohn U.;
 RT "Val244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
 RA "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN
 RP FUNCTION: CIRCULATES IN THE BLOOD IN A ZWYGOEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
 CC BY LIMITED PROTEOLYSES. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PPM: THE VITAMIN K-DEPENDENT. ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -1- PHARMACEUTICAL: Available under the names Nistase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match 81.7%; Score 156; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 7.2e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

1 ANAFLXXLREGSLRXCKXQCSFXAXFIKPDAXRTKLFWISY 44
61 ANAFLEELRPGSLERCKEKGCSFEARVFPKARTKLFWISY 104

RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224; Rel. 33; Created
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brochets A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";
RT Thromb. Res. Suppl. 69:231-238(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruit S.R., Blajchman M.A., Clarke B.J.;
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).
CC - CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
CC - SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).
CC - TISSUE SPECIFICITY: PLASMA.
CC - PM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC - SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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CC -----
CC EMBL: U77477; AAB37326.1; -.
CC HSSP: P08709; 1PAK.
CC MEROPS: S01.215; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.

DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin_1.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Sec; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 363 363
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
FT DISULFID 198 203
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;

Query Match 63.9%; Score 122; DB 1; Length 444;
Best Local Similarity 54.5%; Pred. No. 7.1e-14;
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

1 ANAFLXXLREGSLRXCKXQCSFXAXFIKPDAXRTKLFWISY 44
40 ANAFLEELRPGSLERCKEKGCSFEARVFPKARTKLFWISY 83

RESULT 3

FA7_BOVIN
ID FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.
OC NCBI_TaxId=9913;
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008362; PubMed=3049594;
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,
RA Iwanaga S.,
RT "Bovine factor VII. Its purification and complete amino acid sequence."
RT J. Biol. Chem. 263:14868-14877(1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.,
RT "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX."
RT J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."
RT Adv. Exp. Med. Biol. 281:121-131(1990).
RL J. Biochem. 104:867-868(1988).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC PIR: A31979; A31979.
DR HSSP: P08709; 1BF9.
DR MEROPS: S01.215; .
DR InterPro: IPR000152; Aex_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_T1.
DR InterPro: IPR002383; GLA_Blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin_1.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 1.

DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; KM EGF-like domain; Repeat.
FT CHAIN 1 152
FT CHAIN 153 407
FT DOMAIN 6 35
FT DOMAIN 46 82
FT DOMAIN 87 128
FT DOMAIN 153 407
FT SITE 152 153
FT ACT SITE 193 193
FT ACT SITE 242 242
FT ACT SITE 344 344
FT BINDING 338 338
FT DISULFID 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 72 81
FT DISULFID 91 102
FT DISULFID 98 112
FT DISULFID 114 127
FT DISULFID 135 262
FT DISULFID 153 164
FT DISULFID 178 194
FT DISULFID 310 329
FT DISULFID 340 368
FT MOD_RES 6 7
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 35 35
FT CARBOHYD 52 52
FT CARBOHYD 145 145
FT CARBOHYD 203 203
SQ SEQUENCE 407 AA; 44431 MW; 703E1FB0636F7F10 CRC64;
Query Match 59.7%; Score 114; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 1,7e-12;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
OY 1 ANAFLLXLRBESLKRKXKQCSFYXAFIKDAXRKLFWISY 44
DB 1 ANGFLBLLPGLSRLERECRELCSEEAHEIFRNEERTQFVWSY 44
RESULT 4
FA7_MOUSE STANDARD; PRT; 446 AA.
ID FA7_MOUSE
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97127167; PubMed=8972017;
 RX Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood
 coagulation factor VII gene."
 RL Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIa BY FACTOR XIa, FACTOR XIIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U66079; AAC3796.1; -.
 DR HSSP; P08709; 1BR9.
 DR MEROPS; S01.215; -.
 DR MCD; MGI:109325; F7.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SMO0179; EGF_CA; 1.
 DR SMART; SMO0001; EGF_like; 1.
 DR SMART; SMO0069; GLA; 1.
 DR SMART; SMO0020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SSR; 1.
 KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 24
 FT PROPEP 25 41 POTENTIAL.
 FT CHAIN 42 193 FACTOR VII LIGHT CHAIN.
 FT CHAIN 194 446 FACTOR VII HEAVY CHAIN.
 FT DOMAIN 47 76 GLA-RICH.
 FT DOMAIN 87 123 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 128 169 EGF-LIKE 2.
 FT DOMAIN 194 446 SERINE PROTEASE.
 FT SITE 193 194 CLEAVAGE (BY FACTOR Xa, FACTOR XIa,
 FT ACT_SITE 234 234 FACTOR IXa OR THROMBIN) (BY SIMILARITY).
 FT ACT_SITE 283 283 BY SIMILARITY.
 FT ACT_SITE 385 385 BY SIMILARITY.
 FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).
 FT DISULFID 58 63 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT DISULFID 96 111 BY SIMILARITY.
 FT DISULFID 113 122 BY SIMILARITY.
 FT DISULFID 132 143 BY SIMILARITY.
 FT DISULFID 139 153 BY SIMILARITY.
 FT DISULFID 155 168 BY SIMILARITY.
 FT DISULFID 176 303 BY SIMILARITY.
 FT DISULFID 200 205 BY SIMILARITY.
 FT DISULFID 219 235 BY SIMILARITY.
 FT DISULFID 351 370 BY SIMILARITY.
 FT DISULFID 381 409 BY SIMILARITY.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 104 104 HYDROXYLATION (BY SIMILARITY).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 446 AA; 50276 MW; 2512B44A5CB96E CRC64;
 Query Match 58.1%; Score 111; Length 446;
 Best Local Similarity 54.5%; Pred. No. 6.3e-12;
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;
 QY 1 ANAFLLXRLREGSLKXKCKXKQCSFKXAFYFDKARTKLFWISY 44
 DB 42 ANSLLEELWPGSLRECNCEQCSFEFAREIFXSPERTKQFWIVY 85
 AC 019045;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97256311; PubMed=9101642;
 RA Pendurthi U.R., Anderson K.D., James H.L.;
 RT "Characterization of a full-length cDNA for rabbit factor X."
 RL Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC		CALCIUM (BY SIMILARITY).	
CC	-I-	PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY)	
CC	-I-	PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY) (BY SIMILARITY).	
CC	-I-	MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.	
CC	-I-	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.	
CC	-I-	SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.	
CC		-----	
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch). -----	
CC		EMBL: AF003200; AAB62542.1; -.	
DR	HSEF,	P00742, IHCG.	
DR	MEROPL,	SOL_216; -.	
DR	InterPro;	IPR000152; Asx_hydroxy1.	
DR	InterPro;	IPR001314; Chymotrypsin.	
DR	InterPro;	IPR000561; EGF-like.	
DR	InterPro;	IPR000742; EGF_2.	
DR	InterPro;	IPR001881; EGF_Ca.	
DR	InterPro;	IPR002383; GLA_blood.	
DR	InterPro;	IPR001254; Ser_protease_Try.	
DR	InterPro;	IPR002294; VILK_dep_GLA.	
DR	pfam;	PF000089; EGF_2.	
DR	pfam;	PF00089; trypsin; 1.	
DR	pfam;	PF00594; gla; 1.	
DR	PRINTS;	PR00722; CHYMOTRYPSIN.	
DR	PRINTS;	PR00001; GLABLOOD.	
DR	SMART;	SMO00179; EGF_CA; 1.	
DR	SMART;	SMO0001; EGF_like; 1.	
DR	SMART;	SMO0069; GLA; 1.	
DR	SMART;	SMO0020; Tryp_Spc; 1.	
DR	PROSITE;	PS00010; ASX_HYDROXYL; 1.	
DR	PROSITE;	PS00022; EGF_1; 1.	
DR	PROSITE;	PS01186; EGF_2; 2.	
DR	PROSITE;	PS01187; EGF_CA; 1.	
DR	PROSITE;	PS00011; GLU-CARBOXYLTION; 1.	
DR	PROSITE;	PS50240; TRYPSIN_DOM; 1.	
DR	PROSITE;	PS00134; TRYP SIN_HIS; 1.	
KW	PROSITE;	PS00135; TRYP SIN_SER; 1.	
KW	Glycoprotein;	Hydrolase; Serine protease; Plasma; Blood coagulation; K; Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K; Signal; Zymogen; EGF-like domain; Repeat.	
FT	SIGNAL	1 20 POTENTIAL.	
FT	PROPEP	21 40 BY SIMILARITY.	
FT	CHAIN	41 180 FACTOR X LIGHT CHAIN.	
FT	CHAIN	164 490 FACTOR X HEAVY CHAIN.	
FT	PROPEP	164 232 ACTIVATION PEPTIDE.	
FT	CHAIN	233 490 ACTIVATED FACTOR XN, HEAVY CHAIN.	
FT	DOMAIN	86 122 EGF-LIKE 1, CALCIDIUM-BINDING (POTENTIAL).	
FT	DOMAIN	125 165 EGF-LIKE 2.	
FT	MOD_RES	233 490 SERINE PROTEASE.	
FT	MOD_RES	46 46 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	47 47 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	54 54 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	56 56 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	59 59 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	60 60 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	65 65 GAMMA-CARBOXYGUTAMIC ACID (BY SIMILARITY).	
FT	MOD_RES	66 66 GAMMA-CARBOXYGUTAMIC ACID (BY	

Query Match	Best Local Similarity	Score 102;	DB 1;	Length 490;	
Matches 18;	Conservative	8;	Mismatches 18;	Indels 0;	Gaps 0;
1 ANAFXXLRREGSLXRXCKXXQCSFYXAFYFXFDXARXRLFLWISY 44	41 ANSFLEELKXGNLRECKMEENCSYEALLEVFDREKRTNEFWNKY 84				
MOD_RES	MOD_RES	69	69		
MOD_RES	MOD_RES	72	72		
MOD_RES	MOD_RES	75	75		
MOD_RES	MOD_RES	79	79		
MOD_RES	MOD_RES	103	103		
ACT_SITE	ACT_SITE	274	274		
ACT_SITE	ACT_SITE	320	320		
ACT_SITE	ACT_SITE	417	417		
DISULFID	DISULFID	90	101		
DISULFID	DISULFID	95	110		
DISULFID	DISULFID	112	121		
DISULFID	DISULFID	129	140		
DISULFID	DISULFID	136	149		
DISULFID	DISULFID	151	164		
DISULFID	DISULFID	172	340		
DISULFID	DISULFID	239	244		
DISULFID	DISULFID	259	275		
DISULFID	DISULFID	388	402		
DISULFID	DISULFID	413	441		
CARBOHYD	CARBOHYD	61	61		
CARBOHYD	CARBOHYD	187	187		
CARBOHYD	CARBOHYD	205	205		
SEQUENCE	SEQUENCE	490 AA;	53965 MM;	3A39FA85AF2A6D11 CRC64;	
Query Match	Best Local Similarity	53.4%;	Score 102;	DB 1;	Length 490;
Matches 18;	Conservative	8;	Mismatches 18;	Indels 0;	Gaps 0;
1 ANAFXXLRREGSLXRXCKXXQCSFYXAFYFXFDXARXRLFLWISY 44	41 ANSFLEELKXGNLRECKMEENCSYEALLEVFDREKRTNEFWNKY 84				
MOD_RES	MOD_RES	69	69		
MOD_RES	MOD_RES	72	72		
MOD_RES	MOD_RES	75	75		
MOD_RES	MOD_RES	79	79		
MOD_RES	MOD_RES	103	103		
ACT_SITE	ACT_SITE	274	274		
ACT_SITE	ACT_SITE	320	320		
ACT_SITE	ACT_SITE	417	417		
DISULFID	DISULFID	90	101		
DISULFID	DISULFID	95	110		
DISULFID	DISULFID	112	121		
DISULFID	DISULFID	129	140		
DISULFID	DISULFID	136	149		
DISULFID	DISULFID	151	164		
DISULFID	DISULFID	172	340		
DISULFID	DISULFID	239	244		
DISULFID	DISULFID	259	275		
DISULFID	DISULFID	388	402		
DISULFID	DISULFID	413	441		
CARBOHYD	CARBOHYD	61	61		
CARBOHYD	CARBOHYD	187	187		
CARBOHYD	CARBOHYD	205	205		
SEQUENCE	SEQUENCE	490 AA;	53965 MM;	3A39FA85AF2A6D11 CRC64;	

strongly promoted by thrombomodulin.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
 CC residues allows the modified protein to bind calcium.
 CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the Gla domain. This Gla-independent binding
 CC site is necessary for the recognition of the
 CC thrombin-chromomodulin complex.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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 CC EMBL: AF191307; AAG28380.1; -.
 CC HSSP: P04070; 1PCU.
 CC MEROPS: S01.218; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin; 1.
 DR Pfam: PF00594; gla; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00001; EGF-like; 2.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TYP SPc; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 41
 FT CHAIN 42 459
 FT CHAIN 42 196
 FT CHAIN 199 459
 FT PEPTIDE 199 213
 FT SITE 213 214
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 214 459
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61

FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 255 255
 FT ACT_SITE 301 301
 FT ACT_SITE 400 400
 FT ACT_SITE 400 400
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 321
 FT DISULFID 240 256
 FT DISULFID 371 385
 FT DISULFID 396 424
 FT CARBOHYD 138 138
 FT CARBOHYD 292 292
 FT CARBOHYD 353 353
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 51.3%; Score 98; DB 1; Length 459;
 Best Local Similarity 45.5%; Pred. No. 1.3e-09;
 Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;
 QY 1 ANAFLLXLESGSLRXCKXKCSFKXAFIFDARFKTLFWISY 44
 DB 42 ANSFLELRPSLSRCKEETCDFEAREIFONTENTAFWSKY 85
 RESULT 7
 ID_PRTC_MOUSE STANDARD; PRT; 461 AA.
 AC P33587; O35498;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92316897; PubMed=1618739;
 RA Tada N., Sato M., Tsuchimura A., Iwase R., Hashimoto-Gotoh T.;
 RT "Isolation and characterization of a mouse protein C cDNA.";
 RL J. Biochem. 111:491-495(1992).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=98152576; PubMed=9493582;
 RA Jaldert L.R., Rosen B.D., Lissens A., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine gene encoding
 RT anticoagulant protein C.";
 RL Thromb. Haemost. 79:310-316(1998).
 RN [3]
 RP SEQUENCE OF 274-434 FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=94318474; PubMed=8043441;
 RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;

RT "A comparative study of partial primary structures of the catalytic
 RT region of mammalian protein C".
 RL Br. J. Haematol. 86:590-600(1994).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIA.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: D10445; BAA01235.1; .
 DR EMBL: AF034569; AAC3795.1; .
 DR EMBL: D43755; BAA07812.1; .
 DR PIR: JX0210; JX0210.
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218; .
 DR MOD: MGI:97771; Piroc.
 DR InterPro: IPR000152; Axx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR002383; GLA_Blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR Pfam: PF00594; glaf; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYR_SPC; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Glycoprotein; Serine protease;
 DR Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT STGNLT 1
 FT PROPEP 34
 FT CHAIN 42
 FT CHAIN 199
 FT PEPTIDE 199
 FT SITE 212
 FT DOMAIN 96

FT DOMAIN 135 175 EGF-LIKE 2.
 FT DOMAIN 213 461 SERINE PROTEASE.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 48 48 (BY SIMILARITY).
 FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 55 55 (BY SIMILARITY).
 FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 57 57 (BY SIMILARITY).
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 61 61 (BY SIMILARITY).
 FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 66 66 (BY SIMILARITY).
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 67 67 (BY SIMILARITY).
 FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 70 70 (BY SIMILARITY).
 FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
 FT ACT_SITE 253 253 CHARGE RELAY SYSTEM.
 FT ACT_SITE 299 299 CHARGE RELAY SYSTEM.
 FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
 FT DISULFID 58 63 BY SIMILARITY.
 FT DISULFID 91 110 BY SIMILARITY.
 FT DISULFID 100 105 BY SIMILARITY.
 FT DISULFID 104 119 BY SIMILARITY.
 FT DISULFID 121 130 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 146 159 BY SIMILARITY.
 FT DISULFID 161 174 BY SIMILARITY.
 FT DISULFID 182 319 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 238 254 BY SIMILARITY.
 FT DISULFID 373 387 BY SIMILARITY.
 FT DISULFID 398 426 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 328 328 MISSING (IN REF. 2).
 FT CONFLICT 393 393 N -> D (IN REF. 2).
 SQ SEQUENCE 461 AA; 51945 MW; 53FAAD85B194D6E CRC64;
 Query Match Score 97; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 1.9e-09;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 ANAFLLXLRREGSLRXCKXXQCSFXAFLFKDAXRTKLFMISY 44
 Db 42 ANSLFEMRPGSLERECMEIODEEBAQELFQNVEDTLAWIKY 85
 RESULT 8
 ID_PRTC RAT STANDARD; PRT; 461 AA.
 AC P1354;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistar; TISSUE=Liver;
 RX MEDLINE=92329550; PubMed=1627650;
 RA Okafor T., Maekawa K., Nawa K., Marumoto Y.;
 RT "The cDNA cloning and mRNA expression of rat protein C.";

```

CC Biochem Biophys. Acta 1131:339-332(1992).
CC
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAITC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC
CC -----
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CC
CC -----
CC
CC EMBL, X64336; CAA45617.1; -.
CC
CC PIR, S18994; S18994.
CC
CC PIR, S24312; S24312.
CC
CC HSSP, P04070; 1PCU.
CC
CC MEROPS, S01.218; -.
CC
CC InterPro, IPR000152; Asx_hydroxyl.
CC
CC InterPro, IPR001314; Chymotrypsin.
CC
CC InterPro, IPR000561; EGF-like.
CC
CC InterPro, IPR001881; EGF-Ca.
CC
CC InterPro, IPR002183; GLA blood.
CC
CC InterPro, IPR001254; Ser_protease_Try.
CC
CC InterPro, IPR000294; Vitk_dep_GLA.
CC
CC Pfam, PF00068; EGF_2.
CC
CC Pfam, PF00089; Trypsin_1.
CC
CC Pfam, PF00594; Gla_1.
CC
CC PRINTS, PRO0722; CHYMOTRYPSIN.
CC
CC PRINTS, PR00001; GLABLOOD.
CC
CC SMART, SM00179; EGF_CA_1.
CC
CC SMART, SM00001; EGF_like_1.
CC
CC SMART, SM00069; GLA_1.
CC
CC SMART, SM00020; Tryp_Spc_1.
CC
CC PROSITE, PS00010; ASX_HYDROXYL, 1.
CC
CC PROSITE, PS00022; EGF_1; 1.
CC
CC PROSITE, PS01186; EGF_2; 2.
CC
CC PROSITE, PS01187; EGF_CA_1.
CC
CC PROSITE, PS00011; GLU_CARBOXYLATION; 1.
CC
CC PROSITE, PS50240; TRYPSIN_DOM; 1.
CC
CC PROSITE, PS00134; TRYPSIN_HIS; 1.
CC
CC PROSITE, PS00135; TRYPSIN_SER; 1.
CC
CC Blood coagulation; glycoprotein; Serine protease;
CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
CC EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
CC
CC FT SIGNAL 1 32
CC FT PROPEP 33 41
CC FT CHAIN 42 196
CC FT CHAIN 199 461
CC FT PEPTIDE 199 212
CC FT SITE 212 213
CC FT DOMAIN 96 131
CC FT DOMAIN 135 175
CC FT DOMAIN 213 461
CC FT MOD_RES 47 47
CC
CC GAMMA-CARBOXYGLUTAMIC ACID
CC (BY SIMILARITY).

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Query	1 ANAPLXLREGSLRXCKXKXOCSEFXARFPRDXKRTLPWISY 44	Score 96; DB 1; Length 461;
Beat Local Similarity	45.5%;	Pred. No. 2.9e-09;
Matches 20; Conservative	4;	Mismatches 20; Indels 0; Gaps 0;
Db	42 ANSFLVLRAGSLERECMEBICDFEEAOGTFQWEDTLAFWIKY 85	
RESULT 9		
FA10_HUMAN		
ID_FA10_HUMAN	STANDARD;	PRT; 488 AA.
AC	P00742; Q14340;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	01-OCT-1989 (Rel. 12, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).	
GN	P10.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=91216473; PubMed=1902434;	
RA	Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;	
RT	"Cloning and expression in COS-1 cells of a full-length cDNA encoding	
RL	human coagulation factor X.";	
RL	Gene 99:291-294(1991).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=87026600; PubMed=3768336;	
RA	Leytus S.P., Foster D.C., Kirsch K., Davie E.W.;	
RT	"Gene for human factor X: a blood coagulation factor whose gene	
RT	organization is essentially identical with that of factor IX and	
RT	protein C.";	

RL Biochemistry 25:5098-5102(1986).
 RN [3]
 RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RX TISSUE=Liver;
 RC MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 cDNA.";
 RL Gene 41:311-314(1986).
 RN [5]
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kisiel W., Saegawa T., Howard W.N.,
 Kwa B.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 coagulation factor X: evidence for identification of residue 63 as
 beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884(1983).
 RN [6]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3659-3702(1984).
 RN [7]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 peptides of blood coagulation factor X. The role of the carbohydrate
 moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [8]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=9012829; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 encoding human factor X.";
 RL Gene 84:517-519(1989).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tullinsky A., Park C.H., Bode W.,
 Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966(1993).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283987; PubMed=9618463;
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 converts prothrombin to thrombin in the presence of factor Va,
 calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CALCIUM.

CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: K03194; AAA52490.1; -
 DR EMBL: M57285; AAA52421.1; -
 DR EMBL: L29433; AAA52764.1; -
 DR EMBL: L00390; AAA52764.1; JOINED.
 DR EMBL: L00391; AAA52764.1; JOINED.
 DR EMBL: L00392; AAA52764.1; JOINED.
 DR EMBL: L00393; AAA52764.1; JOINED.
 DR EMBL: L00394; AAA52764.1; JOINED.
 DR EMBL: L00395; AAA52764.1; JOINED.
 DR EMBL: L00396; AAA52764.1; JOINED.
 DR EMBL: M22613; AAA51984.1; -
 DR EMBL: K01886; AAA52486.1; -
 DR EMBL: M33297; AAA52636.1; -
 DR PIR: A09824; EXHU.
 DR PIR: A25853; A25853.
 DR PIR: A24478; A24478.
 DR PDB: 1HCX; 08-MAY-95.
 DR PDB: 1FAK; 29-OCT-97.
 DR PDB: 1EXY; 17-JUN-98.
 DR PDB: 1XKA; 23-MAR-99.
 DR PDB: 1XXB; 23-MAR-99.
 DR MEROPS: S01.216; -.
 DR GLYCOSULEDB: P00742; -.
 DR Genew: HGNC:3528; P10.
 DR MIM: 134530; -.
 DR MIM: 227600; -.
 DR InterPro: IPR000152; Axx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF 2.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; Vltk_dep_GLA.
 DR Pfam: PF00089; EGF; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR Pfam: PF00594; gla_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF-like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; Tryp_SPC; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLUT CARBOXYLATION; 1.
 DR PROSITE: PSS0240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KM Glycoprotein; Hydrolase; Serine protease; Plasma; blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KC Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 FT SIGNAL 1 31
 FT PROPEP 32 40
 FT CHAIN 41 179 FACTOR X LIGHT CHAIN.
 FT CHAIN 183 488 FACTOR X HEAVY CHAIN.
 FT PROPEP 183 234 ACTIVATION PEPTIDE.

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FT CHAIN 235 488 ACTIVATED FACTOR Xa, HEAVY CHAIN.
FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 125 122 EGF-LIKE 2.
FT DOMAIN 235 488 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 221 221 /FTID=CAR_000012.
FT CARBOHYD 231 231 /FTID=CAR_000013.
FT ACT_SITE 276 276 CHARGE RELAY SYSTEM.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110
FT DISULFID 112 121
FT DISULFID 129 140

Query Match 50.3%; Score 96; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 3.1e-09;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFKXLRGSLKRYCKXQCSFXXAFKIDAKRTKLFWISY 44
Db 41 ANSFLEMKKGLHRECMETCSYEAREVFEDSDKTNEFMNKY 84

RESULT 10
ID FA10 BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 1
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN 12
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN 13
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kistiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
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RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN 14
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN 15
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN 16
RP ACTIVE SITE.
RX MEDLINE=73053114; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN 17
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN 18
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
RN 19
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
RN 110
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X.";
RL Biochemistry 29:8111-8118(1990).
RN 111
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telemann O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding.";
RL Biochemistry 31:5974-5983(1992).
RN 112
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Sunnerhagen M., Ullner M., Persson E., Telemann O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X.";
```

RL J. Biol. Chem. 267:19642-19649 (1992).

RN [13]

RX MEDLINE=96387194; PubMed=8794734;

RA Sumnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,

RA Tremhella J.;

RT "The relative orientation of Glu and EGF domains in coagulation factor X is altered by Ca²⁺ binding to the first EGF domain. A combined NMR-small angle X-ray scattering study.";

RL Biochemistry 35:11547-11559 (1996).

CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin.

CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS.

CC -1- GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.

CC -1- PTM: N- AND O-GLYCOSYLATED.

CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).

CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -----

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CC -----

DR EMBL; X00673; CA25286.1; -.

DR FMR; A00925; EXBO.

DR PDB; IAP0; 31-JAN-94.

DR PDB; 1CCF; 31-MAY-94.

DR PDB; 1MHE; 15-MAY-97.

DR PDB; 1MHF; 15-MAY-97.

DR MEROPS; S01.216; -.

DR GlycosultedB; P00743; -.

DR InterPro; IPR000152; Aex_hydroxyl.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF-ca.

DR InterPro; IPR002383; GLA_Blood.

DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00089; trypsin; 1.

DR Pfam; PF00594; gla; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 1.

DR SMART; SM00001; EGF_1like; 1.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; TRYP_Spc; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS00011; GIU_CARBOXYLATION; 1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00133; TRYPSIN_SER; 1.

DR Glycoprotein; Hydroxylase; Serine protease; Plasma; Blood coagulation; Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K; Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.

FT	SIGNAL	1	23	POTENTIAL.
FT	PROPEP	24	40	FACTOR X LIGHT CHAIN.
FT	CHAIN	41	180	FACTOR X HEAVY CHAIN.
FT	CHAIN	183	482	ACTIVATION PEPTIDE.
FT	PROPEP	183	233	ACTIVATED FACTOR XA, HEAVY CHAIN.
FT	CHAIN	234	492	MAY BE REMOVED BUT IS NOT NECESSARY FOR ACTIVATION.
FT	PROPEP	476	492	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	86	122	EGF-LIKE 2.
FT	DOMAIN	125	165	SERINE PROTEASE.
FT	DOMAIN	234	482	CHARGE RELAY SYSTEM.
FT	ACT SITE	275	275	CHARGE RELAY SYSTEM.
FT	ACT SITE	321	321	CHARGE RELAY SYSTEM.
FT	ACT SITE	418	418	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	46	46	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	54	54	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	56	56	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	59	59	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	65	65	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID.

Query Match Best Local Similarity 50.3%; Score 96; DB 1; Length 492; Pred. No. 3.1e-09; Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLXKCKXQCSPXAXFXFKDAXTKLFWISY 44

Db 41 ANSFLEVRKQGNRECELEBACSLREAREVFEDAEQTDERSKY 84

RESULT 11

TMGI_HUMAN	STANDARD;	PRT;	218 AA.
AC	Q14668;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DE	Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein 1).		
GN	PRRG1 OR TMGI OR PRGP1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97404347; PubMed=9256434;		
RA	Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;		
RT	"Primary structure and tissue distribution of two novel proline-rich gamma-carboxyglutamic acid proteins."		
RL	Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062 (1997).		
CC	-1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.		
CC	-1- PTM: Gla residues are produced after subsequent posttranslational modifications of glutamic acid by a vitamin K-dependent gamma-carboxylase.		
CC	-----		
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CC	-----		
DR	EMBL; AF09242; AAB67070.1; -.		
DR	HSP; P00740; 1CFH.		
DR	GeneW; HGNC:9469; PRRG1.		
DR	MTM; 604428; -.		
DR	InterPro; IPR002383; GLA blood.		
DR	InterPro; IPR000294; VitK_dep_GLA.		

DR	Pfam: PF00594; glia; 1.
DR	PRINTS; PR00001; GLABLOOD.
DR	SMART; SM00069; GLA; 1.
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW	Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT	PROPEP
FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
SO	SEQUENCE
OY	1 ANAFLLXLRREGSLKRCCKKKQCSFFKXAIFFDPAKTKFLWISY 44
DB	21 ANGFEIEIRGNIERECKECFCTFEAREAFENNEKTKEFWSTY 64
RESULT 12	
ID	THRB_HUMAN
AC	P00734;
DT	21-JUL-1986 (Rel. 01, Created)
DT	01-JAN-1990 (Rel. 13, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).
GN	F2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OK	NCBI_TaxId=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=86077877; PubMed=2825773;
RA	Degen S.J.F., Davie E.W.;
RT	"Nucleotide sequence of the gene for human prothrombin.";
RL	Biochemistry 26:6165-6177(1987).
RN	[2]
RP	SEQUENCE FROM N.A.; AND VARIANT MET-165.
RA	Rieger M.J., Armet L.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA	Ozuna M., Poel C.L., Toch E.J., Yi O., Nickerson D.A.;
RL	Submitted (JAN-2002) to the EMBL/genbank/DBD databases.
RN	[3]
RP	SEQUENCE OF 8-622 FROM N.A.
RX	MEDLINE=83231469; PubMed=6305407;
RA	Degen S.J.F., McGilivray R.T.A., Davie E.W.;
RT	"Characterization of the complementary deoxyribonucleic acid and gene
RL	coding for human prothrombin.";
RN	Biochemistry 22:2087-2097(1983).
RN	[4]
RP	SEQUENCE OF 44-314.
RX	MEDLINE=77193964; PubMed=873923;
RA	Walz D.A., Hewett-Emmett D., Seegers W.H.;
RT	"Amino acid sequence of human prothrombin fragments 1 and 2.";
RL	Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
RN	[5]
RP	SEQUENCE OF 315-622.
RX	MEDLINE=77207112; PubMed=873923;
RA	Buckowski R.J., Elion J., Downing M.R., Mann K.G.;
RT	"Primary structure of human prothrombin 2 and alpha-thrombin.";
RL	J. Biol. Chem. 252:4942-4957(1977).
RN	[6]
RP	PROCESSING.
RX	MEDLINE=87008532; PubMed=3759958;
RA	Rabiet M.J., Blaesill A., Furie B., Furie B.C.;
RT	"Prothrombin fragment 1 X 2 X 3, a major product of prothrombin
RT	activation in human plasma."

RL J. Biol. Chem. 261:13210-13215(1986).
 [7]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=90059942; PubMed=2583108;
 RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
 RT "The refined 1.9 Å crystal structure of human alpha-thrombin:
 interaction with D-Phe-Pro-Arg chloromethylketone and significance of
 the Tyr-Pro-Tyr insertion segment."; EMO J. 8:3467-3475(1989).
 RL [8]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RP MEDLINE=90327074; PubMed=2374926;
 RX Rygel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
 RA Rottsch C., Fenton J.W. II; "The structure of a complex of recombinant hirudin and human alpha-thrombin."; Science 249:277-280(1990).
 RL [9]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RP MEDLINE=94350942; PubMed=8071320;
 RX Rygel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
 RA Correa P.E., Fenton J.W. II, Tulinsky A.;
 RT "Crystallographic structure of human gamma-thrombin."; J. Biol. Chem. 269:22000-22006(1994).
 RL [10]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RP MEDLINE=97357286; PubMed=9214615;
 RX van de Loch A., Bode W., Huber R., Je Bonnicc B.F., Stone S.R.,
 RA Esmon C.T., Stubbs M.T.;
 RT "The thrombin E1920-BPTI complex reveals gross structural rearrangements: implications for the interaction with antithrombin and thrombomodulin."; EMBO J. 16:2977-2984(1997).
 RL [11]
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
 RP MEDLINE=99162521; PubMed=10051558;
 RX Guinco E.R., Caccia S., Rose T., Fuetterer K., Waksman G., di Cera E.;
 RA "Unexpected crucial role of residue 225 in serine proteases."; Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
 RL [12]
 RN VARIANT BARCELONA.
 RP MEDLINE=87033739; PubMed=3771562;
 RX Rabiet M.-J., Furie B.C., Furie B.;
 RA "Molecular defect of prothrombin Barcelona. Substitution of cysteine for arginine at residue 273."; J. Biol. Chem. 261:15045-15048(1986).
 RL [13]
 RN VARIANT FRANKFURT.
 RP MEDLINE=95513001; PubMed=7792730;
 RX Degen S.J.F., McDowell S.A., Sparks L.M., Scharrer I.;
 RA "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by substitution of Glu-466 by Ala."; Thromb. Haemost. 73:203-209(1995).
 RL [14]
 RN VARIANTS HIMI-1 AND HIMI-2.
 RP MEDLINE=93043342; PubMed=1421388;
 RX Morishita E., Saito M., Kumabaehiri I., Asakura H., Matsuda T.,
 RA Yamaguchi K.;
 RT "Prothrombin Himi: a compound heterozygote for two dysfunctional prothrombin molecules (Met-337-->Thr and Arg-368-->His)."; Blood 80:2275-2280(1992).
 RL [15]
 RN VARIANT PADUA-1.
 RP MEDLINE=95169898; PubMed=7865694;
 RX James H.L., Kim D.J., Zheng D.-Q., Girolami A.;
 RA "Prothrombin Padua I: incomplete activation due to an amino acid substitution at a factor Xa cleavage site."; Blood Coagul. Fibrinolysis 5:841-844(1994).
 RL [16]
 RN VARIANT QUICK-1.
 RP MEDLINE=89207504; PubMed=3242619;
 RX Henriksen R.A., Mann K.G.;
 RA "Identification of the primary structural defect in the dysfibrinogen

RT thrombin Quick I: substitution of cysteine for arginine-382."
 RL Biochemistry 27:9160-9165(1988).
 RN
 RP VARIANT QUICK-2.
 RA MEDLINE=89247398; PubMed=2719946;
 RX Henriksen R.A., Mann K.G.;
 RT "Substitution of valine for glycine-558 in the congenital dysfibrinogen
 RT thrombin Quick II alters primary substrate specificity."
 RL Biochemistry 28:2078-2082(1989).
 RN
 RP VARIANT SALAKTA.
 RA MEDLINE=92378975; PubMed=1354985;
 RX Miyata T., Aruga R., Uneyama H., Bezeaud A., Guillin M.-C.,
 RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
 RT reduces the fibrinogen clotting activity and the esterase activity."
 RL Biochemistry 31:7457-7462(1992).
 RN
 RP VARIANT TOKUSHIMA.
 RA MEDLINE=87185407; PubMed=3567158;
 RX Miyata T., Morita T., Inomoto T., Kawachi S., Shirakami A.,
 RA Iwanaga S.;
 RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
 RT that impairs the fibrinogen clotting activity of derived thrombin
 RT Tokushima."
 RL Biochemistry 26:1117-1122(1987).
 RN
 RP VARIANT TOKUSHIMA.
 RA MEDLINE=87101511; PubMed=3801671;
 RX Inomoto T., Shirakami A., Kawachi S., Shigekiyo T., Saito S.,
 RA Miyoshi K., Morita T., Iwanaga S.;
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
 RT derived from a variant of human prothrombin."
 RL Blood 69:565-569(1987).
 RN
 RP VARIANT TOKUSHIMA.
 RA MEDLINE=92256838; PubMed=1349838;
 RX Iwahana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,
 RA Itakura M.;
 RT "Detection of a single base substitution of the gene for prothrombin
 RT Tokushima. The application of PCR-SSCP for the genetic and molecular
 RT analysis of dysprothrombinemia."
 RL Int. J. Hematol. 55:93-100(1992).
 RN
 RP VARIANT TYPE-3.
 RX MEDLINE=83204687; PubMed=6405779;
 RA Board P.G., Shaw D.C.;
 RT "Determination of the amino acid substitution in human prothrombin
 RT type 3 (157 Glu leads to Lys) and the localization of a third
 RT thrombin cleavage site."
 RL Br. J. Haematol. 54:245-254(1983).
 CC
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
 CC fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
 CC
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC
 CC -1- DISEASE: DEFECTS IN F2 ARE THE CAUSE OF VARIOUS FORMS OF
 CC DYSPROTHROMBINEMIA.
 CC
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.

CC
 CC -1- MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION
 CC PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN
 CC NATURAL BLOOD CLOTTING.
 CC
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC
 CC -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO, DOES
 CC
 CC Query Match 49.2%; Score 94; DB 1; Length 622;
 CC Best Local Similarity 38.6%; Pred. No. 8.9e-09;
 CC Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
 CC
 CC Db 1 ANAFXXLRGSLXRXCKXQCSFXAXFIFKDXRKLFWISY 44
 CC 44 ANTFLEVRKGNLRECVETCTYEAFELSESTADVWMARY 87
 CC
 CC RESULT 13
 CC THRB RAT STANDARD; PRT; 617 AA.
 CC ID THRB RAT
 CC AC P18252;
 CC DT 01-NOV-1990 (Rel. 16, Created)
 CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Prothrombin precursor (EC 3.4.21.5).
 CC GN P2.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_TaxID=10116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC SPRAIN-Sprague-Dawley; TISSUE=Liver;
 CC RX MEDLINE=9032426; PubMed=2377469;
 CC RA Dhanich M., Monard D.;
 CC RT "cDNA sequence of rat prothrombin."
 CC RL Nucleic Acids Res. 18:4251-4251(1990).
 CC RN [2]
 CC RP SEQUENCE OF 383-617 FROM N.A.
 CC RC TISSUE=Liver;
 CC RX MEDLINE=92212913; PubMed=1557383;
 CC RA Banfield D.K., Macgillivray R.T.;
 CC RT "Partial characterization of vertebrate prothrombin cDNAs:
 CC RT amplification and sequence analysis of the B chain of thrombin from
 CC RT nine different species."
 CC RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
 CC
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
 CC fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.
 CC
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC
 CC -----
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EMBL; X52835; CA37017.1; -
EMBL; M81397; AAA4240.1; -
PIR; S10511; S10511.
HSSP; P00734; 1UVS.
MEROPS; S01.217; -
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GLA_blood.
InterPro; IPR000001; Kringle.
InterPro; IPR003966; Prothrombin.
InterPro; IPR001254; Ser protease_Try.
InterPro; IPR000294; Vitr_dep_GLA.
Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
ProDom; PD000395; kringle; 2.
SMART; SM00069; GLA; 1.
SMART; SM00130; KR; 2.
SMART; SM00020; TRY_SPC; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS00070; KRINGLE_2; 2.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver; Hydroxylase; Serine protease; Kringle; Signal.
SIGNAL 1 24
PROPEP 25 43
CHAIN 44 617
PEPTIDE 200 323
PEPTIDE 201 323
CHAIN 324 359
CHAIN 360 617
DOMAIN 109 187
DOMAIN 215 292
DOMAIN 360 617
SITE 200 201
SITE 323 324
SITE 359 360
ACT_SITE 402 402
ACT_SITE 458 458
ACT_SITE 564 564
MOD_RES 50 50
MOD_RES 51 51
MOD_RES 58 58
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MOD_RES 69 69
MOD_RES 70 70
MOD_RES 73 73
MOD_RES 76 76
CARBOHYD 120 120
CARBOHYD 144 144
CARBOHYD 412 412
CARBOHYD 552 552
DISULFID 61 66
DISULFID 91 104
DISULFID 109 187
DISULFID 130 170
DISULFID 158 182
DISULFID 215 292
DISULFID 236 276

FT DISULFID 264 287 BY SIMILARITY.
FT DISULFID 332 478 INTERCHAIN (BY SIMILARITY).
FT DISULFID 387 403 BY SIMILARITY.
FT DISULFID 532 546 BY SIMILARITY.
FT DISULFID 560 590 BY SIMILARITY.
SQ SEQUENCE 617 AA; 70411 MW; AD27D1B71450BD1D CRC64;
Query Match 47.1%; Score 90; DB 1; Length 617;
Best local Similarity 39.5%; Pred. No. 4.5e-08;
Matches 17; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
QY 2 MAFLLXLRGSLXKCKXQCSFXKAFIFKAKRTKLFWISY 44
DB 46 SGFLBELRKGNLERECVEECQSYEAFALESFQDVFWMAXY 88
RESULT 14
THRB_MOUSE STANDARD; PRT; 618 AA.
AC P19221;
DT 01-NOV-1990 (Rel. 16, Last Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prothrombin precursor (BC 3.4.21.5).
GN F2 OR CP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=9102551; PubMed=2222810;
RA Fritzenner Degen S.O., Schaffer L.A., Jamison C.S., Grant S.G., Fitzgibbon J.V., Pai J.-A., Chapman V.M., Elliott R.W.;
RT "Characterization of the cDNA coding for mouse prothrombin and RT localization of the gene on mouse chromosome 2.";
RL DNA Cell Biol. 9:487-496(1990).
RN [2]
RP SEQUENCE OF 384-618 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs: RT amplification and sequence analysis of the B chain of thrombin from nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII, AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg|-Gly, activates fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS, RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOVAL ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION OF PROTHROMBIN TO THROMBIN.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF THROMBIN.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION BY FACTOR XA.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
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DR EMBL: X52308; CAA36548.1; -.
DR EMBL: M81394; AAA40435.1; -.
DR PIR: A35827; A35827.
DR HSSP: P00734; 187X.
DR MEROPS: S01.217; -.
DR MGD: MGI:88380; F2.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00051; kringle_2.
DR Pfam: PF00089; trypsin_1.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR ProDom: PD000395; Kringle; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00130; KR; 2.
DR SMART: SM00020; TRY_P_SPC; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS50070; KRINGLE_2; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KM Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
KM Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KM Hydrolyase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24
FT PROPEP 25 43
FT CHAIN 44 618
FT PEPTIDE 44 200
FT PEPTIDE 201 324
FT CHAIN 325 360
FT CHAIN 361 618
FT DOMAIN 109 187
FT DOMAIN 215 292
FT DOMAIN 361 618
FT SITE 200 201
FT SITE 324 325
FT SITE 360 361
FT ACT_SITE 403 403
FT ACT_SITE 459 459
FT ACT_SITE 565 565
FT MOD_RES 50 50
FT MOD_RES 51 51
FT MOD_RES 58 58
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FT MOD_RES 69 69
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 76 76
FT DISULFID 61 66
FT DISULFID 91 104
FT DISULFID 109 187
FT DISULFID 130 170
FT DISULFID 158 182
FT DISULFID 215 293
FT DISULFID 236 276
FT DISULFID 264 288
FT DISULFID 333 479

FT DISULFID 388 404 BY SIMILARITY.
FT DISULFID 533 547 BY SIMILARITY.
FT DISULFID 561 591 BY SIMILARITY.
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .)
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .)
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .)
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .)
SQ SEQUENCE 618 AA; 70268 MW; B89F719AAFD601E0 CRC64;

Query Match 47.1%; Score 90; DB 1; Length 618;
Best Local Similarity 39.5%; Pred. No. 4.5e-08;
Matches 17; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 2 NAFLLXLRGSLRXCKXQCFXAFXIFKDXARTLFWISY 44
DB 46 SGFLIELRKGNLEHCEVEECSTIEAEALAEFPDIDVFWAKY 88

RESULT 15
ID PRTC_BOVIN STANDARD; PRT; 456 AA.
AC P00745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
GN PROC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014826; PubMed=6091100;
RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
RT "Cloning and sequencing of liver cDNA coding for bovine protein C";
RT Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
RN [2]
RP SEQUENCE OF 40-194.
RX MEDLINE=83007325; PubMed=6896876;
RA Fernlund P., Stenflo J.;
RT "Amino acid sequence of the light chain of bovine protein C";
RL J. Biol. Chem. 257:12170-12179(1982).
RN [3]
RP REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
RT "beta-hydroxyaspartic acid in vitamin K-dependent protein C";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
RN [4]
RP SEQUENCE OF 197-456.
RX MEDLINE=83007326; PubMed=6896877;
RA Stenflo J., Fernlund P.;
RT "Amino acid sequence of the heavy chain of bovine protein C";
RL J. Biol. Chem. 257:12180-12190(1982).
RN [5]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Emon N.L., Debault L.E., Emon C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
RT domainless protein C";
RL J. Biol. Chem. 258:5548-5553(1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Emon N.L., Laue T.M., Emon C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid";
RL J. Biol. Chem. 258:5554-5560(1983).

CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADCAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K02435; AAA30685.1; -
CC DR PIR; A00928; KXBO.
CC DR HSSP; P04070; 1PCU.
CC DR MEROPS; S01.218; -
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR001881; EGF Ca.
CC InterPro; IPR001254; Ser_protease_Try.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00089; trypsin; 1.
CC Pfam; PF00594; gla; 1.
CC SMART; SM00181; EGF; 2.
CC SMART; SM00069; GLA; 1.
CC SMART; SM00020; TYPD_SPC; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01187; EGF CA; 1.
CC PROSITE; PS00011; GLU CARBOXYLATION; 1.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Glycoprotein; Serine protease;
CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
CC EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
CC KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
CC FT NON_TER 1 1
FT SIGNAL <1 29
FT PROPEP 30 39
FT CHAIN 40 194
FT PEPTIDE 197 456
FT DOMAIN 94 129
FT DOMAIN 133 173
FT DOMAIN 211 456
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 62 62
FT MOD_RES 64 64
FT MOD_RES 65 65
PROTEIN C LIGHT CHAIN.
PROTEIN C HEAVY CHAIN.
ACTIVATION PEPTIDE.
EGF-LIKE 1.
EGF-LIKE 2.
SERINE PROTEASE.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.

FT MOD_RES 68 68 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 74 74 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 110 110 HYDROXYLATION.
FT ACT_SITE 252 252 CHARGE RELAY SYSTEM.
FT ACT_SITE 258 258 CHARGE RELAY SYSTEM.
FT ACT_SITE 298 298 CHARGE RELAY SYSTEM.
FT ACT_SITE 397 397 CHARGE RELAY SYSTEM.
FT DISULFID 56 61 BY SIMILARITY.
FT DISULFID 89 108 BY SIMILARITY.
FT DISULFID 98 103 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 119 128 BY SIMILARITY.
FT DISULFID 137 148 BY SIMILARITY.
FT DISULFID 144 157 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 180 318 INTERCHAIN.
FT DISULFID 227 253
FT DISULFID 368 382
FT DISULFID 393 421
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .).
FT VARIANT 82 82 F -> K.
FT CONFLICT 455 456 VP -> PV (IN REF. 4).
SQ SEQUENCE 456 AA; 51407 MW; 51407 MW; CAA6833F894C209 CRC64;

Query Match 46.1%; Score 88; DB 1; Length 456;
Best Local Similarity 40.9%; Pred. No. 7.5e-08;
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANAFLLXLRREGSLRXKXKXCSFXXAFXIFPDAXRTKLFMTSY 44
DB 40 ANSFLELRPGNVERSCSEVCEFEARKEIFONTEDTMAFMSFY 83

Search completed: March 19, 2003, 14:52:50
Job time : 6.625 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10GLU28PHE
Perfect score: 191
Sequence: 1 ANAFPLXLRGSLXRXCKX.....XXAFXIFKDAKRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	81.7	701	4 Q96PQ8	Q96PQ8 homo sapien
2	111	58.1	446	11 Q61109	Q61109 mus musculu
3	97	50.8	460	11 Q91WN8	Q91WN8 mus musculu
4	94	49.2	100	4 Q15253	Q15253 homo sapien
5	91	47.6	460	11 Q99PC6	Q99PC6 mus musculu
6	90	47.1	482	11 Q63207	Q63207 rattus norv
7	88	46.1	456	6 Q9TTR0	Q9TTR0 canis famli
8	88	46.1	469	6 Q9GMD9	Q9GMD9 ornithorhyn
9	88	46.1	481	11 Q54740	Q54740 mus musculu
10	88	46.1	481	11 Q99L32	Q99L32 mus musculu
11	88	46.1	481	11 Q88947	Q88947 mus musculu
12	78	40.8	49	6 Q95ME8	Q95ME8 bos taurus
13	77	40.3	456	4 Q14316	Q14316 homo sapien
14	77	40.3	461	6 Q95ND7	Q95ND7 pan troglod
15	77	40.3	461	6 Q95ND6	Q95ND6 pan troglod
16	73	38.2	179	4 Q8TMS3	Q8TMS3 homo sapien

17	73	38.2	198	11 Q8R182	Q8R182 mus musculu
18	72	37.7	608	13 Q9PTW7	Q9PTW7 struthio ca
19	71	37.2	138	6 Q28994	Q28994 sus scrofa
20	69	36.1	607	13 Q91001	Q91001 gallus gall
21	67	35.1	433	13 Q90YK1	Q90YK1 brachydanto
22	64	33.5	648	6 Q29094	Q29094 sus scrofa
23	62	32.5	98	13 P82807	P82807 notechis sc
24	61	31.9	399	11 Q9CQW3	Q9CQW3 mus musculu
25	59	30.9	650	4 Q9NSD0	Q9NSD0 homo sapien
26	59	30.9	650	4 Q16519	Q16519 homo sapien
27	55.5	29.1	431	10 Q94EY5	Q94EY5 arabidopsis
28	55.5	29.1	492	10 Q9SMJ7	Q9SMJ7 clethr artel
29	55.5	29.1	543	10 Q9MB23	Q9MB23 arabidopsis
30	55.5	29.1	576	10 Q9CV94	Q9CV94 arabidopsis
31	55.5	29.1	589	10 Q9LMS2	Q9LMS2 arabidopsis
32	55	28.8	25	11 Q9QVH6	Q9QVH6 rattus sp.
33	54.5	28.5	196	10 Q04284	Q04284 selaginella
34	54.5	28.5	542	5 Q8T613	Q8T613 halocynthia
35	53.5	28.0	459	10 Q9SE22	Q9SE22 oryza sativ
36	52.5	27.5	506	10 Q9SPF0	Q9SPF0 oryza sativ
37	52.5	27.5	506	10 Q9SE23	Q9SE23 oryza sativ
38	52.5	27.5	567	10 Q8W4J2	Q8W4J2 arabidopsis
39	51.5	27.0	510	10 Q9MB22	Q9MB22 arabidopsis
40	51.5	27.0	619	10 Q9LV37	Q9LV37 arabidopsis
41	50	26.2	673	11 Q61592	Q61592 mus musculu
42	50	26.2	674	11 Q99K57	Q99K57 mus musculu
43	49.5	25.9	588	10 Q9LM33	Q9LM33 arabidopsis
44	49.5	25.9	603	10 Q9LPG7	Q9LPG7 arabidopsis
45	49.5	25.9	606	10 Q9SUG9	Q9SUG9 arabidopsis

ALIGNMENTS

RESULT 1
Q96PQ8 PRELIMINARY; PRT; 701 AA.
ID Q96PQ8
AC Q96PQ8; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor VII active site mutant immunocjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RL EMBL; AF272774; AAK58686.1; -
DR InterPro: IPR000152; Asx hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001254; Ser protease Try.
DR InterPro: IPR000294; Vitr_deg_GLA.
DR Pfam; PR00008; EGF; 2.
DR Pfam; PR00094; gla; 1.
DR Pfam; PR00047; Ig; 2.
DR Pfam; PR00089; trypsin; 1.
DR SMART; SM00181; EGF; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.

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DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match
Best Local Similarity 81.7%; Score 156; DB 4; Length 701;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXXLRGSLRKCKXXQCSFXAFAIFKDAKRTKLFWISY 44
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 61 ANAFLEELRPGSLRECKECCSFEEAREIFKDAERTKLFWISY 104

RESULT 2
Q61109 PRELIMINARY; PRT; 446 AA.
ID Q61109;
AC Q61109;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=96276538; PubMed=8701412;
RA Idusogile E., Kosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487(1996).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY

DR EMBL; U04795; AAC52570.1; -.
DR HSSP; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002086; Aldohyde dehydr.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_spc; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 58.1%; Score 111; DB 11; Length 446;
```

```
Best Local Similarity 54.5%; Pred. No. 3.3e-12;
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXXLRGSLRKCKXXQCSFXAFAIFKDAKRTKLFWISY 44
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 42 ANSLLEELWPGSLRECKNECCSFEEAREIFKSPERTKQWIVY 85

RESULT 3
Q91WN8 PRELIMINARY; PRT; 460 AA.
ID Q91WN8;
AC Q91WN8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013896; AAH13896.1; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;

Query Match 50.8%; Score 97; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 1.5e-09;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXXLRGSLRKCKXXQCSFXAFAIFKDAKRTKLFWISY 44
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 42 ANSLLEELWPGSLRECKNECCSFEEAREIFQNVEDTLAFWIKY 85

RESULT 4
Q15253 PRELIMINARY; PRT; 100 AA.
ID Q15253;
AC Q15253;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thrombin precursor (Fragment).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=87182874; PubMed=3471151;
RA MacGillivray R.T., Irwin D.M., Guinno E.R., Stone J.C.;
```


[illegible]

Qy	1	ANAFILXLRBESGLKRXCKXKQCSFYXAFIFPKDAXRTLFWISY	44
Db	42	ANSFLEEMRPGSLERECEMEIEICDLEAEQIFONVEDTLAFWIKY	85
Query Match			47.6%; Score 91; DB 11; Length 460;
Best Local Similarity			43.2%; Pred. No. 1,9e-08;
Matches	19;	Conservative	4; Mismatches 21; Indels 0; Gaps 0
RESULT 6			
ID	Q63207	PRELIMINARY;	PRT; 482 AA.
AC	Q63207;		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, last sequence update)	
DT	01-MAR-2002	(TREMBLrel. 20, last annotation update)	
DE	Factor X.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY;		
RX	MEDLINE=96093366; PubMed=8578539;		
RA	Stanton C., Ross R.P., Hutson S., Wallin R.;		
RT	"Evidence for competition between vitamin K-dependent clotting factors		
RT	for intracellular processing by the vitamin K-dependent gamma-		
RT	carboxylase.";		
RL	Thromb. Res. 80:63-73(1995).		
CC	-1 -SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE		
CC	TRYPSIN FAMILY.		
DR	EMBL; X79807; CAAS6202.1; -		
DR	HSSP; P00742; 1XKA.		
DR	MEROPS; S01.216;		
DR	InterPro; IPR000152; Asx_hydroxyl.		
DR	InterPro; IPR001314; Chymotrypsin.		
DR	InterPro; IPR000561; EGF-like.		
DR	InterPro; IPR000742; EGF 2.		
DR	InterPro; IPR001881; EGF_Ca.		
DR	InterPro; IPR002383; GLA_blood.		
DR	InterPro; IPR001254; Ser_protease_Try.		
DR	InterPro; IPR000294; Vitk_dep_GLA.		
DR	Pfam; PF00008; EGF 2.		
DR	Pfam; PF00594; GLA; 1.		
DR	Pfam; PF00089; trypsin. 1.		
DR	PRINTS; PR00072; CHYMOTRYPSIN.		
DR	PRINTS; PR00001; GLABLOOD.		
DR	SMART; SM00179; EGF_CA; 1.		
DR	SMART; SM00001; EGF-like; 1.		
DR	SMART; SM00069; GLA; 1.		
DR	SMART; SM00020; Tryp_SPC; 1.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.		
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.		
DR	PROSITE; PS01186; EGF_2; 2.		
DR	PROSITE; PS01187; EGF_CA; 1.		
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.		
DR	PROSITE; PS02040; TRYPSIN_DOM; 1.		
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.		
DR	PROSITE; PS00135; TRYPSIN_SER; 1.		
KW	Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylase;		
KW	Hydroxylation; Repeat; Serine protease.		
SQ	SEQUENCE 482 AA; 54265 MW; 0284678E3954A638 CRC64;		
Query March		47.1%; Score 90; DB 11; Length 482;	
Best Local Similarity		38.6%; Pred. No. 3.1e-08;	
Matches	17;	Conservative	8; Mismatches 19; Indels 0; Gaps 0


```
GN F10 OR FA10.
OS Mus musculus (Mouse).
OC Plasmid pBluescript.
OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=96454993; PubMed=9783672;
RT Heidtman H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: A222677; CAA10933.1; -.
DR HSSP: P00742; 1XKA.
DR MEROPS: S01.216; -.
DR MGD: MGI:103107; F10.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00001; EGF_CA; 1.
DR SMART: SM00179; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRY_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702DSEFD97AE CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.4e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFLLXLRBGLSRXCKXKQCSFXXAFIFKDAKXTKLFWISY 44
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 41 ANSFEEFKGNLRECMETICSYEEVREIFEDDEKTEKWTXY 84

RESULT 10
O99L32 PRELIMINARY; PRT; 481 AA.
AC O99L32;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
```

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RP SEQUENCE FROM N.A.
RA Strausberg R.;
RA Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: BC03877; AAH03877.1; -.
DR HSSP: P00742; 1XKA.
DR MEROPS: S01.216; -.
DR MGD: MGI:103107; F10.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_11.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00001; EGF_CA; 2.
DR SMART: SM00001; EGF_Like; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRY_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 7.4e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFLLXLRBGLSRXCKXKQCSFXXAFIFKDAKXTKLFWISY 44
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 41 ANSFEEFKGNLRECMETICSYEEVREIFEDDEKTEKWTXY 84

RESULT 11
O88947 PRELIMINARY; PRT; 481 AA.
AC O88947;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RA MEDLINE=98347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RT Thromb. Haemost. 80:87-91(1998).
RN (2)
RP SEQUENCE FROM N.A.
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Query Match 40.3%; Score 77; DB 4; Length 456;
Best Local Similarity 40.0%; Pred. No. 8.3e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 10 EGSIXRXXCKXQCSFYXAFIFPDARTKLFWISY 44
DB 52 QGNLRECKMEKCSFEAREVFENTERTEFWKQY 86

RESULT 14

ID Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees.";
RT Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; JOINED.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
DR Hydroxylase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 40.3%; Score 77; DB 6; Length 461;
Best Local Similarity 40.0%; Pred. No. 8.3e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 10 EGSIXRXXCKXQCSFYXAFIFPDARTKLFWISY 44
DB 57 QGNLRECKMEKCSFEAREVFENTERTEFWKQY 91

RESULT 15

ID Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE Coagulation factor XI.

GN F9.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

OX NCBI_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=505;

RA Sacta Y.;

RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees.";

RT Genes Genet. Syst. 0:0-0(2001).

DR EMBL; AB062471; BAB58885.1; JOINED.

DR EMBL; AB062459; BAB58885.1; JOINED.

DR EMBL; AB062461; BAB58885.1; JOINED.

DR EMBL; AB062463; BAB58885.1; JOINED.

DR EMBL; AB062465; BAB58885.1; JOINED.

DR EMBL; AB062467; BAB58885.1; JOINED.

DR EMBL; AB062469; BAB58885.1; JOINED.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF 2.

DR Pfam; PF00594; gla; 1.

DR Pfam; PF00089; trypsin; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01186; EGF_2; UNKNOWN_2.

DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.

DR PROSITE; PS50240; TRYPsin_DOM; 1.

DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.

DR Hydroxylase; Serine protease.

KW SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 40.3%; Score 77; DB 6; Length 461;
Best Local Similarity 40.0%; Pred. No. 8.3e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 10 EGSIXRXXCKXQCSFYXAFIFPDARTKLFWISY 44
DB 57 QGNLRECKMEKCSFEAREVFENTERTEFWKQY 91

Search completed: March 19, 2003, 15:13:32
Job time : 47.3125 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10GLU28PHE

Perfect score: 191

Sequence: 1 ANAFIXLREGSLRXRCXXX.....XXAFXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	86.4	44	3	US-08-955-636-28 Sequence 28, Appl
2	162	84.8	44	3	US-08-955-636-26 Sequence 26, Appl
3	159	83.2	44	3	US-08-955-636-27 Sequence 27, Appl
4	156	81.7	44	3	US-08-955-636-3 Sequence 3, Appl
5	156	81.7	406	1	US-08-293-778-24 Sequence 24, Appl
6	156	81.7	406	1	US-08-295-411-5 Sequence 5, Appl
7	156	81.7	406	2	US-08-955-471-5 Sequence 5, Appl
8	156	81.7	406	5	PCT-US92-10242-5 Sequence 5, Appl
9	156	81.7	444	1	US-08-475-845-2 Sequence 2, Appl
10	156	81.7	444	2	US-08-327-690-2 Sequence 2, Appl
11	156	81.7	444	2	US-08-660-289-2 Sequence 2, Appl
12	156	81.7	444	2	US-08-537-807-2 Sequence 2, Appl
13	156	81.7	444	2	US-08-871-003-2 Sequence 2, Appl
14	156	81.7	444	4	US-08-464-233-2 Sequence 2, Appl
15	156	81.7	444	4	US-09-189-607-2 Sequence 2, Appl
16	156	81.7	444	4	US-09-378-907-2 Sequence 2, Appl
17	156	81.7	444	5	PCT-US94-05779-2 Sequence 2, Appl
18	156	81.7	466	1	US-07-882-2024-4 Sequence 4, Appl
19	156	81.7	466	1	US-08-921-615A-4 Sequence 4, Appl
20	156	81.7	466	1	US-08-321-777-4 Sequence 4, Appl
21	156	81.7	466	4	US-09-009-217-14 Sequence 14, Appl
22	156	81.7	466	4	US-09-009-656-14 Sequence 4, Appl
23	156	81.7	466	5	PCT-US93-04493-4 Sequence 4, Appl
24	155	81.2	44	3	US-08-955-636-30 Sequence 30, Appl
25	150	78.5	44	3	US-08-955-636-29 Sequence 4, Appl
26	141	73.8	41	1	US-08-229-280-4 Sequence 4, Appl
27	122	63.9	44	3	US-08-955-636-4 Sequence 4, Appl

28	105	55.0	139	1	US-08-330-978-2 Sequence 2, Appl
29	105	55.0	139	1	US-08-474-042-2 Sequence 2, Appl
30	105	55.0	139	1	US-08-484-558-2 Sequence 2, Appl
31	105	55.0	139	1	US-08-774-529-2 Sequence 2, Appl
32	105	55.0	437	1	US-08-487-037-2 Sequence 2, Appl
33	105	55.0	437	1	US-08-487-037-3 Sequence 3, Appl
34	105	55.0	488	1	US-08-487-037-1 Sequence 1, Appl
35	97	50.8	44	3	US-08-955-636-35 Sequence 35, Appl
36	96	50.3	44	3	US-08-955-636-18 Sequence 18, Appl
37	96	50.3	448	1	US-08-295-411-3 Sequence 3, Appl
38	96	50.3	448	2	US-08-955-471-3 Sequence 3, Appl
39	96	50.3	448	5	PCT-US92-10068-1 Sequence 1, Appl
40	96	50.3	448	5	PCT-US92-10242-3 Sequence 3, Appl
41	96	50.3	487	1	US-08-469-486-53 Sequence 53, Appl
42	96	50.3	487	2	US-08-469-658-53 Sequence 2, Appl
43	96	50.3	492	1	US-08-469-486-2 Sequence 2, Appl
44	96	50.3	492	2	US-08-469-658-2 Sequence 2, Appl
45	95	49.7	44	3	US-08-955-636-25 Sequence 25, Appl

ALIGNMENTS

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RESULT 1
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisseu, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28

Query Match      86.4%; Score 165; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 36-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFIXLREGSLRXRCXXXQCSFXAIFKDXRTKLFWISY 44
DB 1 ANAFIXLREGSLRXRCXXXQCSFXAIFKDXRTKLFWISY 44

RESULT 2
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisseu, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match
Best Local Similarity 97.7%; Pred. No. 9, 6e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44
DB 1 ANAFLXXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44

RESULT 3
US-08-955-636-27
Sequence 27, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelisseuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match
Best Local Similarity 95.5%; Pred. No. 3, 1e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44
DB 1 ANAFLXXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44

RESULT 4
US-08-955-636-3
Sequence 3, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelisseuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match
Best Local Similarity 95.5%; Pred. No. 1e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44
DB 1 ANAFLXXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44

RESULT 5
US-08-293-778-24
Sequence 24, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION:
APPLICANT: Nicolaisen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agri's, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129,224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24

Query Match
Best Local Similarity 91.7%; Score 156; DB 1; Length 406;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44
DB 1 ANAFLXXLRGSLRXCKXXQCSFXAXFIKDXARTKLFWISY 44

RESULT 6
US-08-295-411-5


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/ Sequence 5, Application US/08295411
/ Patent No. 5679639
/ GENERAL INFORMATION:
/ APPLICANT: Griffin, John H.
/ APPLICANT: Meesters, Rolf M.
/ TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
/ TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
/ TITLE OF INVENTION: for Inhibiting Coagulation
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Office of Patent Counsel, The Scripps
/ ADDRESSER: Research Institute
/ STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
/ CITY: La Jolla
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/295,411
/ FILING DATE: 22-AUG-1994
/ CLASSIFICATION: 530
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 07/793,989
/ FILING DATE: 18-NOV-1991
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: TSPR263.0C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 406 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..152
/ OTHER INFORMATION: /note= "Factor VII Light Chain"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 153..406
/ OTHER INFORMATION: /note= "Factor VII Heavy Chain"
/ US-08-295-411-5

Query Match      81.7%; Score 156; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1,1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY 1 ANAFLXLRGSLRXCKXKQCSFXXAFXIFKDXARTKLFWISY 44
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DB 1 ANAFLELRPGSLERCKEKGCSFEERAREIFKDAERTKLFWISY 44
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RESULT 7
US-08-955-471-5
/ Sequence 5, Application US/08955471
/ Patent No. 5968751
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/ GENERAL INFORMATION:
/ APPLICANT: Griffin, John H.
/ APPLICANT: Meesters, Rolf M.
/ TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
/ TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
```

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/ TITLE OF INVENTION: for Inhibiting Coagulation
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Office of Patent Counsel, The Scripps
/ ADDRESSER: Research Institute
/ STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
/ CITY: La Jolla
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/955,471
/ FILING DATE:
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 08/295,411
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: TSPR263.0C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 406 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..152
/ OTHER INFORMATION: /note= "Factor VII Light Chain"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 153..406
/ OTHER INFORMATION: /note= "Factor VII Heavy Chain"
/ US-08-955-471-5

Query Match      81.7%; Score 156; DB 2; Length 406;
Best Local Similarity 72.7%; Pred. No. 1,1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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DB 1 ANAFLELRPGSLERCKEKGCSFEERAREIFKDAERTKLFWISY 44
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RESULT 8
PCT-US92-10242-5
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/ Sequence 5, Application PC/TUS9210242
/ GENERAL INFORMATION:
/ APPLICANT: Griffin, John H.
/ APPLICANT: Meesters, Rolf
/ TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
/ TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
/ TITLE OF INVENTION: for Inhibiting Coagulation
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Office of Patent Counsel, The Scripps
/ ADDRESSER: Research Institute
/ STREET: 10666 North Torrey Pines Road, TPC 8
/ CITY: La Jolla
/ STATE: CA
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/
/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/10242
/ FILING DATE: 19921118
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/793,989
/ FILING DATE: 18-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Filting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCRO472P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 406 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..152
/ OTHER INFORMATION: /note= "Factor VII Light Chain"
/
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 153..406
/ OTHER INFORMATION: /note= "Factor VII Heavy Chain"
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PCT-US92-10242-5

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Best Local Similarity 72.7%; Pred. No. 1,1e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRBGSIXRCKXQCSFXAXFKDAERTKLFWISY 44
DB 1 ANAFLBELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 9
US-08-475-845-2
/ Sequence 2, Application US/08475845
/ Patent No. 5788965
/ GENERAL INFORMATION:
/ APPLICANT: Berkner, Kathleen L.
/ APPLICANT: Petersen, Lars C.
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Hedner, Ulla
/ APPLICANT: Bregengaard, Claus
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Stuart Street Tower
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.24
/ CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/08/475,845
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/327,690
/ FILING DATE: 24-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/065,725
/ FILING DATE: 21-MAY-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/662,920
/ FILING DATE: 28-FEB-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parmelee, Steven W.
/ REGISTRATION NUMBER: 31,990
/ REFERENCE/DOCKET NUMBER: 13952-8-4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-467-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-475-845-2

Query Match 81.7%; Score 156; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 1,2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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DB 39 ANAFLBELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 10
US-08-327-690-2
/ Sequence 2, Application US/08327690
/ Patent No. 5817788
/ GENERAL INFORMATION:
/ APPLICANT: Berkner, Kathleen L.
/ APPLICANT: Petersen, Lars C.
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Hedner, Ulla
/ APPLICANT: Bregengaard, Claus
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Stuart Street Tower
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/327,690
/ FILING DATE: 24-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/065,725
/ FILING DATE: 21-MAY-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/662,920
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FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match 81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRGSLRXCKXQCSFXAXFIPODARTKLFWISY 44
Db 39 ANAFLELRPGSLRCKEKCQCSFEAREIFDAERTKLFWISY 82

RESULT 11
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,289
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

Query Match 81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRGSLRXCKXQCSFXAXFIPODARTKLFWISY 44
Db 39 ANAFLELRPGSLRCKEKCQCSFEAREIFDAERTKLFWISY 82

RESULT 12
US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 81.7%; Score 156; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRGSLRXCKXQCSFXAXFIPODARTKLFWISY 44
Db 39 ANAFLELRPGSLRCKEKCQCSFEAREIFDAERTKLFWISY 82

RESULT 13
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.

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; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-871-003-2

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Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY 1 ANAFLLXLRGSLKRXCKXQCSFXAXFIKDXARTKLFWISY 44
Db 39 ANAFLELRPGSLRECKECCSFEEAREIFKDXARTKLFWISY 82

RESULT 14
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; Sequence 2, Application US/08464233
; Patent No. 6039944
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: Patentn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,233
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-233-2

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RESULT 15
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; Sequence 2, Application US/09189607
; Patent No. 618789
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.24
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; APPLICATION NUMBER: US/09/189,607
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/660,289
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-189-607-2

Query Match 81.7%; Score 156; DB 4; Length 444;
Best Local Similarity 72.7%; Pred. No. 1,2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Db 39 ANAFLEELRPGSLRECKEQQCSFEARBIFKDAERTKLFWISY 82

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GenCore version 5.1.4 ps_4578
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OM protein - protein search, using sw model

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280.876 Million cell updates/sec

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Perfect score: 191
Sequence: 1 ANAFILXLRGSLRXKCKX.....XXAFYIFDAXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	94	49.2	419	US-10-182-263-6	Sequence 6, Appli
3	92	48.2	419	US-10-182-263-3	Sequence 3, Appli
4	92	48.2	419	US-10-182-263-4	Sequence 4, Appli
5	92	48.2	419	US-10-182-263-5	Sequence 5, Appli
6	81	42.4	419	US-10-182-263-1	Sequence 1, Appli
7	81	42.4	419	US-09-978-917A-4	Sequence 4, Appli
8	81	42.4	461	US-10-182-263-2	Sequence 2, Appli
9	81	42.4	461	US-09-978-917A-2	Sequence 2, Appli
10	77	40.3	415	US-09-118-748-2	Sequence 2, Appli
11	77	40.3	461	US-10-132-829-5	Sequence 5, Appli
12	77	40.3	461	US-09-884-901-3	Sequence 3, Appli
13	66.5	34.8	96	US-09-759-1308-313	Sequence 313, App
14	66.5	34.8	209	US-09-759-1308-312	Sequence 312, App
15	66.5	34.8	226	US-09-759-1308-310	Sequence 310, App
16	51.5	27.0	95	US-09-759-1308-356	Sequence 356, App
17	51.5	27.0	208	US-09-759-1308-355	Sequence 355, App
18	51.5	27.0	225	US-09-759-1308-353	Sequence 353, App
19	45.5	23.8	729	US-10-145-396-11	Sequence 11, Appli

20	44.5	23.3	347	10	US-09-780-053-4	Sequence 4, Appli
21	44.5	23.3	730	9	US-10-145-396-12	Sequence 12, Appli
22	44.5	23.3	730	10	US-09-780-053-2	Sequence 2, Appli
23	43	22.5	447	10	US-09-815-242-13490	Sequence 13490, A
24	43	22.5	447	10	US-09-815-242-13612	Sequence 13612, A
25	43	22.5	447	10	US-09-735-564-2	Sequence 2, Appli
26	41	21.5	447	10	US-09-735-564-2	Sequence 194, App
27	40	20.9	88	10	US-09-811-284-194	Sequence 4, Appli
28	40	20.9	273	9	US-09-764-868-968	Sequence 968, App
29	39	20.4	115	9	US-09-883-152-21	Sequence 21, Appli
30	39	20.4	115	9	US-09-986-480-152	Sequence 192, App
31	39	20.4	130	9	US-09-986-480-345	Sequence 345, App
32	39	20.4	254	9	US-10-104-019-21	Sequence 21, Appli
33	39	20.4	873	9	US-10-200-154-2	Sequence 2, Appli
34	39	20.4	873	10	US-09-954-043-2	Sequence 2, Appli
35	38.5	20.2	111	10	US-09-899-896-7	Sequence 109, App
36	38	19.9	47	10	US-09-738-254-109	Sequence 109, App
37	38	19.9	47	10	US-09-904-615-109	Sequence 109, App
38	38	19.9	176	9	US-10-078-770-106	Sequence 106, App
39	38	19.9	179	9	US-09-738-626-6259	Sequence 6259, App
40	38	19.9	333	9	US-09-738-626-5683	Sequence 5683, App
41	38	19.9	400	9	US-10-078-770-114	Sequence 114, App
42	38	19.9	467	10	US-09-912-020-381	Sequence 381, App
43	38	19.9	608	10	US-09-908-664-5	Sequence 5, Appli
44	38	19.9	1266	9	US-09-931-969A-2	Sequence 2, Appli
45	38	19.9	1266	9	US-10-079-699-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match 81.7%; Score 156; DB 9; Length 406;
Best Local Similarity 95.5%; Pred. No. 5.2e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFILXLRGSLRXKCKXCCGFFXAFYIFDAXRTKLFWISY 44
DB 1 ANAFILXLRGSLRXKCKXCCGFFXAFYIFDAXRTKLFWISY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E

```

; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          49.2%; Score 94; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 7.1e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSEFXAFXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDPEEAKEIFEDVDTLAFW 41

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          48.2%; Score 92; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.6e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSEFXAFXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDPEEAKEIFEDVDTLAFW 41

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          48.2%; Score 92; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.6e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSEFXAFXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDPEEAKEIFEDVDTLAFW 41

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          48.2%; Score 92; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.6e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSEFXAFXIFKDXARTKLFW 41
Db 1 ANSFLELRHGSLEKCEIEICDPEEAKEIFEDVDTLAFW 41

RESULT 6
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 419;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFIFKDAKRTKLFW 41
DB 1 ANSFLELRHSSLERECIEICDFEAKETIQVDDTLAFW 41

RESULT 7
US-09-978-917A-4
; Sequence 4, Application US/09978917A
; Publication No. US20030027299A1

; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219u8310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 419;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFIFKDAKRTKLFW 41
DB 1 ANSFLELRHSSLERECIEICDFEAKETIQVDDTLAFW 41

RESULT 8
US-10-182-263-2
; Sequence 2, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 461;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFIFKDAKRTKLFW 41
DB 43 ANSFLELRHSSLERECIEICDFEAKETIQVDDTLAFW 83

RESULT 9

US-09-978-917A-2
; Sequence 2, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:

; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219u8310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(42)
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (43)...(461)
US-09-978-917A-2

Query Match
Best Local Similarity 42.4%; Score 81; DB 9; Length 461;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAFIFKDAKRTKLFW 41
DB 43 ANSFLELRHSSLERECIEICDFEAKETIQVDDTLAFW 83

RESULT 10
US-09-118-748-2
; Sequence 2, Application US/09118748A
; Patent No. US20020031799A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Darrel W.
; APPLICANT: Chang, Jindl
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 5470-183
; CURRENT APPLICATION NUMBER: US/09/118,748A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/053,571
; EARLIER FILING DATE: 1997-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-118-748-2

Query Match
Best Local Similarity 40.3%; Score 77; DB 10; Length 415;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 10 EGSLLRXCKXQCSFXXAFIFKDAKRTKLFWISY 44
DB 11 QGNLERECWEKCSFEAREVEFENTERTEFPWKQY 45

RESULT 11
US-10-132-829-5
; Sequence 5, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:

; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masaaki
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
; FILE REFERENCE: 6627-P41170

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; CURRENT APPLICATION NUMBER: US/10/132.829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-132-829-5

Query Match          40.3%; Score 77; DB 9; Length 461;
Best Local Similarity 40.0%; Pred. No. 8.8e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY      10 EGSIXRXXKXXQCSFXAXFXIFKDXARTKLFWISY 44
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Db      57 QGNLRECMEEKCSFEERAREVFENTERTTTFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18/212,902
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-884-901-3

Query Match          40.3%; Score 77; DB 10; Length 461;
Best Local Similarity 40.0%; Pred. No. 8.8e-06;
Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY      10 EGSIXRXXKXXQCSFXAXFXIFKDXARTKLFWISY 44
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      57 QGNLRECMEEKCSFEERAREVFENTERTTTFWKQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Kirtz, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-759-130B-313

Query Match          34.8%; Score 66.5; DB 9; Length 96;
Best Local Similarity 36.4%; Pred. No. 0.00013;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2 NAF-LXXLRGSLXRXKXXQCSFXAXFXIFKDXARTKLFWISY 44
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Db      36 NRPDLLEFTPGNLERECNEBLCNVEAREIFVDEDKTIAFWQEX 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-312

Query Match      34.8%; Score 66.5; DB 9; Length 209;
Best Local Similarity 36.4%; Pred. No. 0.00029;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2 NAF-LXXLRGSLRXCKXQCSFXXAFKIDAXRTKLFWISY 44
DB      36 NRFDLELFTPGNLERECNELCNVEEARLIFVDEDKTIAFWQEX 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: KIRST, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-759-130B-310

Query Match      34.8%; Score 66.5; DB 9; Length 226;
Best Local Similarity 36.4%; Pred. No. 0.00032;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2 NAF-LXXLRGSLRXCKXQCSFXXAFKIDAXRTKLFWISY 44
DB      53 NRFDLELFTPGNLERECNELCNVEEARLIFVDEDKTIAFWQEX 96
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OM protein - protein search, using sw model

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	81.6	44	20	AAV18306
2	155	81.6	44	22	AAAB36396
3	125	65.8	44	20	AAV18311
4	124	65.3	44	20	AAV18310
5	122	64.2	44	20	AAV18302
6	122	64.2	44	20	AAV18305
7	122	64.2	44	22	AAAB36395
8	122	64.2	401	22	AAAB4870
9	122	64.2	401	22	AAAB4871
10	122	64.2	406	14	AAAB35764

11	122	64.2	406	18	AAW14509	Modified blood coa
12	122	64.2	406	18	AAW14510	Modified blood coa
13	122	64.2	406	22	AAU77745	Human factor VIIa
14	122	64.2	406	22	AAW52171	Human FVII SEQ ID
15	122	64.2	406	22	AAW52172	Mammalian expresse
16	122	64.2	406	22	AAW52181	Human FVII mutant
17	122	64.2	406	22	AAW52182	Human FVII mutant
18	122	64.2	406	22	AAW52183	Human FVII mutant
19	122	64.2	406	22	AAW52184	Human FVII mutant
20	122	64.2	406	22	AAW52185	Human FVII mutant
21	122	64.2	406	22	AAW52186	Human FVII mutant
22	122	64.2	406	22	AAW52187	Human FVII mutant
23	122	64.2	406	22	AAW52188	Human FVII mutant
24	122	64.2	406	22	AAW52189	Human FVII mutant
25	122	64.2	406	22	AAW52190	Human FVII mutant
26	122	64.2	406	22	AAW52191	Human FVII mutant
27	122	64.2	406	22	AAW52192	Human FVII mutant
28	122	64.2	406	22	AAW52193	Human FVII mutant
29	122	64.2	406	22	AAW52194	Human FVII mutant
30	122	64.2	406	22	AAW52195	Human FVII mutant
31	122	64.2	406	22	AAW52196	Human FVII mutant
32	122	64.2	406	22	AAW52197	Human FVII mutant
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35	122	64.2	406	22	AAW52200	Human FVII mutant
36	122	64.2	406	22	AAW52201	Human FVII mutant
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38	122	64.2	406	22	AAW52203	Human FVII mutant
39	122	64.2	406	22	AAW52204	Human FVII mutant
40	122	64.2	406	22	AAW52205	Human FVII mutant
41	122	64.2	406	22	AAW52206	Human FVII mutant
42	122	64.2	406	22	AAW52207	Human FVII mutant
43	122	64.2	406	22	AAW52208	Human FVII mutant
44	122	64.2	406	22	AAW52209	Human FVII mutant
45	122	64.2	406	22	AAW52210	Human FVII mutant

ALIGNMENTS

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AC	AAV18306;
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DT	17-AUG-1999 (first entry)
XX	
DE	Bovine factor VII GLA domain.
XX	
KW	GLA domain; vitamin K-dependent protein; clotting disorder;
KM	therapy.
XX	
OS	Bos taurus.
XX	
FT	Key location/Qualifiers
FT	Misc-difference 1..44
FT	/note="Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX	
PN	WO9920767-A1.
XX	
PD	29-APR-1999.
XX	
XX	
PF	20-OCT-1998; 98WO-US22152.
XX	
PR	23-OCT-1997; 97US-0955636.
XX	
PA	(MINU) UNIV MINNESOTA.
XX	
XX	Nejsestuen GL;
PI	
XX	
DR	WPI; 1999-288309/24.

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure; Page 15; 86pp; English.
 XX
 CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA;
 Query Match 81.6%; Score 155; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 5.8e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAXEIRFNXXRTQFWVSY 44
 1 ANGFLXLRPGSLXRXCRXXLCSPFXAXHIFRNXXRTQFWVSY 44
 Db
 RESULT 2
 AAB36396
 ID AAB36396 standard; peptide; 44 AA.
 XX
 AC AAB36396;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Bovine factor VII gamma-carboxyglutamic acid domain SRQ ID NO:4.
 XX
 KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KW factor X; prothrombin; enhanced membrane binding affinity;
 KW clot formation; thrombolytic; haemostatic; bleeding disorder;
 KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KW liver disease.
 XX
 OS Bos taurus.
 XX
 OS WC0200066753-A2.
 XX
 PN 09-NOV-2000.
 XX
 PD 28-APR-2000; 2000WO-US11416.
 XX
 PE 29-APR-1999; 99US-0302239.
 XX
 PR 29-APR-1999; 99US-0302239.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Neiseetuen GL;
 XX
 PS WPI; 2001-007226/01.
 XX
 DR Novel vitamin K-dependent polypeptide useful for treating clotting
 XX disorders such as thrombosis and hemophilia, comprises modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity -
 XX
 PS Disclosure; Page 12; 81pp; English.
 XX
 CC The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified
 CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type bovine factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 44 AA;
 Query Match 81.6%; Score 155; DB 22; Length 44;
 Best Local Similarity 95.5%; Pred. No. 5.8e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAXEIRFNXXRTQFWVSY 44
 1 ANGFLXLRPGSLXRXCRXXLCSPFXAXHIFRNXXRTQFWVSY 44
 Db
 RESULT 3
 AAY18311
 ID AAY18311 standard; peptide; 44 AA.
 XX
 AC AAY18311;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX
 PN WO9920767-A1.
 XX
 PD 29-APR-1999.
 XX
 PE 20-OCT-1998; 98WO-US22152.
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Neiseetuen GL;
 XX
 PS WPI; 1999-288309/24.
 XX
 DR Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 PT
 XX
 PS Disclosure; Page 80; 86pp; English.
 XX
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA;
 Query Match 65.8%; Score 125; DB 20; Length 44;
 Best Local Similarity 75.0%; Pred. No. 4.5e-13;
 Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;


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XX 29-APR-1999.
PD 20-OCT-1998; 98WO-US22152.
XX 23-OCT-1997; 97US-0955636.
XX (MINU ) UNIV MINNESOTA.
XX Neiseetuen GL;
XX WPI; 1999-288309/24.
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX Disclosure; Page 15; 86pp; English.
XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX Sequence 44 AA;
SQ
Query Match 64.2%; Score 122; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.4e-12;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 ANGFLXXLRNGSLXRXCRXXLCSPFXAEXIFRNXXRTQFWVS 44
Db 1 ANAFLXXLRPGSLXRXCRXXQCSFXAXRXIFPDAXRTKLFWISY 44
RESULT 7
AAB36395
ID AAB36395 standard; peptide; 44 AA.
XX AAB36395;
AC 27-FEB-2001 (first entry)
XX Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder;
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
KW liver disease.
XX Homo sapiens.
XX OS
XX WO20006753-A2.
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US11416.
XX 29-APR-1999; 99US-0302239.
XX (MINU ) UNIV MINNESOTA.
XX Neiseetuen GL;
XX WPI; 2001-007226/01.
XX Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified

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PT gamma-carboxy glutamic acid domain that enhances membrane binding
XX affinity -
XX Disclosure; Page 12; 81pp; English.
XX The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX Sequence 44 AA;
SQ
Query Match 64.2%; Score 122; DB 22; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.4e-12;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 ANGFLXXLRNGSLXRXCRXXLCSPFXAEXIFRNXXRTQFWVS 44
Db 1 ANAFLXXLRPGSLXRXCRXXQCSFXAXRXIFPDAXRTKLFWISY 44
RESULT 8
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX AAB84870;
AC 31-JUL-2001 (first entry)
XX Mutant blood coagulant factor VII (FVII-31).
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutlein.
XX Homo sapiens.
XX OS
XX Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 311..317
FT /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Ser substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX JP2001061479-A.
XX 13-MAR-2001.
XX 24-AUG-1999; 99JP-0237610.
XX 24-AUG-1999; 99JP-0237610.
XX 24-AUG-1999; 99JP-0237610.
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX WPI; 2001-310677/33.
XX N-PSDB; AAH19463.
XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -
XX Claim 14; Page 20-21; 29pp; Japanese.
XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients.

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XX Sequence      401 AA;
SO Query Match          64.2%; Score 122; DB 22; Length 401;
   Best Local Similarity 52.3%; Pred. No. 1.2e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
Qy 1 ANGFLLXLRNGSLRXCRXXLCSPFXXAEXIFENXXRTROFWMVSY 44
    |||||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 ANAFLEELRPGSLERCKEEOCSFEAREEIFDASRTKLFWISY 44

RESULT 9
ID AAB84871 standard; Protein; 401 AA.
XX AAB84871;
AC
XX AA84871;
DT 31-JUL-2001 (first entry)
DE Mutant blood coagulant factor VII (FVII-39).
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KM mutant; muteln.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 235..239 /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
FT FT Asp-Arg-Lys-Thr-Leu"
FT Misc-difference 311..317 /note= "Wild-type Leu-Gln-Gin-Ser-Arg-Lys-Val-Gly-Asp
FT FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX XX
PN JP2001061479-A.
XX
XX 13-MAR-2001.
PD
PF 24-AUG-1999; 99JP-0237610.
XX
PR 24-AUG-1999; 99JP-0237610.
XX
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI: 2001-310677/33.
DR N-PADB: AAH19464.
XX
PT Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -
XX
PS Claim 16; Page 23-24; 29pp; Japanese.
XX
CC The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients.
XX
SQ Sequence 401 AA;

Query Match          64.2%; Score 122; DB 22; Length 401;
Best Local Similarity 52.3%; Pred. No. 1.2e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
Qy 1 ANGFLLXLRNGSLRXCRXXLCSPFXXAEXIFENXXRTROFWMVSY 44
    |||||::|||::|||::|||::|||::|||::|||::|||
Db 1 ANAFLEELRPGSLERCKEEOCSFEAREEIFDASRTKLFWISY 44

RESULT 10
ID AAR35764 standard; protein; 406 AA.
AAR35764

```

[illegible]

KW Factor VIIa, human, shock heat treatment; protein stability;
KM protein manufacture; protein conformation; mutant; mutain.
OS Homo sapiens.
OS Synthetic.
XX
XX
FT Key Location/Qualifiers
FT Active-site 193
FT /note= "Member of the factor VIIa catalytic triad"
FT Active-site 242
FT /note= "Member of the factor VIIa catalytic triad"
FT Active-site 344
FT /note= "Member of the factor VIIa catalytic triad"
FT Misc-difference 344
FT /label= Gly, Met, Thr
FT /note= "Preferably Ala. Wild type Ser"
XX
XX WO200177141-A1.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-DK00234.
XX
XX 06-APR-2000; 2000DK-0000573.
XX 17-APR-2000; 2000US-197650P.
XX
XX (NOVO) NOVO NORDISK AS.
XX
XX Matchless F:
XX
XX WPI; 2001-657162/75.
XX
XX Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX involves a shock heat treatment -
XX
XX Disclosure: Page -: 22pp; English.
XX
XX The invention describes a method of stabilising a polypeptide involving
XX shock heat treatment of the polypeptide. The method is useful in a
XX pharmaceutical composition, in the industrial or large scale method of
XX manufacturing a polypeptide, also as a unit operation during preparation,
XX purification, recovery and/or formulation of polypeptides. The shock heat
XX treatment improves the protein stability without substantial loss of
XX biological activity. The method can be applied to change polypeptide
XX conformation in a very fast and non-invasive manner. The polypeptide
XX formed is stable. The method is also useful for decreasing the
XX association of the polypeptide. This sequence represents a modified
XX human factor VIIa protein, mutated at the catalytic site, described
XX in the invention.
XX Note: This sequence does not appear in the specification but has
XX been obtained using information given in the invention.
XX
XX Sequence 406 AA:
SQ
Query Match 64.2%; Score 122; DB 22; Length 406;
Best Local Similarity 52.3%; Pred. No. 1.2e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
OY 1 ANGFLXXLNGSLXRCXRLCSFXAEXIFRXXXTRQFWXSY 44
DB 1 ANAFLEELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 14
AAMS2171
ID AAMS2171 standard; Protein; 406 AA.
XX
XX AAMS2171;
XX
XX 07-FEB-2002 (first entry)
XX
XX Human FVII SEQ ID NO 1.
XX
XX

KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KM cardiac; hepatocutrophic; cerebroprotective; haemophilia; liver disease;
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis.
OS Homo sapiens.
XX
XX
FT Key Location/Qualifiers
FT Misc-difference 6
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 7
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 14
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 16
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 19
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 20
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 25
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 26
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 29
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 35
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Modified-site 52
FT /note= "O-glycosylated"
FT Modified-site 60
FT /note= "O-glycosylated"
FT Modified-site 145
FT /note= "N-glycosylated"
FT Cleavage-site 152..153
FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322
FT /note= "N-glycosylated"
XX
XX WO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-DK00094.
XX
XX 11-FEB-2000; 2000DK-0000218.
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX
XX WPI; 2001-581807/65.
XX N-PSDB; AAI99982.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently
XX attached to polypeptide group -
XX
XX Claim 1; Page 81-83; 89pp; English.
XX
XX

CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections.

CC Sequence 406 AA;

Query Match 64.2%; Score 122; DB 22; Length 406;

Best Local Similarity 75.0%; Pred. No. 1.2e-11;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLXRCXRXLCSPFXAEXIFRNXXRTROPWVS 44

DB 1 ANAFLLXLRPGSLXRCXKXQCSFXXARXIFKDAERTKLFWISY 44

RESULT 15
 AAM52172
 ID AAM52172 standard; Protein; 406 AA.

AC AAM52172;

DT 07-FEB-2002 (first entry)

XX Mammalian expressed human FVII SEQ ID NO 3.

XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;

KM cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;

KM myocardial infarction; thrombotic stroke; deep-vein thrombosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 52 /note= "O-glycosylated"

FT Modified-site 60 /note= "O-glycosylated"

FT Modified-site 145 /note= "N-glycosylated"

FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
 to an activated form, comprising two chains
 linked by a single disulphide bridge"

FT Modified-site 322 /note= "N-glycosylated"

XX WO200158935-A2.

XX 16-AUG-2001.

PF 12-FEB-2001; 2001WO-DK00094.

PR 11-FEB-2000; 2000DK-0000218.

PR 18-OCT-2000; 2000DK-0001558.

XX (MAXY-) MAXYGEN APS.

PI Andersen KV, Pedersen AH, Bornaes C;

XX WPI; 2001-581807/65.

DR N-PSDB; AA199983.

PT New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -

XX Disclosure; Page 85-86; 89pp; English.

XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections.

XX Sequence 406 AA;

Query Match 64.2%; Score 122; DB 22; Length 406;

Best Local Similarity 52.3%; Pred. No. 1.2e-11;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLXRCXRXLCSPFXAEXIFRNXXRTROPWVS 44

DB 1 ANAFLEELRPGSLERECKEQCSFEARELIFKDAERTKLFWISY 44

Search completed: March 19, 2003, 14:51:14
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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10ASN28GLU_4
Perfect score: 190
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Scoring table: BLOSUM62
Gapop 10.0 , Gapevt 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	148	77.9	407	1	KFB07	coagulation factor
2	130	68.4	443	2	I46932	coagulation factor
3	122	64.2	466	1	KFH07	coagulation factor
4	108	56.8	461	1	JX0210	protein C (activat
5	107	56.3	461	1	S18994	protein C (activat
6	96	50.5	456	1	KXBO	protein C (activat
7	95	50.0	482	1	EXRT	coagulation factor
8	95	50.0	488	1	EXHU	coagulation factor
9	94	49.5	461	1	KXHU	protein C (activat
10	90	47.4	492	1	EXBO	coagulation factor
11	88	46.3	416	1	KFBO	coagulation factor
12	88	46.3	461	1	KFHU	coagulation factor
13	83	43.7	452	1	A30351	coagulation factor
14	83	43.7	459	2	JQ0419	coagulation factor
15	82	43.2	475	1	EXCH	coagulation factor
16	77	40.5	622	1	TBHU	thrombin (EC 3.4.2
17	75	39.5	642	2	S53433	thrombin (EC 3.4.2
18	74	38.9	617	2	S10511	thrombin (EC 3.4.2
19	74	38.9	618	2	A35827	thrombin (EC 3.4.2
20	71	37.4	675	1	KXBO	plasma protein S p
21	70	36.8	642	2	S53434	plasma protein S p
22	70	36.8	646	2	S38819	plasma protein S p
23	70	36.8	676	1	KXHU	plasma protein S p
24	68	35.8	625	1	TBBO	thrombin (EC 3.4.2
25	68	35.8	675	1	KXRT	plasma protein S p
26	67	35.3	422	1	KXHU	plasma protein Z p
27	63	33.2	396	1	KXBO	plasma protein Z p
28	61	32.1	675	1	KXMS	plasma protein S p
29	59	31.1	678	2	B48089	growth arrest-spec

30	58	30.5	673	2	A48089	growth arrest-spec
31	56	29.5	413	1	VHVN1H	nucleoprotein - in
32	56	29.5	674	2	I55476	growth potentiatin
33	53	27.9	605	1	W1WLB2	El protein - bovin
34	53	27.9	620	1	W1WLB2	El protein - bovin
35	49.5	26.1	594	2	D84859	probable MAP kinase
36	49.5	26.1	603	2	C96575	probable MAP kinase
37	49	25.8	1217	2	T21403	hypothetical prote
38	48.5	25.5	576	2	G96763	probable MAP kinase
39	45	23.7	687	2	T08528	probable DNA copol
40	44	23.2	1101	2	T26919	hypothetical prote
41	43	22.6	219	2	A2449	hypothetical prote
42	43	22.6	297	2	JC1527	coat protein - pot
43	43	22.6	440	2	C83368	probable MFS trans
44	42.5	22.4	907	2	T15792	hypothetical prote
45	42	22.1	320	2	G84993	glutathione syntha

ALIGNMENTS

RESULT 1

KFB07 coagulation factor VIIa (EC 3.4.21.21) - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999

C/Accession: A31979; C20274

R/Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A/Title: Bovine factor VII. Its purification and complete amino acid sequence.

A/Reference number: A31979; PMID:89008362; PMID:3049594

A/Accession: A31979

A/Molecule type: protein

A/Residues: 1-407 <RAK>

R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A/Reference number: A20274; PMID:83308813; PMID:6688526

A/Accession: C20274

A/Molecule type: protein

A/Residues: 58-62, 'X', 64-68 <MCM>

A/Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R/Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.

J. Biochem. 104, 867-868, 1988

A/Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A/Reference number: A44556; PMID:89213999; PMID:3149637

A/Contents: annotation

A/Note: structure and location of covalently bound carbohydrate

C/Function:

A/Description: catalyzes the proteolytic activation of coagulation factor X in the preser

gulation factor IX in the presence of calcium and tissue factor

A/Pathway: blood coagulation extrinsic pathway

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam

F.1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>

F.1-144/Domain: Gla domain homology (fragment) <GLA>

F.50-81/Domain: EGF homology <EGF>

F.91-127/Domain: EGF homology <EGF>

F.153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F.153-387/Product: trypsin homology <TRY>

F.6-7-14-16-19-20-25-26-29-34-35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F.17-22-50-61-55-70-72-81-91-102-98-112-114-127-135-262-159-164-178-194-310-329-340-368/I

F.63/Binding site: carbohydrate (Ser) (covalent) #status experimental

F.145-203/Binding site: carbohydrate (Asn) (covalent) #status experimental

F.152-153/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental

F.193-242-344/Active site: His, Asp, Ser #status predicted

F.290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 77.9%; Score 148; DB 1; Length 407;

Best Local Similarity 68.2%; Pred. No. 7, 7e-18;

Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

C.Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 08-Dec-2000
C.Accession: S49075; J04670; P50191; P50190; 162745
R.Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A.Title: Evidence for competition between vitamin K-dependent clotting factors for intracellular binding sites
A.Reference number: A58498; MUID:96093366; PMID:8578539
A.Accession: S49075
A.Molecule type: mRNA
A.Residues: 1-482 <STA>
A.Cross-references: EMBL:X79807; NID:9506600; PIDN:CA56202.1; PID:g506601
A.Note: submitted to the EMBL Data Library, June 1994
A.Note: neither the complete nucleic acid sequence nor the complete translation are shown
R.Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A.Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A.Reference number: J04670; MUID:96194815; PMID:8647460
A.Accession: J04670
A.Molecule type: mRNA
A.Residues: 1-482 <STA2>
A.Cross-references: EMBL:X79807; NID:9506600; PIDN:CA56202.1; PID:g506601
A.Experimental source: Cos-1 cell
R.Enyoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A.Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma
A.Reference number: P50190; MUID:92041742; PMID:1718949
A.Accession: P50191
A.Molecule type: protein
A.Residues: 41-58, 'X', 60-65 <ENU1>
A.Accession: P50190
A.Molecule type: protein
A.Residues: 183-186, 'X', 188-207 <ENU2>
R.Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A.Title: Analysis of the partial nucleotide sequences and deduced primary structures of factor Xa
A.Reference number: I46196; MUID:94223160; PMID:8168596
A.Accession: I62745
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 295-383, 'G', 385-455 <MUR>
A.Cross-references: GB:D21315; NID:g415309; PIDN:BAA04756.1; PID:g455396
C.Function:
A.Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor Va
A.Pathway: blood coagulation
C.Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C.Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
R.1-23/Domain: signal sequence #status predicted <SIG>
F.24-40/Domain: propeptide #status predicted <PRO>
F.25-84/Domain: Gla domain homology <GLA>
F.41-179/Product: coagulation factor X light chain #status predicted <LCH>
F.190-121/Domain: EGF homology <EG1>
F.129-164/Domain: EGF homology <EG2>
F.183-483/Product: coagulation factor X heavy chain #status predicted <HCH>
F.183-231/Domain: activation peptide #status predicted <AP1>
F.232-483/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F.232-460/Domain: trypsin homology <TRY>
F.46/47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F.57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402, 410-419, 421-430, 432-433, 435-436, 438-439, 441-442, 444-445, 447-448, 450-451, 453-454, 456-457, 459-460, 462-463, 465-466, 468-469, 471-472, 474-475, 477-478, 480-481, 483-484, 486-487, 489-490, 492-493, 495-496, 498-499, 501-502, 504-505, 507-508, 510-511, 513-514, 516-517, 519-520, 522-523, 525-526, 528-529, 531-532, 534-535, 537-538, 540-541, 543-544, 546-547, 549-550, 552-553, 555-556, 558-559, 561-562, 564-565, 567-568, 570-571, 573-574, 576-577, 579-580, 582-583, 585-586, 588-589, 591-592, 594-595, 597-598, 599-600, 602-603, 605-606, 608-609, 611-612, 614-615, 617-618, 620-621, 623-624, 626-627, 629-630, 632-633, 635-636, 638-639, 641-642, 644-645, 647-648, 650-651, 653-654, 656-657, 659-660, 662-663, 665-666, 668-669, 671-672, 674-675, 677-678, 680-681, 683-684, 686-687, 689-690, 692-693, 695-696, 698-699, 701-702, 704-705, 707-708, 710-711, 713-714, 716-717, 719-720, 722-723, 725-726, 728-729, 731-732, 734-735, 737-738, 740-741, 743-744, 746-747, 749-750, 752-753, 755-756, 758-759, 761-762, 764-765, 767-768, 770-771, 773-774, 776-777, 779-780, 782-783, 785-786, 788-789, 791-792, 794-795, 797-798, 799-800, 802-803, 805-806, 808-809, 811-812, 814-815, 817-818, 820-821, 823-824, 826-827, 829-830, 832-833, 835-836, 838-839, 841-842, 844-845, 847-848, 850-851, 853-854, 856-857, 859-860, 862-863, 865-866, 868-869, 871-872, 874-875, 877-878, 880-881, 883-884, 886-887, 889-890, 892-893, 895-896, 898-899, 901-902, 904-905, 907-908, 910-911, 913-914, 916-917, 919-920, 922-923, 925-926, 928-929, 931-932, 934-935, 937-938, 940-941, 943-944, 946-947, 949-950, 952-953, 955-956, 958-959, 961-962, 964-965, 967-968, 970-971, 973-974, 976-977, 979-980, 982-983, 985-986, 988-989, 991-992, 994-995, 997-998, 999-1000
F.1231-233/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #status predicted
F.274, 320, 417/Active site: His, Asp, Ser #status predicted

RESULT 8

ex:AMU
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
 N.Alternate names: Stuart factor
 C.Species: Homo sapiens (man)
 C.Date: 15-Nov-1984 #sequence, revision 02-May-1994 #text change 08-Dec-2000
 C.Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00
 R.Leytus, S.P.; Foster, D.C.; Kutarchi, K.; Davie, E.W.
 Biochemistry 25, 5098-5102, 1986
 A.Title: Gene for human Factor X: a blood coagulation factor whose gene organization is
 A.Reference number: A24478; PMID:87026600; PMID:3768336
 A.Accession: A24478
 A.Molecule type: DNA
 A.Residues: 1-488 <LE2>
 A.Cross-references: GB:I:29433; GB:M14327; NID:945960; PIDN:AAA52764.1; PID:G182831
 R.Messler, T.L.; Plittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
 Gene 99, 291-294, 1991
 A.Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor X
 A.Reference number: J00917; PMID:91216473; PMID:1902434
 A.Accession: J00917
 A.Molecule type: mRNA
 A.Residues: 1-488 <MES>
 A.Cross-references: GB:M57285; NID:G182389; PIDN:AAA52421.1; PID:G182390
 R.Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
 U. Biol. Chem. 267, 7395-7401, 1992
 A.Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation factor
 A.Reference number: A42485; PMID:92218390; PMID:1313736
 A.Accession: A42485
 A.Molecule type: DNA
 A.Residues: 1-15 <MTA>
 A.Experimental source: liver
 A.Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBIPI:93787)
 R.Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagdeeswaran, P.
 Gene 41, 311-314, 1986
 A.Title: Isolation and characterization of human blood-coagulation factor X cDNA.
 A.Reference number: A25853; PMID:86221723; PMID:3011603
 A.Accession: A25853
 A.Molecule type: mRNA
 A.Residues: 19-284, 'E', 289-488 <KAU>
 A.Cross-references: C.W:MacGillivray, R.T.A. 1985
 R.Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A. 1985
 Proc. Natl. Acad. Sci. U.S.A. 82, 3531-3595, 1985
 A.Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X
 A.Reference number: A22208; PMID:85216545; PMID:2582420
 A.Accession: A22208
 A.Molecule type: mRNA
 A.Residues: 13-441, 'S', 443-488 <FUN>
 A.Cross-references: GB:K03194; NID:G182840; PIDN:AAA52490.1; PID:G182841
 R.Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kutarchi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
 A.Title: Characterization of a cDNA coding for human factor X.
 A.Reference number: A21284; PMID:84222026; PMID:6587384
 A.Accession: A21284
 A.Molecule type: mRNA
 A.Residues: 13-284, 'E', 289-488 <LE2>
 A.Cross-references: GB:K01886
 R.McMillen, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss
 Biochemistry 22, 2875-2884, 1983
 A.Title: Complete amino acid sequence of the light chain of human blood coagulation factor X
 A.Reference number: A20362; PMID:83257207; PMID:6871167
 A.Accession: A20362
 A.Molecule type: protein
 A.Residues: 41-179 <MCW>
 R.Inoue, K.; Morita, T.
 Eur. J. Biochem. 210, 153-163, 1993
 A.Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A.Reference number: S39414; PMID:94062825; PMID:8234361
 A.Accession: S39415
 A.Molecule type: protein
 A.Residues: 183-234 <INO>
 A.Note: glycosylation sites
 A.Note: identification and characterization of beta-hydroxyaspartic acid
 R.Jagdeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.

Gene 84, 517-519, 1989
 A>Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
 A:Reference number: I54051, MUID:90128239; PMID:2612918
 A:Accession: I54051
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23 <RES>
 A:Cross-references: GB:M33297; NID:g18360; PIDN:AA52636.1; PID:g553330
 R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bl
 J. Mol. Biol. 233, 947-966, 1993
 A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
 A:Reference number: A49458; MUID:93360277; PMID:8355279
 A:Accession: A49458
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms
 C:Comment: The two chains held together by one disulfide bond are formed from a single-C
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
 C:Genetic:
 A:Gene: GDB:F10
 A:Cross-references: GDB:119890; OMIM:227600
 A:Map position: 13q34-13q34
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
 A:Note: deficiency of this factor causes Stuart disease
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:41-179/Domain: Gla domain homology <Gla>
 F:183-488/Domain: EGF homology <EGF>
 F:129-164/Domain: EGF homology <EG2>
 F:183-488/Domain: coagulation factor X heavy chain #status experimental <HCH>
 F:183-334/Domain: activation peptide #status experimental <APT>
 F:235-488/Domain: coagulation factor Xa heavy chain #status experimental <ACT>
 F:235-462/Domain: trypsin homology <TRY>
 F:46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:57-63/Disulfide bonds: #status predicted
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:199,211/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 50.0%; Score 95; DB 1; Length 488;
 Best Local Similarity 36.4%; Pred. No. 1.6e-08;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRCRXXKCSFXAEXIFRNXXRTROFVSV 44
 Db 41 ANSFLBEMKXGHLRECEMETCTSYEARVEFEDSDKTNEFNKY 84

RESULT 9
 KXHU
 protein C (activated) (EC 3.4.21.69) precursor - human
 N:Alternate names: autoproteolysin IIA; plasma protein C
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
 C:Accession: A22331; A25426; A21781; A23789; A00927
 R:Postner, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A>Title: The nucleotide sequence of the gene for human protein C.
 A:Reference number: A22331; MUID:85270390; PMID:2991887
 A:Accession: A22331
 A:Molecule type: DNA
 A:Residues: 1-461 <ROS1>
 A:Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A>Title: Evolution and organization of the human protein C gene.
 A:Reference number: A25426; MUID:86120978; PMID:3511471

A:Accession: A25426
 A:Molecule type: DNA
 A:Residues: 1-445, '1', 446-461 <PLU>
 A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
 R:Postner, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A>Title: Characterization of a cDNA coding for human protein C.
 A:Reference number: A21781; MUID:84272714; PMID:6589623
 A:Accession: A21781
 A:Molecule type: mRNA
 A:Residues: Q, 107-461 <ROS2>
 A:Cross-references: GB:K02059; NID:g190322; PIDN:AAA60164.1; PID:g190323
 R:Beckmann, R.J.; Schmidt, R.J.; Sauter, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5233-5247, 1985
 A>Title: The structure and evolution of a 461 amino acid human protein C precursor and it
 A:Reference number: A23789; MUID:85269639; PMID:2991859
 A:Accession: A23789
 A:Molecule type: mRNA
 A:Residues: 1-461 <BEC>
 A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
 R:Millerich, J.P.; Broeze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A>Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me
 A:Reference number: A44605; MUID:90293094; PMID:1694179
 A:Accession: A44605
 A:Contents: annotation; carboxylate binding sites; activation peptide
 A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
 R:Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A>Title: O-linked fucose is present in the first epidermal growth factor domain of factor
 A:Reference number: A44606; MUID:92184750; PMID:1544994
 A:Accession: A44606
 A:Contents: annotation; beta-hydroxyaspartic acid
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine protease that in
 ization of factor Va is synthesized in the liver as a single chain precursor, which is c
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
 C:Genetic:
 A:Gene: GDB:PROC
 A:Cross-references: GDB:120317; OMIM:176860
 A:Map position: 2q13-2q21
 A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding;
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:27-86/Domain: Gla domain homology <Gla>
 F:33-42/Domain: propeptide #status predicted <PRO>
 F:43-197/Domain: protein C light chain #status predicted <LCH>
 F:92-131/Domain: EGF homology <EGF>
 F:140-175/Domain: EGF homology <EG2>
 F:200-461/Domain: activation peptide #status experimental <APT>
 F:212-445/Domain: trypsin homology <TRY>
 F:46-49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status expe
 F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/Di
 F:106-111/Disulfide bonds: #status predicted
 F:110/Binding site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asn) (covalent) #status experimental
 F:119,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
 F:233,299,402/Active site: His, Asp, Ser #status predicted
 F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 49.5%; Score 94; DB 1; Length 461;
 Best Local Similarity 46.3%; Pred. No. 2.2e-08;
 Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRCRXXKCSFXAEXIFRNXXRTROFV 41
 Db 43 ANSFLBEMKXGHLRECEMETCTSYEARVEFEDSDKTNEFNKY 83

RESULT 10
 EXBO
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine

C:Comment: Factor IX is activated by factor XII, which excises the activation peptide pC:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strC:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the presenA:Pathway: blood coagulation intrinsic pathway

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam F:1-146/Product: coagulation factor IXa light chain #status experimental <Ato>

F:1-45/Domain: Gla domain homology (fragment) <Gla>

F:51-82/Domain: EGF homology <EG1>

F:88-124/Domain: EGF homology <EG2>

F:147-181/Domain: activation peptide #status experimental <APT>

F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>

F:182-409/Domain: trypsin homology <TRY>

F:7, 8, 15, 17, 20, 21, 26, 27, 30, 33, 36, 40/Modified site: gamma-carboxyglutamic acid (Glu) #sta F:18-23, 51-62, 56-71, 73-82, 88-99, 95-109, 111-124, 132-290, 207-223, 337-351, 362-390/Disulfide F:53/Binding site: carboxylate (Ser) (covalent) #status experimental

F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:158, 168, 173, 261/Binding site: carboxylate (Asn) (covalent) #status experimental

F:222, 270, 366/Active site: His, Asp, Ser #status predicted

Query Match 46.3%; Score 88; DB 1; Length 416;
Best Local Similarity 37.2%; Pred. No. 2, 3e-07;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRNGSLKRCXXLCSPFXAXEIRNXXRTQFWVSY 44
Db 3 SGKLEFVRNGLRECKEKCKSEAEAREVEFTEKTEFWKQY 45

RESULT 12

KFHU

coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human

N:Alternative names: antihemophilic factor B; Christmas factor

C:Species: Homo sapiens (man)

C:Date: 17-Dec-1982 #sequence, revision 30-Jun-1987 #text change 15-Sep-2000

C:Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20 R:Yoshitake, S.; Schnap, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.

Biochemistry 24, 3736-3750, 1985

A:Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).

A:Reference number: A00922; PMID:8600558; PMID:2994716

A:Accession: A00922

A:Molecule type: DNA

A:Residues: 1-461 <YOS>

A:Cross-references: GB:K02402; NID:g182612; PIDN:AA59620.1; PID:g182613

R:Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giamelli, F.; Gould, K.; Huddleston, J.A.; Bro EMO J. 3, 1053-1060, 1984

A:Title: The gene structure of human anti-haemophilic factor IX.

A:Reference number: A37570; PMID:84236100; PMID:6329734

A:Accession: A37570

A:Molecule type: DNA

A:Residues: 1-461 <ANS>

A:Cross-references: GB:K02048

R:Reitsma, P.H.; Bettina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Brier, E. Blood 72, 1074-1076, 1988

A:Title: The putative factor IX gene promoter in hemophilia B Leyden.

A:Reference number: A30511; PMID:88327116; PMID:3416069

A:Accession: A30511

A:Molecule type: DNA

A:Residues: 8-24 <REI>

A:Cross-references: EMBL:X55008; NID:g311288; PIDN:CAH38245.2; PID:g4469253

R:Koeberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S. Am. J. Hum. Genet. 45, 448-457, 1989

A:Title: Functionally important regions of the factor IX gene have a low rate of polymor A:Reference number: A32989; PMID:893171752; PMID:2773937

A:Accession: A32989

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 30-92 <KOB>

R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985

A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat

A:Reference number: A22673; PMID:85190593; PMID:3857619

A:Accession: A22673

A:Molecule type: mRNA

A:Residues: 1-193, 'T', 195-461 <MCG>

A:Cross-references: GB:M11309; NID:g180552; PIDN:AA52023.1; PID:g180553

A:Note: the authors translated the codon ACA for residue 29 as Tyr

R:Raye, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Finkel, A.; Tolstoshe Nucleic Acids Res. 11, 2325-2335, 1983

A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-bas A:Reference number: A21337; PMID:83220788; PMID:6687940

A:Accession: A21337

A:Molecule type: mRNA

A:Residues: 1-193, 'T', 195-461 <JAY>

A:Cross-references: GB:J00137; NID:g182610; PIDN:AA522763.1; PID:g182611

R:Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandes, T.; Warren, S.T. Somat. Cell Mol. Genet. 10, 465-473, 1984

A:Title: Isolation and characterization of a cDNA coding for human factor IX

A:Reference number: A37546; PMID:84300526; PMID:6089357

A:Accession: A37546

A:Molecule type: mRNA

A:Residues: 38-193, 'T', 195-326 <JAG>

A:Cross-references: GB:M35672

R:Kurachi, K.; Davie, E.W. Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982

A:Title: Isolation and characterization of a cDNA coding for human factor IX.

A:Reference number: A30623; PMID:83065193; PMID:6959130

A:Accession: A30623

A:Molecule type: mRNA

A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A', 3 A:Cross-references: GB:J00136; NID:g182608; PIDN:AA58726.1; PID:g182609

A:Experimental source: liver

R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B. Vox Sang. 58, 21-29, 1990

A:Title: Development of an immunoaffinity process for factor IX purification.

A:Reference number: A60486; PMID:90194857; PMID:2316207

A:Accession: A60486

A:Molecule type: protein

A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>

R:McMillen, B.A.; Fujikawa, K.; Kistiel, W. Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co A:Reference number: A20274; PMID:83308813; PMID:6688526

A:Accession: A20274

A:Molecule type: protein

A:Residues: 105-109, 'X', 111-115 <MCN>

R:Balland, A.; Faure, T.; Carralio, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle Eur. J. Biochem. 172, 565-572, 1988

A:Title: Characterization of two differently processed forms of human recombinant factor A:Reference number: S02527; PMID:8816735; PMID:3280312

A:Accession: S02527

A:Molecule type: protein

A:Residues: 29-63 <BAL>

A:Note: processed forms expressed in recombinant system

R:Ballat, S.; Perraud, F.; Dalemans, W.; Ballard, A.; Dieterle, A.; Faure, T.; Meulien, f EMO J. 9, 3395-3301, 1990

A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice and A:Reference number: S12058; PMID:91006024; PMID:2209546

A:Accession: S12058

A:Molecule type: mRNA; protein

A:Residues: 1-68 <JAL>

A:Note: processed forms expressed in recombinant system

R:Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campeel EMO J. 9, 475-480, 1990

A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium A:Reference number: S12377; PMID:90151623; PMID:2406129

A:Accession: S12377

A:Molecule type: protein

A:Residues: 92-130 <HAN>

A:Note: NMR detection of calcium binding by domain expressed in recombinant system

R:de la Salle, C.; Charmanlier, J.L.; Baas, M.C.; Schwartz, A.; Wiesel, M.L.; Grunbaum, Thromb. Haemost. 70, 370-371, 1993

A:Title: A deletion located in the 3' non translated part of the factor IX gene responsit A:Reference number: I59612; PMID:94054330; PMID:8236150

A/Accession: 159612
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 444-461 <RES>
 A/Cross-references: GB:566752; NID:9439773; PIDN:AA826588.1; PID:9439774
 R/Stolett, E.S.; Koeberl, D.D.; Sarker, G.; Sommer, S.S.
 Science 239, 491-494, 1998
 A/Title: Genomic amplification with transcript sequencing.
 A/Reference number: 159529; MUID:86127096; PMID:3340835
 A/Accession: 159529
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 290-359 <RES>
 A/Cross-references: GB:M19063; NID:g182622; PIDN:AA52456.1; PID:g182623
 R/Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw
 Biochemistry 33, 5167-5171, 1994
 A/Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically 11r
 A/Reference number: A54255; MUID:94227047; PMID:8172892
 A/Accession: A54255
 A/Molecule type: protein
 A/Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>
 A/Note: the residues designated 'X' were determined to be threonine bound to carbohydrate
 R/Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A/Title: Activation of human factor IX (Christmas factor).
 A/Reference number: A18483; MUID:78194509; PMID:659613
 A/Contents: annotation; activation; active site; carbohydrate binding
 R/McGraw, R.A.; Davie, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
 A/Reference number: A37569
 A/Contents: annotation
 A/Note: 194-Thr was also found
 R/Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5698-5704, 1984
 A/Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
 A/Reference number: A37543; MUID:84185715; PMID:6425296
 A/Contents: annotation; calcium binding
 R/Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A/Reference number: A37544
 A/Contents: annotation; calcium binding, correction
 R/Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A/Title: Defective propeptide processing of blood clotting factor IX caused by mutation
 A/Reference number: A37545; MUID:86189477; PMID:3009023
 A/Contents: annotation; signal sequence cleavage site
 R/Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya, J.
 J. Biol. Chem. 264, 21257-21265, 1989
 A/Title: Blood clotting factor IX (BIM) Nagoya: substitution of arginine 180 by tryptophan
 A/Contents: annotation; sequence of mutant BIM Nagoya
 A/Note: carboxylation, glycosylation, and cleavage sites
 R/Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle
 submitted to the Brookhaven Protein Data Bank, November 1991
 A/Reference number: A51252; PDB:1IXA
 A/Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A/Note: recombinant form expressed in yeast
 C/Comment: Factor IX is activated by factor Xla, which excises the activation peptide pr
 C/Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
 C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc
 C/Genetics:
 A/Gene: GDB:F9
 A/Cross-references: GDB:119900; OMIM:306900
 A/Map position: Xq27.1-Xq27.2
 A/Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 C/Function:
 A/Description: catalyzes the proteolytic activation of coagulation factor X in the prese
 A/Pathway: blood coagulation intrinsic pathway
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-46/Domain: propeptide #status experimental <PPT>
 F:31-91/Domain: Gla domain homology <Gla>

F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:97-128/Domain: EGF homology <EG1>
 F:134-170/Domain: EGF homology <EG2>
 F:192-226/Domain: activation peptide #status experimental <ACT>
 F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F:227-454/Domain: trypsin homology <TRY>
 F:53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #st
 F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D
 F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:191-192/Cleavage site: Arg-Ala (coagulation factor IXa) #status experimental
 F:203,213/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:205,215/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental
 Query Match 46.3%; Score 88; DB 1; Length 461;
 Best Local Similarity 39.5%; Pred. No. 2,Se-07;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;
 Oy 2 NGFLXLLNGSLXRCXRCXLCSPFXAXEIPFNXXRTQFWYSY 44
 Db 49 SGKLEEFVQGNLRECEMEKCSFEAREVFENTERTTEFWKQY 91
 RESULT 13
 coagulation factor IXa (EC 3.4.21.22) precursor - dog
 C/Species: Canis lupus familiaris (dog)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A/Accession: A30351; 146201
 R/Evans, J.P.; Matzke, H.H.; Ware, J.L.; Stafford, D.W.; High, K.A.
 Blood 74, 207-212, 1989
 A/Title: Molecular cloning of a cDNA encoding canine factor IX.
 A/Reference number: A30351; MUID:89323338; PMID:2752110
 A/Accession: A30351
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-452 <EVA>
 A/Cross-references: GB:M21757; NID:g972719; PIDN:AA75006.1; PID:g163948
 R/Axelrod, J.H.; Read, M.S.; Brinkhouse, K.M.; Vermo, I.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990
 A/Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic
 A/Reference number: 146201; MUID:90311364; PMID:2367529
 A/Accession: 146201
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-452 <AXE>
 A/Cross-references: GB:M3826; NID:g163949; PIDN:AA30844.1; PID:g163950
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-40/Domain: propeptide #status predicted <PRO>
 F:24-84/Domain: Gla domain homology <Gla>
 F:41-45/Product: coagulation factor IX #status predicted <MAT>
 F:90-121/Domain: EGF homology <EG1>
 F:127-163/Domain: EGF homology <EG2>
 F:216-445/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,66,67,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
 F:57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/D
 F:258,306,402/Active site: His, Asp, Ser #status predicted
 Query Match 43.7%; Score 83; DB 1; Length 452;
 Best Local Similarity 37.2%; Pred. No. 1,8e-06;
 Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;
 Oy 2 NGFLXLLNGSLXRCXRCXLCSPFXAXEIPFNXXRTQFWYSY 44
 Db 42 SGKLEEFVQGNLRECEMEKCSFEAREVFENTERTTEFWKQY 84
 RESULT 14
 J00419
 coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
 C/Accession: J00419.1;19667
 R:Mu, S.M.; Stafford, D.W.; Ware, J.
 Gene 86, 275-278, 1990
 A>Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.
 A/Reference number: J00419; MWID:90215309; PMID:2323576
 A/Accession: J00419
 A/Molecule type: mRNA
 A/Residues: 1-459 <MUS>
 A/Cross-references: GB:M23109; NID:g193317; PIDN:AAA37629.1; PID:g387158
 A/Experimental source: liver
 R:Sarkar, G.; Koebel, D.D.; Sommer, S.S.
 Genomics 6, 133-143, 1990
 A>Title: Direct sequencing of the activation peptide and the catalytic domain of the fad
 A/Reference number: I46580; MWID:90152675; PMID:2303254
 A/Accession: I49667
 A/Status: preliminary; translated from GB/EMBL/DBU
 A/Molecule type: mRNA
 A/Residues: 168-362, 'Q', 364-387, 'I', 389-451 <RES>
 A/Cross-references: GB:M26236; NID:g193319; PIDN:AAA37630.1; PID:g193320
 C/Comment: This protein plays a critical role in blood coagulation.
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>
 F:17-34/Domain: propeptide #status predicted <PRO>
 F:19-79/Domain: Gla domain homology <GLA>
 F:35-459/Product: coagulation factor IX #status predicted <MAY>
 F:85-116/Domain: EGF homology <EG1>
 F:122-158/Domain: EGF homology <EG2>
 F:225-452/Domain: trypsin homology <TRY>
 F:41,42,49,51,54,55,60,61,64,67,70,74/Modified site: gamma-carboxylglutamic acid (Glu) #S
 F:52-57,85-96,90-105,107-116,122-133,129-143,145-158,166-333,250-266,380-394,405-433/DLS
 F:265,313,409/Active site: His, Asp, Ser #status predicted

Query Match 43.7%; Score 83; DB 2; Length 459;
 Best Local Similarity 37.2%; Pred. No. 1.8e-06;
 Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 2 NGFLXLRNGSLKRCXXLCSEFYXAEIIFRNXXRTROFWVSY 44
 Db 37 SKLEEFVGRNLTRECEERCSFEAREVEFENTKTEPFWKQY 79

RESULT 15

EXCH
 coagulation factor Xa (EC 3.4.21.6) precursor - chicken
 N/Alternate names: virus-activating proteinase
 C:Species: Gallus gallus (chicken)
 C>Date: 12-Feb-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
 C/Accession: S15838; S20389; S20381
 R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotch, B.; Ogasawara, T.; Na
 FEBS Lett. 283, 281-285, 1991
 A>Title: Primary structure of the virus activating protease from chick embryo. Its ident
 A/Reference number: S15838; MWID:91257322; PMID:2044767
 A/Accession: S15838
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-475 <SUZ>
 A/Cross-references: DBU:DO0844; NID:g222869; PIDN:BAA0724.1; PID:g222870
 R:Gotch, B.; Yamuchi, F.; Ogasawara, T.; Nagai, Y.
 FEBS Lett. 296, 274-278, 1992
 A>Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsi
 A/Reference number: S20380; MWID:92164779; PMID:1537403
 A/Accession: S20380
 A/Molecule type: protein
 A/Residues: 41-55 <GOT>
 A/Accession: S20381
 A/Molecule type: protein
 A/Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A/Pathway: blood coagulation

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-185/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-167/Domain: EGF homology <EG2>
 F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:186-240/Domain: activation peptide #status predicted <APT>
 F:241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
 F:241-468/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #st
 F:57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,421
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:196,207,228,285/Binding site: carbonylate (Asn) (covalent) #status predicted
 F:282,328,423/Active site: His, Asp, Ser #status predicted

Query Match 43.2%; Score 82; DB 1; Length 475;
 Best Local Similarity 34.1%; Pred. No. 2.8e-06;
 Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 ANGFLXLRNGSLKRCXXLCSEFYXAEIIFRNXXRTROFWVSY 44
 Db 41 ANSLEEMKQGNTERECNEBRCSEAREAFEDNEKTEPFWNJY 84

Search completed: March 19, 2003, 15:00:58
 Job time : 30.125 secs

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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10ASN28GLU_4
Perfect score: 190
Sequence: 1 ANGFLXLXNGSLXRCRX.....XXAEXIFRXRXRTQFWVS 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	77.9	407	1	FA7_BOVIN
2	130	68.4	444	1	FA7_RABIT
3	122	64.2	466	1	P98139 oryctolagus
4	108	56.8	218	1	TMGI_HUMAN
5	108	56.8	461	1	PRTC_MOUSE
6	107	56.3	461	1	PRTC_RAT
7	105	55.3	446	1	FA7_MOUSE
8	102	53.7	231	1	TMG3_HUMAN
9	101	53.2	459	1	PRTC_PIG
10	96	50.5	486	1	PRTC_BOVIN
11	95	50.0	488	1	FA10_HUMAN
12	94	49.5	461	1	PRTC_HUMAN
13	93	48.9	490	1	FA10_RABIT
14	90	47.4	492	1	FA10_BOVIN
15	88	46.3	416	1	FA9_BOVIN
16	88	46.3	461	1	FA9_HUMAN
17	85	44.7	488	1	PRTC_RABIT
18	83	43.7	452	1	FA9_CANFA
19	83	43.7	459	1	FA9_MOUSE
20	82	43.2	475	1	FA10_CHICK
21	77	40.5	622	1	THRB_HUMAN
22	74	38.9	617	1	THRB_RAT
23	74	38.9	618	1	THRB_MOUSE
24	71	37.4	675	1	PRIS_BOVIN
25	70	36.8	202	1	TMG2_HUMAN
26	70	36.8	226	1	TMG4_HUMAN
27	70	36.8	646	1	PRTS_RABIT
28	70	36.8	649	1	PRTS_HUMAN
29	70	36.8	676	1	PRTS_HUMAN
30	68	35.8	376	1	FA10_TROCA
31	68	35.8	625	1	THRB_BOVIN
32	68	35.8	675	1	PRTS_RAT
33	67	35.3	400	1	PRTZ_HUMAN

34	63	33.2	396	1	PRTZ_BOVIN
35	61	32.1	675	1	PRTS_MOUSE
36	56	29.5	413	1	NCAI_HNV
37	53	27.9	604	1	VE1_BPV2
38	53	27.9	605	1	VE1_BPV1
39	45	23.7	818	1	CDBI_HUMAN
40	43	22.6	350	1	V001_DROME
41	42	22.1	320	1	GSHB_BUCAT
42	42	22.1	473	1	AM13_MYCTU
43	42	22.1	473	1	FP2_MYCTA
44	42	22.1	484	1	SLR2_YEAST
45	42	22.1	1275	1	RFBC_MYXCA

ALIGNMENTS

RESULT 1	ID	FA7_BOVIN	STANDARD;	PRT;	407 AA.
AC	P22457;				
DT	01-AUG-1991 (Rel. 19, Last sequence update)				
DT	01-AUG-1991 (Rel. 19, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Coagulation factor VII (BC 3.4.21.21) (Serum prothrombin conversion accelerator).				
DE	accelerator).				
GN	F7.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OX	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=69008362; PubMed=3049594;				
RA	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,				
RA	Iwanaga S.;				
RT	"Bovine factor VII. Its purification and complete amino acid				
RT	sequence.";				
RL	J. Biol. Chem. 263:14868-14877(1988).				
RN	[2]				
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.				
RX	MEDLINE=91344709; PubMed=2129367;				
RA	Iwanaga S., Nishimura H., Kawabata S., Kisei W., Hase S., Ikenaka T.;				
RT	"A new trisaccharide sugar chain linked to a serine residue in the				
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";				
RL	Adv. Exp. Med. Biol. 281:121-131(1990).				
CC	- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS				
CC	CONVERTED TO FACTOR VIIA BY FACTOR XA. FACTOR XIA, FACTOR IXA, OR				
CC	THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR				
CC	AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA				
CC	BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO				
CC	FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.				
CC	- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -Ile bond in factor X to				
CC	form factor Xa.				
CC	- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED				
CC	BY A DISULFIDE BOND.				
CC	- TISSUE SPECIFICITY: PLASMA.				
CC	- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME				
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND				
CC	CALCIUM.				
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.				
CC	- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.				
DR	PIR; A31979; A31979.				
DR	HSSP; P08709; 1BF9.				

DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_Like; 1.
 DR SMART; SM00020; GLA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPsin DOM; 1.
 DR PROSITE; PS00134; TRYPsin HIS; 1.
 DR PROSITE; PS00135; TRYPsin SER; 1.
 KM Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KM liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KM EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 39 POTENTIAL.
 FT CHAIN 40 191 FACTOR VII LIGHT CHAIN.
 FT CHAIN 192 444 FACTOR VII HEAVY CHAIN.
 FT DOMAIN 45 74 GLA-RICH.
 FT DOMAIN 85 121 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 126 167 EGF-LIKE 2.
 FT DOMAIN 192 444 SERINE PROTEASE.
 FT SITE 191 192 CLEAVAGE (BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN) (BY SIMILARITY).
 FT ACT_SITE 232 232 BY SIMILARITY.
 FT ACT_SITE 281 281 BY SIMILARITY.
 FT ACT_SITE 383 383 BY SIMILARITY.
 FT BINDING 377 377 SUBSTRATE (BY SIMILARITY).
 FT DISULFID 56 61 BY SIMILARITY.
 FT DISULFID 89 100 BY SIMILARITY.
 FT DISULFID 94 109 BY SIMILARITY.
 FT DISULFID 111 120 BY SIMILARITY.
 FT DISULFID 130 141 BY SIMILARITY.
 FT DISULFID 137 151 BY SIMILARITY.
 FT DISULFID 153 166 BY SIMILARITY.
 FT DISULFID 174 301 BY SIMILARITY.
 FT DISULFID 198 203 BY SIMILARITY.
 FT DISULFID 217 233 BY SIMILARITY.
 FT DISULFID 349 368 BY SIMILARITY.
 FT DISULFID 379 407 BY SIMILARITY.
 FT MOD_RES 45 45 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 53 53 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 68 68 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 74 74 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 102 102 HYDROXYLATION (BY SIMILARITY).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 444 AA; 49011 MW; 0481ABCF5427F8 CRC64;

Query Match 68.4%; Score 130; DB 1; Length 444;
 Best Local Similarity 52.3%; Pred. No. 4,9e-16;
 Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

OY 1 ANGFLXLLRNGSLKRXCRXXLCISFXKXEXIFRNXXRRTRQFVSVY 44
 DB 40 ANSFLLELRPGSLRECKEELCSFEAREVQSTERTKQFWITY 83

RESULT 3
 PAF HUMAN STANDARD; PRT; 466 AA.
 AC P08709; Q14339;
 DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 DE conversion accelerator) (Eptacog alfa).
 GN F7.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86205965; PubMed=3486420;
 RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
 RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
 RA Davie E.W.;
 RT "Characterization of a cDNA coding for human factor VII";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87260948; PubMed=3037537;
 RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
 RA Hagen F.S., Murray M.J.;
 RT "Nucleotide sequence of the gene coding for human factor VII, a
 RT vitamin K-dependent protein participating in blood coagulation";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
 RA Rieder W.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=8908153; PubMed=3264725;
 RA Talm L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
 RA Pedersen A.H., Hedner U.;
 RT "Amino acid sequence and posttranslational modifications of human
 RT factor VIIa from plasma and transfected baby hamster kidney cells";
 RL Biochemistry 27:7785-7793(1988).
 RN [5]
 RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
 RX MEDLINE=91250411; PubMed=1904059;
 RA Bjorn S., Foster D.C., Thim L., Woberg F.C., Christensen M.,
 RA Komiyama Y., Pedersen A.H., Kistiel W.;
 RT "Human plasma and recombinant factor VII. Characterization of O-
 RT glycosylations at serine residues 52 and 60 and effects of site-
 RT directed mutagenesis of serine 52 to alanine";
 RL J. Biol. Chem. 266:11051-11057(1991).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=9062160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [7]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903;
 RA Banner D.W., P'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kitchener D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor";
 RL Nature 380:41-46(1996).

[9] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RP MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 inhibited with a Bp1 mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950;
 RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.W., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 molecule with reduced activity isolated from a clinically unaffected
 male.";
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patrachini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casenato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patrachini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamaya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Fellen A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 polymorphism (SSCP) analysis in five dysfunctional variants of
 coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94264305; PubMed=8204879;
 RA Chaign S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Caecaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RP VARIANT MET HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Met: homozygous asymptomatic type I deficiency caused by
 an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 catalytic domain.";

RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arfink A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [19]
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8893260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Koroetlshavsky M.,
 RA Zaitov R., Seligson U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PMM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -1- PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match 64.2%; Score 122; DB 1; Length 466;
 Best Local Similarity 52.3%; Pred. No. 1,5e-14; Indels 0; Gaps 0;
 Matches 23; Conservative 5; Mismatches 16;

QY 1 ANGFLXLRLNGSLXRXCRXXLCSPFXAEXIFRNXXRTQFNVSY 44
 DB 61 ANAFLEELRPSLRECKEEOCSFEAREIRFKDAERTLTFWISY 104

RESULT 4
 TMG1_HUMAN STANDARD; PRT; 218 AA.
 AC 014668;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
 DE rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
 DE 1).
 GN PRG1 OR TMG1 OR PRGPI.
 OS Homo sapiens (Human).


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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_HIS; 1.
DR PROSITE; PS00134; TRYPSIN_SER; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 33
FT PROPEP 34 41
FT CHAIN 42 196
FT CHAIN 199 461
FT PEPTIDE 199 212
FT SITE 212 213
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 213 461
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 253 253
FT ACT_SITE 299 299
FT ACT_SITE 402 402
FT DISULFID 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 319
FT DISULFID 238 254
FT DISULFID 373 387
FT DISULFID 398 426
FT CARBOHYD 214 214
FT CARBOHYD 290 290
FT CARBOHYD 355 355
FT CARBOHYD 328 328
FT CONFLICT 393 393
FT CONFLICT 393 393
SQ SEQUENCE 461 AA; 51945 MW; 53FAAD0858194D6E CRC64;

Query Match 56.8%; Score 108; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 5,4e-12;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

```

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DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=92329550; PubMed=1627650.
RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
RT "The cDNA cloning and mRNA expression of rat protein C.";
RL Biochim. Biophys. Acta 1131:329-332(1992).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X64336; CAA45617.1; -.
DR PIR; S18994; S18994.
DR PIR; S24312; S24312.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin_1.
DR Pfam; PF00594; gla_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

```

DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 32
 FT PROPEP 33 41
 FT CHAIN 42 196
 FT PEPTIDE 199 461
 FT SITE 212 213
 FT DOMAIN 135 175
 FT DOMAIN 213 461
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 254 254
 FT ACT_SITE 300 300
 FT ACT_SITE 402 402
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 320
 FT DISULFID 239 255
 FT DISULFID 373 387
 FT DISULFID 398 426
 FT CARBOHYD 215 215
 FT CARBOHYD 291 291
 FT CARBOHYD 355 355
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF9364EDACD5 CRC64;

Query Match 56.3%; Score 107; DB 1; Length 461;
 Best local Similarity 45.5%; Pred. No. 8.3e-12;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXLLNGSLKRXCRXXLCGXXAEXIFRXKXRRPQVSVY 44
 DB 42 ANSFLEVRAGSLERECMEBICDFEEAOEIFQVNEVDLAFWIKY 85

RESULT 7
 ID_FAT_MOUSE STANDARD; PRT; 446 AA.
 AC P70375;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
 GN F7 OR CF7.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:97127167; PubMed:8972017;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood
 coagulation factor VII gene."
 RL Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U66079; AAC3796.1; -.
 DR HSSP; P08709; 1BP9.
 DR MEROPS; S01.215; -.
 DR MGD; MGI:109325; F7.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VltK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00584; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 24
 FT PROPEP 25 41
 FT CHAIN 42 193
 FT CHAIN 194 446
 FT DOMAIN 47 76
 FT DOMAIN 194 446
 FT DOMAIN 47 76

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FT DOMAIN 87 123 EGF-LINE 1, CALCTUM-BINDING (POTENTIAL).
FT DOMAIN 128 169 EGF-LINE 2,
FT DOMAIN 194 446 SERINE PROTEASE.
FT SITE 193 194 CLEAVAGE (BY FACTOR IXA, FACTOR XIIA,
  FACTOR IXA, OR THROMBIN) (BY SIMILARITY).
FT ACT_SITE 234 234 BY SIMILARITY.
FT ACT_SITE 283 283 BY SIMILARITY.
FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 96 111 BY SIMILARITY.
FT DISULFID 113 122 BY SIMILARITY.
FT DISULFID 132 143 BY SIMILARITY.
FT DISULFID 139 153 BY SIMILARITY.
FT DISULFID 155 168 BY SIMILARITY.
FT DISULFID 176 303 BY SIMILARITY.
FT DISULFID 200 205 BY SIMILARITY.
FT DISULFID 219 235 BY SIMILARITY.
FT DISULFID 351 370 BY SIMILARITY.
FT DISULFID 381 409 BY SIMILARITY.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 104 104 HYDROXYLATION (BY SIMILARITY).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 446 AA; 50276 MM; 2512E44A5C8C96E CRC64;

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Query Match 55.3%; Score 105; DB 1; Length 446;
Best Local Similarity 47.7%; Pred. No. 1.9e-11;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

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Qy 1 ANGFLXLRNGSLRXCRXLCSPFXAEXIFRNXXRTQFWVSY 44
Db 42 ANSLLEELPQSLERECNEBQCSEBARIETFSPEPTKQFWIV 85

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RESULT 8
TMG3_HUMAN STANDARD; PRT; 231 AA.
AC Q9BZD7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=spinal cord;
RA MEDLINE=2117044; PubMed=1171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
  proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Glu residues are produced after subsequent posttranslational
  modifications of glutamic acid by a vitamin K-dependent gamma-
  carboxylase.
CC -----
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DR EMBL; AF226350; AA00955.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
  PROTEIN 3.
FT DOMAIN 20 78 EXTRACELLULAR (POTENTIAL).
FT TRANSME 79 101 POTENTIAL.
FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25848 MM; 8A37E48490D81 CRC64;

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Query Match 53.7%; Score 102; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 3.4e-11;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

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Qy 1 ANGFLXLRNGSLRXCRXLCSPFXAEXIFRNXXRTQFWVSY 44
Db 20 ANFLLELRQGTIERECMEICISIEYKVEVENKEKTFPKGY 63

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RESULT 9
PRTC_PIG STANDARD; PRT; 459 AA.
AC Q9GLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
  factor XIV).
GN PROC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=liver;
RX MEDLINE=21121490; PubMed=11229814;
RX Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
  Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
  protein modeling of membrane binding sites and comparative anatomy of
  domains.";
RL Cell. Mol. Life Sci. 58:148-159(2001).
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
  regulates blood coagulation by inactivating factors Va and VIIIa
  in the presence of calcium ions and phospholipide.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
  and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
  into a light chain and a heavy chain held together by a disulfide
  bond. The enzyme is then activated by thrombin, which cleaves a
  tetradecapeptide from the amino end of the heavy chain; this
  reaction, which occurs at the surface of endothelial cells, is
  strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
  residues allows the modified protein to bind calcium.
CC -----

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CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the
 CC thrombin-thrombomodulin complex.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: AF191307; MAG28380.1; -.
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin; 1.
 DR Pfam: PF00594; gla; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00001; EGF-like; 2.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYP_Spc; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_Ca; 1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KM Blood coagulation; Glycoprotein; Serine protease;
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT STGNL 1 18
 FT PROPP 19 41
 FT CHAIN 42 459
 FT CHAIN 42 196
 FT CHAIN 199 459
 FT CHAIN 199 213
 FT SITE 213 214
 FT SITE 213 214
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 214 459
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 67 67

FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 255 255
 FT ACT_SITE 301 301
 FT ACT_SITE 400 400
 FT ACT_SITE 400 400
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 321
 FT DISULFID 240 256
 FT DISULFID 371 385
 FT DISULFID 396 424
 FT CARBOHYD 138 138
 FT CARBOHYD 292 292
 FT CARBOHYD 353 353
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 53.2%; Score 101; DB 1; Length 459;
 Best Local Similarity 45.5%; Pred. No. 1e-10; Mismatches 22; Indels 0; Gaps 0;
 Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;
 QY 1 ANGFLXXLRNGSLRXRCRXLCSPFXAEXIFRNXXRTQGWVS 44
 Db 42 ANSFLELRPSLSIERCKEFTCDFEAREIFONTENTMAFWMSKY 85
 RESULT 10
 ID PRTC_BOVIN STANDARD; PRT; 456 AA.
 AC P00745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
 DE (Autoproteolytic cleavage of protein C precursor (BC 3.4.21.69)
 DE factor XIV) (Fragment).
 GN PROC.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85014826; PubMed=6091100;
 RA Long G.L., Balgaje R.M., McGillivray R.T.A.;
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
 RN [2]
 RP SEQUENCE OF 40-194
 RX MEDLINE=83007325; PubMed=6896876;
 RA Fernlund P., Stenflo J.;
 RT "Amino acid sequence of the light chain of bovine protein C";
 RL J. Biol. Chem. 257:12170-12179(1982).
 RN [3]
 RP REVISION TO 110.
 RX MEDLINE=83169769; PubMed=6572939;
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
 RN [4]
 RP SEQUENCE OF 197-456.
 RX MEDLINE=83007326; PubMed=6896877;
 RA Stenflo J., Fernlund P.;
 RT "Amino acid sequence of the heavy chain of bovine protein C";
 RL J. Biol. Chem. 257:12180-12190(1982).

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RN [5]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Esmon N.L., Debault L.E., Esmon C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
  domainless protein C.";
RL J. Biol. Chem. 258:5548-5553 (1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmon N.L., Lau T.M., Esmon C.T.;
RT "Structural changes required for activation of protein C are induced
  by Ca2+ binding to a high affinity site that does not contain gamma-
  carboxyglutamic acid.";
RL J. Biol. Chem. 258:5554-5560 (1983).
CC -1 FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
  REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
  IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1 CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
  and VIIIA.
CC -1 SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
  INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
  BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
  TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN: THIS
  REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
  STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1 TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1 PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
  GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1 MISCELLANEOUS: CALCIUM ALSO BINDS WITH STRONGER AFFINITY TO
  ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
  SITE IS NECESSARY FOR THE RECOGNITION OF THE
  THROMBIN-THROMBOMODULIN COMPLEX.
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1 SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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CC
DR EMBL, K02435; AAA30685.1; -.
DR PIR, A00928; KXBO.
DR HSSP, P04070; 1PCU.
DR MEROPS, S01.218; -.
DR InterPro, IPR000152; Asx_hydroxyl.
DR InterPro, IPR000561; EGF-like.
DR InterPro, IPR001881; EGF_CA.
DR InterPro, IPR001254; Ser_protease_Try.
DR InterPro, IPR000294; VitK_dep_GLA.
DR Pfam, PF00008; EGF_2.
DR Pfam, PF00089; trypsin; 1.
DR Pfam, PF00594; gla; 1.
DR SMART, SM00181; EGF_2.
DR SMART, SM00069; GLA; 1.
DR SMART, SM00020; Tryp_Spc; 1.
DR PROSITE, PS00010; ASX_HYDROXYL; 1.
DR PROSITE, PS00022; EGF_1; 1.
DR PROSITE, PS01186; EGF_2; 2.
DR PROSITE, PS01187; EGF_CA; 1.
DR PROSITE, PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE, PS50240; TRYPSIN_DOM; 1.
DR PROSITE, PS500134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE, PS500135; TRYPSIN_SER; 1.
KW Blood coagulation, Glycoprotein, Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT NON_TER 1 1
FT SIGNAL <1 29
FT PROPEP 30 39

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FT	CHAIN	40	194	PROTEIN C LIGHT CHAIN.
FT	CHAIN	197	456	PROTEIN C HEAVY CHAIN.
FT	PEPTIDE	197	210	ACTIVATION PEPTIDE.
FT	DOMAIN	94	129	EGF-LIKE 1.
FT	DOMAIN	133	173	EGF-LIKE 2.
FT	DOMAIN	211	456	SERINE PROTEASE.
FT	MOD_RES	45	45	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	46	46	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	53	53	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	58	58	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	59	59	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	62	62	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	64	64	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	65	65	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	68	68	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	74	74	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	110	110	HYDROXYLATION.
FT	ACT_SITE	252	252	CHARGE RELAY SYSTEM.
FT	ACT_SITE	298	298	CHARGE RELAY SYSTEM.
FT	ACT_SITE	397	397	CHARGE RELAY SYSTEM.
FT	DISULFID	56	61	BY SIMILARITY.
FT	DISULFID	89	103	BY SIMILARITY.
FT	DISULFID	98	103	BY SIMILARITY.
FT	DISULFID	102	117	BY SIMILARITY.
FT	DISULFID	119	128	BY SIMILARITY.
FT	DISULFID	137	148	BY SIMILARITY.
FT	DISULFID	144	157	BY SIMILARITY.
FT	DISULFID	159	172	BY SIMILARITY.
FT	DISULFID	230	318	BY SIMILARITY.
FT	DISULFID	237	253	INTERCHAIN.
FT	DISULFID	368	382	
FT	DISULFID	393	421	
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	289	289	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	350	350	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	366	366	N-LINKED (GLCNAC. . .)
FT	VARIANT	82	82	F -> K.
FT	CONFLICT	455	456	VP -> PV (IN REF. 4).
FT	SEQUENCE	456 AA;	51407 MM;	CAAF6833F894C209 CRC64;
Qy	Query Match	50.5%;	Score 96;	DB 1;
Db	Best Local Similarity	43.2%;	Pred. No. 8.4e-10;	Length 456;
	Matches 19;	Conservative 4;	Mismatches 21;	Indels 0;
	Gaps 0;			
1	ANGFLXLRNGSLRXCRXXLCSPFXAEIIFRNXXRTQFWWSY	44		
40	ANSFLELRPGNVERECSEVCEFEENAEIPONTDTNAFMSFY	83		
FA10_HUMAN	STANDARD;	PRT;	488 AA.	
AC	P00742; Q14340;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).			
GN	P10.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91216473; PubMed=1902434;			
RA	Messier T.L., Piltman D.D., Long G.L., Kaufman R.J., Church W.R.;			
RT	"Cloning and expression in COS-1 cells of a full-length cDNA encoding			
RL	human coagulation factor X.";			
RN	Gene 99:291-294 (1991).			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87026600; PubMed=3768336;			

RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RT protein C."; 25:5098-5102(1986).
 RL Biochem J., 25:5098-5102(1986).
 RN (3)
 RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillyray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RT blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN (4)
 RP SEQUENCE OF 19-488 FROM N.A.
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";
 RL Gene 41:311-314(1986).
 RN (5)
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kistiel W., Sasaagawa T., Howald W.N.,
 RA Kwa B.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884(1983).
 RN (6)
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 RN (7)
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN (8)
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanham K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519(1989).
 RN (9)
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tullinsky A., Park C.H., Bode W.,
 RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966(1993).
 RN (10)
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.

CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; K03194; AAA52490.1; -;
 DR EMBL; M57285; AAA52421.1; -;
 DR EMBL; L29433; AAA52764.1; -;
 DR EMBL; L00390; AAA52764.1; JOINED.
 DR EMBL; L00391; AAA52764.1; JOINED.
 DR EMBL; L00392; AAA52764.1; JOINED.
 DR EMBL; L00393; AAA52764.1; JOINED.
 DR EMBL; L00394; AAA52764.1; JOINED.
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 DR EMBL; L00396; AAA52764.1; JOINED.
 DR EMBL; M22613; AAA51984.1; -;
 DR EMBL; K01886; AAA52486.1; -;
 DR EMBL; M33297; AAA52636.1; -;
 DR PIR; A00924; EXHU.
 DR PIR; A25853; A25853.
 DR PIR; A24478; A24478.
 DR PDB; 1HCG; 08-MAY-95.
 DR PDB; 1FXV; 29-OCT-97.
 DR PDB; 1FXV; 17-JUN-98.
 DR PDB; 1XKA; 23-MAR-99.
 DR PDB; 1XKB; 23-MAR-99.
 DR MEROPS; S01.216; -;
 DR GlycoSuiteDB; P00742; -;
 DR Genew; HGNC:3528; F10.
 DR MIM; 134530; -;
 DR MIM; 227600; -;
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF-like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS0186; EGF_2; 2.
 DR PROSITE; PS0187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR GlycoProtein; Hydroxylase; Serine protease; Plasma; Blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KM Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 FT SIGNAL 1 31 POTENTIAL.

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FT CHAIN        41      179
FT CHAIN       183      488
FT PROPEP      183      234
FT CHAIN       235      488
FT DOMAIN      86      122
FT DOMAIN     125      165
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FT MOD_RES     47      47
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FT MOD_RES     69      69
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FT MOD_RES     79      79
FT MOD_RES    103      103
FT CARBOHYD    199      199
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FT DISULFID    112      121
FT DISULFID    129      140

                    50.0%; Score 95; DB 1; Length 488;
Query March      Best Local Similarity 36.4%; Pred. 1.4e-09;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXLRLNGSLKRXCRXXLCSPFYXAEKXIFRNXXRTQFVWSY 44
Db 41 ANSFLEMKKKGHLRECHBETCSYEAREVFEFSDKTNBFWNKY 84

RESULT 12
PRTC_HUMAN STANDARD; PRT; 461 AA.
AC P04070; Q16001; Q15190; Q15189;
DC 01-NOV-1986 (Rel. 03, Created);
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Antiproteolytic IIR) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85270390; PubMed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RA "The structure and evolution of a 461 amino acid human protein C
RA precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs.";
RL Nucleic Acids Res. 13:5233-5247(1985).

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RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120978; PubMed=3511471;
RA Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RT "Evolution and organization of the human protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=84272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN [6]
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Miletich J.P., Broze G.J., Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translocation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN [7]
RP HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN [8]
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Eamon C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN [10]
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN [11]
RP VARIANT CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Haasan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN [12]
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=90098906; PubMed=2602169;
RA Grundy C.B., Chitcliffe A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGC-->TGC) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN [13]

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RP VARIANT CVS-272.
 RX MEDLINE=91329836; PubMed=1868249;
 RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
 RT "The spectrum of genetic defects in a panel of 40 Dutch families with
 RT symptomatic protein C deficiency type I: heterogeneity and founder
 RT effects.";
 RL Blood 78:890-894(1991).
 RN [14]
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
 RX MEDLINE=92190481; PubMed=1347706;
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
 RA Ralville I.R., Long G.L.;
 RT "Protein C Vermont: symptomatic type II protein C deficiency
 RT associated with two GLA domain mutations.";
 RL Blood 79:1456-1465(1992).
 RN [15]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RT a missense mutation.";
 RL Blood 80:126-133(1992).
 RN [16]
 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RT causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [17]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schutman S., Tengborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RT gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [18]
 RP VARIANT GLN-220.
 RX MEDLINE=93250852; PubMed=1301959;
 RA Gaudillie S., Vidau M., Atach M., Albenc-Gelas M., Fischer A.M.,
 RA Gouault-Heilman M., Toulon P., Fiesinger J.N., Goossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
 RT deficiency: characterization by denaturing gradient gel
 RT electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [19]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yamamoto K., Matsushita T., Sugitara I., Takamatsu J., Iwasaaki E.,
 RA Mada H., Deguchi K., Shirakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 RT mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
 RN [20]
 RP VARIANTS TRP-38; CVS-42; HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE=93313192; PubMed=8324221;
 RA Gaudillie S., Albenc-Gelas M., Gaussem P., Aillaud M.-F., Dupuy E.,
 RA Juhán-Vague I., Atach M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RT gene in patients presenting with defective protein C anticoagulant
 RT activity.";
 RL Blood 82:159-168(1993).
 RN [21]
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND
 RP V-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RT with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [22]

RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Millar D.S., Grundy C.B., Bignelli P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A GLA domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 RT causing type 2 protein C deficiency and recurrent venous
 RT thrombosis.";
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [23]
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
 RX MEDLINE=94122329; PubMed=8292730;
 RA Tsay W., Greengard U.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
 RA Koepfer M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with
 RT symptomatic type I protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).
 RN [24]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Patrachini P., Gemmati D., Castaman G., Rodeghiero F.,
 RA Macey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RL Br. J. Haematol. 84:285-289(1993).
 RN [25]
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
 Query Match 49.5%; Score 94; DB 1; Length 461;
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 Db 43 ANSFLELRHSLSRECIETCFERAKETIFQVVDTLAFW 83
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 AC 019065;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN P10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97256311; PubMed=9101642;
 RA Pendurthi U.R., Anderson K.D., James H.L.;
 RT "Characterization of a full-length cDNA for rabbit factor X.";
 RL Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
 CC (BY SIMILARITY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

```

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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CC -----
DR EMBL: AF003200; AAB62542.1; -.
DR HSSP: P00742; IHCG.
DR MEROS; S01.216; -.
DR InterPro: IPR000152; Aax_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
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DR PRINTS; PR00001; GLABLOOD.
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DR SMART; SM00069; GLA; 1.
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DR PROSITE; PS01187; EGF_CA; 1.
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DR PROSITE; PS00133; TRYPSIN_SER; 1.
DR GlycoProtein; Hydroxylase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat.
FT SIGNAL 1 20
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FT SEQUENCE 430 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;

Query Match 48.9%; Score 93; DB 1; Length 490;
Best Local Similarity 38.6%; Pred. No. 3.2e-09;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGSLKRXCRXXLCSPFXAXEIRPNXXRTQFNVS 44
Db 41 ANSFLEELKGNLRECEWNCSEYEALVEFDEKRTNEFNKKY 84

RESULT 14
FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUN-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RX MEDLINE=84247315; PubMed=630671;
RA Fung M.R., Campbell R.M., McGilivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence."
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor)."
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens."
RL Biochem. Biophys. Res. Commun. 115:8-14(1993).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain."

```

RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 RN (5)
 RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moiety in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN (6)
 RP ACTIVE SITE
 RX MEDLINE=73053314; PubMed=4264286;
 RA Titali K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 RT "Bovine factor X Ia (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 RL Biochemistry 11:4899-4903(1972).
 RN (7)
 RP PROCESSING
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Titali K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN (8)
 RP CALCIUM-BINDING DATA
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN (9)
 RP SULFATION
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN (10)
 RP STRUCTURE BY NMR OF 85-126
 RX MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
 RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN (11)
 RP STRUCTURE BY NMR OF 85-126
 RX MEDLINE=92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Teleman O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN (12)
 RP STRUCTURE BY NMR OF 85-126
 RX MEDLINE=92406922; PubMed=1527084;
 RA Selander-Sunnehaugen M., Ullner M., Persson E., Teleman O.,
 RA Stenflo J., Drakenberg T.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
 RL J. Biol. Chem. 267:19642-19649(1992).
 RN (13)
 RP STRUCTURE BY NMR OF 41-126
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Trewhella J.;
 RT "The relative orientation of Gla and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";

RL Biochemistry 35:11547-11559(1996).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; X00673; CAA25286.1; -.
 CC PIR; A00925; EXBO.
 CC PDB; 1AEO; 31-JAN-94.
 CC PDB; 1CCF; 31-MAY-94.
 CC PDB; 1MHE; 15-MAY-97.
 CC PDB; 1MHP; 15-MAY-97.
 CC MEROPS; S01.216; -.
 CC DR GlycosultedB; P00743; -.
 CC DR InterPro; IPR000152; Asx hydroxyl.
 CC DR InterPro; IPR001314; Chymotrypsin.
 CC DR InterPro; IPR000561; EGF-like.
 CC DR InterPro; IPR007742; EGF_2.
 CC DR InterPro; IPR001881; EGF_Ca.
 CC DR InterPro; IPR002383; GLA_blood.
 CC DR InterPro; IPR001254; Ser protease_Try.
 CC DR InterPro; IPR000294; VitK_dep_GLA.
 CC DR Pfam; PF00008; EGF_2.
 CC DR Pfam; PF00089; trypsin; 1.
 CC DR Pfam; PF00594; gla; 1.
 CC DR PRINTS; PR00722; CHYMOTRYPSIN.
 CC DR PRINTS; PR00001; GLABLOOD.
 CC DR SMART; SM00179; EGF_CA; 1.
 CC DR SMART; SM00001; EGF_like; 1.
 CC DR SMART; SM00069; GLA; 1.
 CC DR SMART; SM00020; TRYP_SPC; 1.
 CC DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC DR PROSITE; PS00022; EGF_1; 1.
 CC DR PROSITE; PS01186; EGF_2; 2.
 CC DR PROSITE; PS01187; EGF_CA; 1.
 CC DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 CC DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC DR PROSITE; PS00135; TRYPSIN_SER; 1.
 CC KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 CC FT SIGNAL 1 23
 CC FT PROPEP 24 40
 CC FT CHAIN 41 180
 CC FT CHAIN 183 492
 CC FT PROPEP 183 233
 CC FT CHAIN 234 492
 CC FT PROPEP 476 492
 CC DOMAIN 86 122
 CC
 CC FACTOR X LIGHT CHAIN.
 CC FACTOR X HEAVY CHAIN.
 CC ACTIVATION PEPTIDE.
 CC ACTIVATED FACTOR XA, HEAVY CHAIN.
 CC MAY BE REMOVED BUT IS NOT NECESSARY FOR
 CC ACTIVATION.
 CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

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FT DOMAIN 125 165 EGF-LIKE 2.
FT ACT SITE 234 492 SERINE PROTEASE.
FT ACT SITE 275 275 CHARGE RELAY SYSTEM.
FT ACT SITE 321 321 CHARGE RELAY SYSTEM.
FT ACT SITE 418 418 CHARGE RELAY SYSTEM.
FT MOD RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

Query Match 47.4%; Score 90; DB 1; Length 492;
Best Local Similarity 36.4%; Pred. No. 1,le-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY '1 ANGFLXXLRNGSLXRCXKXLCSPFXAXEIRNXXRTQGVVSY 44
41 ANSFLXEVKQGNLRECELEACSLSEAREVEDEADQDFWFSKY 84

RESULT 15
FA9_BOVIN STANDARD; PRT; 416 AA.
AC P00741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor IX (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=80056619; PubMed=291916;
RA Katayama K., Ericsson L.H., Enfield D.L., Walsh K.A., Neurath H.,
RA Davie E.W., Tiltam K.;
RT "Comparison of amino acid sequence of bovine Coagulation Factor IX
RT (Christmas Factor) with that of other vitamin K-dependent plasma
RT proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4990-4994(1979).
RN [2]
RP REVISION TO 64.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [3]
RP SEQUENCE OF 51-111 FROM N.A.
RX MEDLINE=82272386; PubMed=6287289;
RA Choo K.H., Gould K.G., Rees D.J.G., Brownlee G.G.;
RT "Molecular cloning of the gene for human anti-haemophilic factor IX.";
RL Nature 299:178-180(1982).
RN [4]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA Miyata T., Iwanaga S., Takao T., Shimomichi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine
RT blood coagulation factors VII and IX.";
RL J. Biochem. 104:867-868(1988).
RN [5]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
```

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RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=90130422; PubMed=2105311;
RA Hase S., Nishimura H., Kawabata S., Iwanaga S., Ikenaka T.;
RT "The structure of (xylose)2glucose-O-serine 53 found in the first
RT epidermal growth factor-like domain of bovine blood clotting factor
RT IX.";
RL J. Biol. Chem. 265:1858-1861(1990).
CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
CC IONS. PHOSPHOLIPIDS, AND FACTOR VIIIa.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIa, WHICH EXCISES THE
CC ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2
CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID
CC (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE,
CC BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; J00007; AAA30520.1; -.
CC PIR; A00923; KFB0.
CC HSSP; P00740; ICFH.
CC MEROPS; S01.214; -.
CC GlycoSiteDB; P00741; -.
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR000742; EGF 2.
CC InterPro; IPR001881; EGF Ca.
CC InterPro; IPR001438; EGF II.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR001254; Ser_protease_Try.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00089; trypsin; 1.
CC Pfam; PF00594; gla_1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00010; EGFBL00D.
CC PRINTS; PR00001; GLABLOOD.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00001; EGF_like; 1.
CC SMART; SM00069; GLA; 1.
CC SMART; SM00020; Tryp_Sec; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF 2; 2.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00011; TRY_CARBOXYLATION; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Plasma; Serine protease; Calcium-binding;
CC Hemolysis; Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid;
CC Hemophilic; Hydroxylation; Zymogen; EGF-like domain.
CC CHAIN 1 146 FACTOR IXA (ACTIVE FORM) LIGHT CHAIN.
CC PROPEP 147 181 ACTIVATION PEPTIDE.
CC CHAIN 182 416 FACTOR IXA (ACTIVE FORM) HEAVY CHAIN.
CC DOMAIN 47 83 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
CC DOMAIN 84 125 EGF-LIKE 2.
CC DOMAIN 182 416 SERINE PROTEASE.
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```
FT SITE 146 147 CLEAVAGE (BY FACTOR X1A) .
FT SITE 181 182 CLEAVAGE (BY FACTOR X1A) .
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 8 8 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 15 15 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 17 17 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 21 21 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 27 27 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 30 30 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 33 33 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 36 36 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 40 40 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 HYDROXYLATION.
FT MOD_RES 64 64 BY SIMILARITY.
FT DISULFID 18 23 BY SIMILARITY.
FT DISULFID 51 62 BY SIMILARITY.
FT DISULFID 56 71 BY SIMILARITY.
FT DISULFID 73 82 BY SIMILARITY.
FT DISULFID 88 99 BY SIMILARITY.
FT DISULFID 95 109 BY SIMILARITY.
FT DISULFID 111 124 BY SIMILARITY.
FT CARBOHYD 53 53 O-LINKED (GLC. . .).
FT CARBOHYD 53 53 /FTID=CAR_000008.
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .).
FT ACT_SITE 222 222 CHARGE RELAY SYSTEM.
FT ACT_SITE 270 270 CHARGE RELAY SYSTEM.
FT ACT_SITE 366 366 CHARGE RELAY SYSTEM.
FT VARIANT 64 64 D -> T (IN REF. 1).
SQ SEQUENCE 416 AA; 46785 MW; 34A7DFB916330662 CRC64;
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Query Match 46.3%; Score 88; DB 1; Length 416;
Best Local Similarity 37.2%; Pred. No. 2.2e-08;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

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OY 2 NGFLXKLUNGSLRXCRXXLCSFYKXAEIIFRNXXRTROFWVSY 44
DB 3 SGKLEEFVRGNLBERECKEKCSFEAREVPEENTKTEFWKQY 45
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Search completed: March 19, 2003, 14:52:56
Job time : 6.625 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10ASN28GLU_4
Sequence: 1 ANGFLXLLXNGSLXRCRX...XXAEXIFRNXXRTQFWSEY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_rhodent:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	64.2	701	4	Q96P08
2	108	56.8	460	11	Q91WN8
3	105	55.3	446	11	Q61109
4	102	53.7	460	11	Q99PC6
5	99	52.1	456	6	Q9TTP0
6	95	50.0	482	11	Q63207
7	92	48.4	481	11	Q54740
8	92	48.4	481	11	Q99L32
9	92	48.4	481	11	Q88947
10	88	46.3	456	6	Q95ME8
11	88	46.3	456	6	Q14316
12	88	46.3	461	6	Q95ND7
13	88	46.3	461	6	Q95ND6
14	88	46.3	461	6	Q95ND9
15	81	42.6	138	6	Q28994
16	81	42.6	433	13	Q90YK1

17	77	40.5	100	4	Q15253	Q15253 homo sapien
18	77	40.5	608	13	Q9PTW7	Q9PTW7 struthio ca
19	75	39.5	648	8	Q29094	Q29094 sus scrofa
20	74	38.9	399	11	Q9COW3	Q9COW3 mus musculus
21	71.5	37.6	542	5	Q8T613	Q8T613 halocynthia
22	70	36.8	179	4	Q8TAS3	Q8TAS3 homo sapien
23	70	36.8	198	11	Q8R182	Q8R182 mus musculus
24	70	36.8	650	4	Q9NSD0	Q9NSD0 homo sapien
25	70	36.8	650	4	Q16519	Q16519 homo sapien
26	65	34.2	607	13	Q91001	Q91001 gallus gall
27	59	31.1	678	4	Q14393	Q14393 homo sapien
28	58	30.5	673	11	Q61592	Q61592 mus musculus
29	58	30.5	674	11	Q9PK57	Q9PK57 mus musculus
30	57	30.0	25	11	Q9QVH6	Q9QVH6 rattus sp.
31	56	29.5	98	13	P82807	P82807 notechis sc
32	56	29.5	674	11	Q63772	Q63772 rattus sp.
33	56	29.5	674	11	Q98S05	Q98S05 gasterosteus
34	53	27.9	472	13	Q98S05	Q98S05 gasterosteus
35	53	27.9	613	13	Q98S06	Q98S06 gasterosteus
36	50.5	26.6	575	10	Q98S07	Q98S07 gasterosteus
37	50.5	26.6	608	10	Q9XF36	Q9XF36 medicago sa
38	49.5	26.1	196	10	Q04284	Q04284 selaginella
39	49.5	26.1	557	10	Q8W4J2	Q8W4J2 arabidopsis
40	49.5	26.1	603	10	Q9LPG7	Q9LPG7 arabidopsis
41	49.5	26.1	606	10	Q95JG9	Q95JG9 arabidopsis
42	49.5	26.1	651	10	Q8S218	Q8S218 oryza sativ
43	49	25.8	1217	5	Q9XV62	Q9XV62 caenorhabdi
44	48.5	25.5	431	10	Q94EY5	Q94EY5 arabidopsis
45	48.5	25.5	492	10	Q9SMJ7	Q9SMJ7 cicer ariet

ALIGNMENTS

RESULT 1
Q96P08 PRELIMINARY; PRT; 701 AA.
ID Q96P08
AC Q96P08
DT 01-DEC-2001 (TEMBREL. 19, Created)
DT 01-DEC-2001 (TEMBREL. 19, Last sequence update)
DT 01-MAR-2002 (TEMBREL. 20, Last annotation update)
DE Factor VII active site mutant Immunocoujugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AAKS8686.1; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00181; EGF_2.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01166; EGF_2; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolyase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94ACCEBA2CC992F CRC64;

Query Match 64.2%; Score 122; DB 4; Length 701;
Best Local Similarity 52.3%; Pred. No. 8.2e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAEXIFRNXXRTROFWVS 44
Db 61 ANAFLELRPGSLERECNEQCSFEAREIFDAERTKLFWISY 104

RESULT 2

ID 091NM8 PRELIMINARY; PRT; 460 AA.
AC 091NM8.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strauberg R;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013896; AAH13896.1; -.
DR MGD; MGI:97771; Proc.

DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_Ca; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolyase; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;

Query Match 56.8%; Score 108; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 2.1e-11;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAEXIFRNXXRTROFWVS 44
Db 42 ANSFLEMRPGSLERECNEICDFEAOEIFQNVEDTLAFWIKY 85

RESULT 3

ID 061109 PRELIMINARY; PRT; 446 AA.
AC 061109.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Coagulation factor VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96276538; PubMed=8701412;
RA Idsogte E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII,"
RT Thomb. Haemost. 75:481-487(1996).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY

CC EMBL; U44795; AAC52570.1; -.
DR HSSP; P08709; IFAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Cystealain.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00659; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;
KM Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BBFDA6870 CRC64;

Query Match 55.3%; Score 105; DB 11; Length 446;
Best Local Similarity 47.7%; Pred. No. 7.3e-11;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRXCRXXLCSPFXAEXIFRNXXRTROFWVS 44
Db 42 ANSLLEELMPGSLERECNEQCSFEAREIFKSPRTQFWIVY 85

RESULT 4

ID 099PC6 PRELIMINARY; PRT; 460 AA.
AC 099PC6.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Anticoagulant protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Kott I.;

RT "Complete sequence of UC72A01.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY
DR EMBL; AF318182; AK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; Piroc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_1ke; 2.
DR SMART; SM00001; EGF_1ke; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KM Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;
Query Match 53.7%; Score 102; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 2,7e-10;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
QY 1 ANGFLXXLRNGSLKRCXXKCSFXAXEIPRNXXRTROFVSVY 44
DB 42 ANSFLBEMRPGSLERECMEIEICDLEAQEIPQNVEDTLAIFWIKY 85
RESULT 5
Q9TTR0 PRELIMINARY; PRT; 456 AA.
AC Q9TTR0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein C precursor.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matie U., Brunberg L.,
RT "Molecular characterization and chromosomal assignment of the canine
protein C gene.";
RL Mamm. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99371952; Pubmed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Breen B.,
RT "Analysis of canine protein C gene polymorphisms.";
RL Anim. Genet. 30:237-238(1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.

DR EMBL; A0001979; CAA05126.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_1ke; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KM Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL 1 42
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;
Query Match 52.1%; Score 99; DB 6; Length 456;
Best Local Similarity 43.2%; Pred. No. 9,5e-10;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
QY 1 ANGFLXXLRNGSLKRCXXKCSFXAXEIPRNXXRTROFVSVY 44
DB 43 ANSFLBEMRPGSLERECMEIEICDLEAQEIPQNVEDTLAIFWIKY 86
RESULT 6
Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; Pubmed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.,
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
DR EMBL; X79807; CAA56202.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; tryptain; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KM Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 02846783954A698 CRC64;

Query Match 50.0%; Score 95; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 5.5e-09;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGSLRXCRXXLCSPFXAXEIPRNXXRTROFWVS 44
Db 41 ANSPFEIRKGNLERECVEICISFEBAFEVFDNKTTEFMNKY 84

RESULT 7

OS4740 PRELIMINARY; PRT; 481 AA.
AC OS4740.
DT 01-JUN-1998 (TRENBLREL. 06, Created)
DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR FA10.
OS Mus musculus (Mouse).
OC Plasmid plusscript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=9845493; PubMed=9783672;
RA Heidemann H.H., Kontermann R.B.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AJ222677; CAA10933.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; tryptain; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KM Repeat; Serine protease; Signal.
FT SIGNAL 1
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702D5E5F9D97AE CRC64;

Query Match 48.4%; Score 92; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 2e-08;
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGSLRXCRXXLCSPFXAXEIPRNXXRTROFWVS 44
Db 41 ANSPFEIRKGNLERECVEICISFEBAFEVFDNKTTEFMNKY 84

RESULT 8

O99L32 PRELIMINARY; PRT; 481 AA.
AC O99L32.
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; BC003877; AAH03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; tryptain; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLUT CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88B96C8A0B7E7F CRC64;
Query Match 48.4%; Score 92; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 2e-08;
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
Qy 1 ANGFLXXLRNGSLKRCXKXLCSPFXAEXIFRNXXRTQFWVSY 44
Db 41 ANSFFEFKKNLERECMEICSEYEVEEIFEDEDKTEKWTYK 84
RESULT 9
ID 088947 PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
DE Coagulation factor X precursor.
F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129SvJ;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of the murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
EMBL; AF087644; AAC36345.1; -;
DR HSSP; AF211347; AAF22980.1; -;
DR HSSP; P00742; IYKA.
DR MEROPS; S01.216; -;
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00017; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLUT CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5E9D271E CRC64;
Query Match 48.4%; Score 92; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 2e-08;
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
Qy 1 ANGFLXXLRNGSLKRCXKXLCSPFXAEXIFRNXXRTQFWVSY 44
Db 41 ANSFFEFKKNLERECMEICSEYEVEEIFEDEDKTEKWTYK 84
RESULT 10
ID 095ME8 PRELIMINARY; PRT; 49 AA.
AC 095ME8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mziara M.N., Amaral E.J.;
RT "Partial sequence of bovine F9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB394598; AAK77556.1; -;
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PROSITE; PS00011; GLUT CARBOXYLATION; UNKNOWN_1.
FT NON TER 1 1
FT NON TER 49 49
SQ SEQUENCE 49 AA; 6023 MW; D15C6D59CCBA4A14 CRC64;
Query Match 46.3%; Score 88; DB 6; Length 49;
Best Local Similarity 37.2%; Pred. No. 1.1e-08;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;
Qy 2 NGFLXXLRNGSLKRCXKXLCSPFXAEXIFRNXXRTQFWVSY 44
Db 6 SGKLEEFVGNLERECMEICSEYEVEEIFEDEDKTEKWTYK 48
RESULT 11
ID 014316 PRELIMINARY; PRT; 456 AA.
AC 014316;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas
DE disease, HAEMOPHILIA B) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
  Brier E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
  TRYPSIN FAMILY.
CC EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; ICFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF_1-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_T1.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Glaf; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
  Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 46.3%; Score 88; DB 4; Length 456;
Best Local Similarity 39.5%; Pred. No. 1e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy 2 NGFLXXLNGSLXRYCRXXLCSEFXAXEIRFXXXRTROFWYSY 44
Db 44 SGLKEPVOGNLERCEMEKCSFEAREVFENTERTEFWKQY 86

RESULT 12
O95ND7 PRELIMINARY; PRT; 461 AA.
AC O95ND7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
  chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.

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DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF_1-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; glaf; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00134; TRYPSIN_SER; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 46.3%; Score 88; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 1e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy 2 NGFLXXLNGSLXRYCRXXLCSEFXAXEIRFXXXRTROFWYSY 44
Db 49 SGLKEPVOGNLERCEMEKCSFEAREVFENTERTEFWKQY 91

RESULT 13
O95ND6 PRELIMINARY; PRT; 461 AA.
AC O95ND6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
  chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; -.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF_1-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; glaf; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

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DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolyase; Serine protease.
 SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 46.3%; Score 88; DB 6; Length 461;
 Best Local Similarity 39.5%; Pred. No. 1e-07;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy 2 NGFLXXLRNGSLKRXCRXXLCSPFXAEXIFRNXXRTRQFWVS 44
 Db 49 GGLLEEFVQGNLRECEMEKCSFEARAEVENTERTTEFWKQY 91

RESULT 14

O9GMD9 PRELIMINARY; PRT; 469 AA.
 AC O9GMD9; 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Coagulation factor X.
 OS Ornithorhynchus anatinus (Duckbill platypus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
 OX NCBI_Taxid=9258;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21015017; PubMed=11132153;
 RA Poorafshar M., Aveskogh M., Munday B., Hellman L.;
 RT "Identification and structural analysis of four serine proteases in a
 RT monotreme, the platypus, Ornithorhynchus anatinus";
 RL Immunogenetics 52:19-28(2000).
 CC -! SIMILARITY. BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPsin FAMILY.
 DR EMBL; AF275654; AAG00453.1; -.
 DR HSSP; P00742; 1XKB.
 DR MEROPS; S01.216; -.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF-like; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease.
 SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match 46.3%; Score 88; DB 6; Length 469;
 Best Local Similarity 34.1%; Pred. No. 1.e-07;

Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;
 Oy 1 ANGFLXXLRNGSLKRXCRXXLCSPFXAEXIFRNXXRTRQFWVS 44
 Db 41 ANSLFELKGNLRECEMEKCSFEARAEVENTERTTEFWKQY 84

RESULT 15
 ID Q28994 PRELIMINARY; PRT; 138 AA.

AC Q28994; 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Mature porcine factor IX (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96003866; PubMed=7568220;
 RA Brandstetter H., Bauer M., Huber R., Lollar P., Bode W.;
 RT "X-ray structure of clotting factor IXa: active site and module
 RT structure related to Xase activity and hemophilia B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9796-9800(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Lollar P.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U51135; AAG6318.1; -.
 DR HSSP; P00740; 1EDM.
 DR InterPro; IPR00152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR001438; EGF-II.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00010; EGFBL00D.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
 FT NON TER 1
 FT NON TER 138
 SQ SEQUENCE 138 AA; 15515 MW; 793BBD4D5FAFAD CRC64;

Query Match 42.6%; Score 81; DB 6; Length 138;
 Best Local Similarity 41.2%; Pred. No. 6.1e-07;
 Matches 14; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Oy 11 GSLRXCRXXLCSPFXAEXIFRNXXRTRQFWVS 44
 Db 4 GNLEFCEKCSFEARAEVENTERTTEFWKQY 37

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	124	65.3	44	3	US-08-955-636-26
4	122	64.2	44	3	US-08-955-636-3
5	122	64.2	44	3	US-08-955-636-30
6	122	64.2	406	1	US-08-293-778-24
7	122	64.2	406	1	US-08-295-411-5
8	122	64.2	406	5	US-08-955-471-5
9	122	64.2	406	5	PCT-US92-10242-5
10	122	64.2	444	1	US-08-475-845-2
11	122	64.2	444	2	US-08-327-590-2
12	122	64.2	444	2	US-08-660-289-2
13	122	64.2	444	2	US-08-537-807-2
14	122	64.2	444	2	US-08-871-003-2
15	122	64.2	444	3	US-08-464-233-2
16	122	64.2	444	4	US-09-189-607-2
17	122	64.2	444	4	US-09-378-507-2
18	122	64.2	444	5	PCT-US94-05779-2
19	122	64.2	466	1	US-07-882-202A-4
20	122	64.2	466	1	US-08-021-615A-4
21	122	64.2	466	4	US-08-321-777-4
22	122	64.2	466	4	US-09-009-217-14
23	122	64.2	466	4	US-09-009-656-14
24	122	64.2	466	5	PCT-US93-0493-4
25	119	62.6	44	3	US-08-955-636-28
26	118	62.1	44	3	US-08-955-636-29
27	108	56.8	41	1	US-08-229-280-4

28	100	52.6	139	1	US-08-330-978-2	Sequence 2, Appl
29	100	52.6	139	1	US-08-474-042-2	Sequence 2, Appl
30	100	52.6	139	1	US-08-484-558-2	Sequence 2, Appl
31	100	52.6	139	1	US-08-774-592-2	Sequence 2, Appl
32	100	52.6	437	1	US-08-487-037-2	Sequence 3, Appl
33	100	52.6	437	1	US-08-487-037-3	Sequence 3, Appl
34	100	52.6	488	1	US-08-487-037-1	Sequence 1, Appl
35	99	52.1	44	3	US-08-955-636-23	Sequence 23, Appl
36	96	50.5	44	3	US-08-955-636-2	Sequence 2, Appl
37	95	50.0	448	1	US-08-295-411-3	Sequence 3, Appl
38	95	50.0	448	2	US-08-955-471-3	Sequence 3, Appl
39	95	50.0	448	5	PCT-US92-10068-1	Sequence 1, Appl
40	95	50.0	448	5	PCT-US92-10242-3	Sequence 3, Appl
41	94	49.5	41	1	US-08-229-280-5	Sequence 5, Appl
42	94	49.5	42	2	US-08-745-254A-2	Sequence 2, Appl
43	94	49.5	44	3	US-08-955-636-1	Sequence 1, Appl
44	94	49.5	45	2	US-08-965-832-1	Sequence 1, Appl
45	94	49.5	419	1	US-08-295-411-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      81.6%; Score 155; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.9e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLXRCRX...XXAEXIFRNXXRTQFWVS 44
Db 1 ANGFLXXLRNGSLXRCRX...XXAEXIFRNXXRTQFWVS 44

RESULT 2
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match 65.8%; Score 125; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 2.3e-14;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 1 ANGLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTROFWVS 44
DB 1 ANAFLXLRDGLXRXCKXQCSPFXARXIFPDAXRTLFWISY 44

RESULT 3
US-08-955-636-26

Sequence 26, Application US/08955636A
Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelsestuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 26

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-26

Query Match 65.3%; Score 124; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 ANGLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTROFWVS 44
DB 1 ANAFLXLRGSLXRXCKXQCSPFXARXIFPDAXRTLFWISY 44

RESULT 4

US-08-955-636-3

Sequence 3, Application US/08955636A

Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelsestuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-3

Query Match 64.2%; Score 122; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7.3e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 ANGLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTROFWVS 44
DB 1 ANAFLXLRPGLXRXCKXQCSPFXARXIFPDAXRTLFWISY 44

RESULT 5
US-08-955-636-30

Sequence 30, Application US/08955636A
Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelsestuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 30

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-30

Query Match 64.2%; Score 122; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7.3e-14;
Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 ANGLXLRNGSLXRXCRXXLCSPFXAXEIPFNXXRTROFWVS 44
DB 1 ANAFLXLRQGLXRXCKXQCSPFXARXIFPDAXRTLFWISY 44

RESULT 6
US-08-293-778-24

Sequence 24, Application US/08293778

Patent No. 5580560

GENERAL INFORMATION:

APPLICANT: Nicolaissen, Else M.

APPLICANT: Bjorn, Soren E.

APPLICANT: Wiiberg, Finn C.

APPLICANT: Woodbury, Richard

TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESSES:

ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.

STREET: 405 Lexington Avenue, 62nd Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/293,778

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/104,509

FILING DATE: 25-JUN-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/434,149

FILING DATE: 13-NOV-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24

Query Match 64.2%; Score 122; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPXXAEXIFRNXXRTROPFWSY 44
DB 1 ANAFLLYLRPGSLRYCKYQCSFYARIFYKDAERTKLFWISY 44

RESULT 7
US-08-295-411-5
Sequence 5, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffith, John H.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-295-411-5

Query Match 64.2%; Score 122; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPXXAEXIFRNXXRTROPFWSY 44
DB 1 ANAFLEELRPGSLRECKEKGCSFEAREIFKDAERTKLFWISY 44

RESULT 8
US-08-955-471-5
Sequence 5, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffith, John H.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152

OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 64.2%; Score 122; DB 2; Length 406;
Best Local Similarity 52.3%; Pred. No. 7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRNGSLXRCXRLCSFXXAEIFRNXXRTQFWVS 44
DB 1 ANAFLELRPGSLERECKEEOCSFEAREIFPDARTYLFWISY 44

RESULT 9
PCT-US92-10242-5
Sequence 5, Application PC/TUS9210242

GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Messers, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA

ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match 64.2%; Score 122; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 7e-13;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
QY 1 ANGFLXLRNGSLXRCXRLCSFXXAEIFRNXXRTQFWVS 44
DB 1 ANAFLELRPGSLERECKEEOCSFEAREIFPDARTYLFWISY 44

RESULT 10
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5788965

GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.

ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-845-2

Query Match 64.2%; Score 122; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRNGSLXRCXRLCSFXXAEIFRNXXRTQFWVS 44
DB 39 ANAFLELRPGSLERECKEEOCSFEAREIFPDARTYLFWISY 82

RESULT 11
US-08-327-690-2

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Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

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Qy      64.2%; Score 122; DB 2; Length 444,
Query Match
Best Local Similarity 52.3%; Pred No 7,7e-13;
Matched 23; Conservative 5; Mismatches 16; Indels

          1 ANGFLXXLNGSLRXCRXXLCSPYXAEXIFRXXRTROFWSY 44
           |||.....|..|||...|||...|||...|||...|||
Db    39 ANAFLEELRPGSLERCKEBCQCSFEARERIFKDAERTKLFWISY 82

RESULT 12
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982

GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower

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Query Match 64.2%; Score 122; DB 2; Length 444;
Best Local Similarity 53.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRNGSLKRCXRLCSFYLAKLFRNNKKRTQFWVSY 44
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DB 39 ANAFLEELRPGSLERCKEEOCSFEAEALIFDMDRIKLFWISY 82

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APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 64.2%; Score 122; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRNGSLXRCXRLCSFXXAEXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPGSLRECKEQQCFEAREIFKDAERTKLFWISY 82

RESULT 14
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-0707
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 64.2%; Score 122; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRNGSLXRCXRLCSFXXAEXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPGSLRECKEQQCFEAREIFKDAERTKLFWISY 82

RESULT 15
US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend, Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match 64.2%; Score 122; DB 3; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRNGSLXRCXRLCSFXXAEXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPGSLRECKEQQCFEAREIFKDAERTKLFWISY 82

Search completed: March 19, 2003, 15:16:19
Job time : 10.75 secs

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10ASN28GLU_4
Perfect score: 190
Sequence: 1 ANGFLXLLRNGSLRXCRXX.....XXAEXIFRNXXRRQFWVSX 44

Scoring table: BLOSUM62
Gapex 10.0, Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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14: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	64.2	406	9	US-10-109-498-1
2	94	49.5	419	9	US-10-182-263-1
3	94	49.5	419	9	US-10-182-263-3
4	94	49.5	419	9	US-10-182-263-4
5	94	49.5	419	9	US-10-182-263-5
6	94	49.5	419	9	US-09-978-917A-4
7	94	49.5	461	9	US-10-182-263-2
8	94	49.5	461	9	US-09-978-917A-2
9	93	48.9	419	9	US-10-182-263-6
10	88	46.3	415	10	US-09-118-748-2
11	88	46.3	461	9	US-10-132-829-5
12	88	46.3	461	10	US-09-884-901-3
13	70	36.8	96	9	US-09-759-1308-313
14	70	36.8	209	9	US-09-759-1308-312
15	70	36.8	226	9	US-09-759-1308-310
16	53	27.9	95	9	US-09-759-1308-356
17	53	27.9	208	9	US-09-759-1308-355
18	53	27.9	225	9	US-09-759-1308-353
19	42	22.1	464	10	US-09-801-368-334

20	41.5	21.8	197	9	US-10-076-622-516	Sequence 516, App
21	41.5	21.8	197	12	US-10-007-805-516	Sequence 516, App
22	41.5	21.8	232	9	US-10-076-622-517	Sequence 517, App
23	41.5	21.8	232	12	US-10-007-805-517	Sequence 517, App
24	41.5	21.8	243	9	US-09-938-418-7	Sequence 7, Appl1
25	41.5	21.8	243	9	US-10-045-992-4	Sequence 4, Appl1
26	41.5	21.8	243	9	US-10-063-547-122	Sequence 122, App
27	41.5	21.8	243	9	US-10-174-590-366	Sequence 366, App
28	41.5	21.8	243	9	US-10-175-738-366	Sequence 366, App
29	41.5	21.8	243	9	US-10-063-616-122	Sequence 122, App
30	41.5	21.8	243	9	US-10-175-737-366	Sequence 366, App
31	41.5	21.8	243	9	US-10-063-502-122	Sequence 122, App
32	41.5	21.8	243	9	US-10-076-622-514	Sequence 514, App
33	41.5	21.8	243	9	US-10-173-706-366	Sequence 366, App
34	41.5	21.8	243	9	US-10-175-738-366	Sequence 366, App
35	41.5	21.8	243	9	US-10-175-752-366	Sequence 366, App
36	41.5	21.8	243	9	US-10-176-482-366	Sequence 366, App
37	41.5	21.8	243	9	US-10-176-757-366	Sequence 366, App
38	41.5	21.8	243	9	US-10-176-913-366	Sequence 366, App
39	41.5	21.8	243	9	US-10-180-552-366	Sequence 366, App
40	41.5	21.8	243	9	US-10-180-557-366	Sequence 366, App
41	41.5	21.8	243	9	US-10-173-700-366	Sequence 366, App
42	41.5	21.8	243	9	US-10-174-572-366	Sequence 366, App
43	41.5	21.8	243	9	US-10-174-579-366	Sequence 366, App
44	41.5	21.8	243	9	US-10-174-582-366	Sequence 366, App
45	41.5	21.8	243	9	US-10-174-588-366	Sequence 366, App

ALIGNMENTS

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US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US2003044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/261,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      64.2%; Score 122, DB 9, Length 406;
Best Local Similarity 75.0%; Pred. No. 3e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLXLLRNGSLRXCRXXICSFXXAEXIFRNXXRRQFWVSX 44
DB 1 ANAFLLXLRPSLRLRXCKXXQCSFXARXIFKDXARXRLFWISY 44

RESULT 2
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US2003022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E
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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRXCRXXLCSPYXAEIIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKETIQNVDDTLAFW 41

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRXCRXXLCSPYXAEIIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKETIFDVEDDTLAFW 41

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRXCRXXLCSPYXAEIIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKETIFDVEDDTLAFW 41

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLXRXCRXXLCSPYXAEIIFRNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKETIFDVEDDTLAFW 41

RESULT 6
US-09-978-917A-4
; Sequence 4, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 021998310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.1e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;
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Qy 1 ANGFLXXLRNGSLXRCXKXLCSEFXAXEJIFRNXXRTROFW 41
DB 1 ANSFLEELRHSSLERECIEECDFEEAKEIFQNVDDTLAFW 41

RESULT 7
US-10-182-263-2
; Sequence 2, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 49.5%; Score 94; DB 9; Length 461;
Best Local Similarity 46.3%; Pred. No. 2.3e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRCXKXLCSEFXAXEJIFRNXXRTROFW 41
DB 43 ANSFLEELRHSSLERECIEECDFEEAKEIFQNVDDTLAFW 83

RESULT 8
US-09-978-917A-2
; Sequence 2, Application US/0978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: (1)...(42)
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (43)...(461)
US-09-978-917A-2

Query Match 49.5%; Score 94; DB 9; Length 461;
Best Local Similarity 46.3%; Pred. No. 2.3e-08;
Matches 19; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRCXKXLCSEFXAXEJIFRNXXRTROFW 41
DB 43 ANSFLEELRHSSLERECIEECDFEEAKEIFQNVDDTLAFW 83

RESULT 9

US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match 48.9%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 3.1e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRCXKXLCSEFXAXEJIFRNXXRTROFW 41
DB 1 ANSFLEELRHSSLERECIEECDFEEAKEIFQNVDDTLAFW 41

RESULT 10
US-09-118-748-2
; Sequence 2, Application US/09118748A
; Patent No. US20020031799A1
; GENERAL INFORMATION:
; APPLICANT: Staeford, Darrel W.
; APPLICANT: Chang, Jinli
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 5470-183
; CURRENT APPLICATION NUMBER: US/09/118,748A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/053,571
; EARLIER FILING DATE: 1997-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-118-748-2

Query Match 46.3%; Score 88; DB 10; Length 415;
Best Local Similarity 39.5%; Pred. No. 2.3e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXXLRNGSLXRCXKXLCSEFXAXEJIFRNXXRTROFW 44
DB 3 SKULBEFVQGNLRECEMEKCSFEFAREVENTERTTEFWKQY 45

RESULT 11
US-10-132-829-5
; Sequence 5, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII
; TITLE OF INVENTION: with vesicle vector
; FILE REFERENCE: 6627-Pa1170

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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query March          46.3%; Score 88; DB 9; Length 461;
Best Local Similarity 39.5%; Pred. No. 2.5e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

OY      2  NGFLXLRNGSLXRCRXKXLCGFXAXEYFRNXXRTROPWVSY 44
Db      49  SGKLEFVQGNLRECEMEKCSFEERAREVFENTERITTEFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOPW-1-1396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-901-3

Query March          46.3%; Score 88; DB 10; Length 461;
Best Local Similarity 39.5%; Pred. No. 2.5e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

OY      2  NGFLXLRNGSLXRCRXKXLCGFXAXEYFRNXXRTROPWVSY 44
Db      49  SGKLEFVQGNLRECEMEKCSFEERAREVFENTERITTEFWKQY 91

RESULT 13
US-09-759-1308-313
; Sequence 313, Application US/097591308
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarty, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29

OY      11  GSLXRCRXKXLCGFXAXEYFRNXXRTROPWVSY 44
Db      46  GNLERECNEBLCTYEAREIFVDEKXTIAFWQCY 79

RESULT 14
US-09-759-1308-312
; Sequence 312, Application US/097591308
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarty, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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; PRIOR APPLICATION NUMBER: US 09/608,452
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/393,996
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: US 09/602,871
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US 09/420,707
 ; PRIOR FILING DATE: 1999-10-19
 ; NUMBER OF SEQ ID NOS: 460
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 312
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-759-130B-312

Query Match 36.8%; Score 70; DB 9; Length 209;
 Best Local Similarity 38.2%; Pred. No. 0.00015;
 Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLXRCRXXLCSPXXAEXIFRNXXRTPQFWVS 44
 DB 46 GNLERCNEELCNVEARELFVDEDKTIAFWQEX 79

RESULT 15

; US-09-759-130B-310
 ; Sequence 310, Application US/09759130B
 ; Publication No. US20030022279A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: McCarthy, Sean A
 ; APPLICANT: Fraser, Christopher C
 ; APPLICANT: Sharp, John D
 ; APPLICANT: Barnes, Thomas S
 ; APPLICANT: Kistel, Susan J
 ; APPLICANT: Mackay, Charles R
 ; APPLICANT: Myers, Paul S
 ; APPLICANT: Leiby, Kevin R
 ; APPLICANT: Wrighton, Nicolas
 ; APPLICANT: Goodearl, Andrew
 ; APPLICANT: Holtzman, Douglas A
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
 ; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
 ; TITLE OF INVENTION: USES.
 ; FILE REFERENCE: MPIO0-535OMNIM
 ; CURRENT APPLICATION NUMBER: US/09/759,130B
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: US 09/479,249
 ; PRIOR FILING DATE: 2000-01-07
 ; PRIOR APPLICATION NUMBER: US 09/559,497
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 09/578,063
 ; PRIOR FILING DATE: 2000-05-24
 ; PRIOR APPLICATION NUMBER: US 09/333,159
 ; PRIOR FILING DATE: 1999-06-14
 ; PRIOR APPLICATION NUMBER: US 09/596,194
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/342,364
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: US 09/608,452
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/393,996
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: US 09/602,871
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US 09/420,707
 ; PRIOR FILING DATE: 1999-10-19
 ; NUMBER OF SEQ ID NOS: 460
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 310
 ; LENGTH: 226
 ; TYPE: PRT

; ORGANISM: Homo sapiens
 ; US-09-759-130B-310

Query Match 36.8%; Score 70; DB 9; Length 226;
 Best Local Similarity 38.2%; Pred. No. 0.00016;
 Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLXRCRXXLCSPXXAEXIFRNXXRTPQFWVS 44
 DB 63 GNLERCNEELCNVEARELFVDEDKTIAFWQEX 96

Search completed: March 20, 2003, 13:30:17
 Job time : 9.375 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds
(without alignments)
186.869 Million cell updates/sec

Title: 10ASN28PHE_4
Perfect score: 191
Sequence: 1 ANGFLXLRNGLXRXCRXX.....XXAFYIFRXXRTRQFWWSY 44

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDSI/gcgdata/geneseq/genesqp-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/genesqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154	80.6	44	20	AA19306
2	154	80.6	44	22	AA18306
3	128	67.0	44	20	AA18312
4	122	63.9	44	20	AA18311
5	121	63.4	44	20	AA18310
6	119	62.3	44	20	AA18302
7	119	62.3	44	20	AA18305
8	119	62.3	44	22	AA18305
9	119	62.3	401	22	AA18470
10	119	62.3	401	22	AA18471

11	119	62.3	406	14	AA18306	Factor VII (VII).
12	119	62.3	406	18	AA18306	Modified blood coa
13	119	62.3	406	18	AA18306	Modified blood coa
14	119	62.3	406	22	AA18306	Human factor VIIa
15	119	62.3	406	22	AA18306	Human factor VIIa
16	119	62.3	406	22	AA18306	Mammalian exprese
17	119	62.3	406	22	AA18306	Human FVII mutant
18	119	62.3	406	22	AA18306	Human FVII mutant
19	119	62.3	406	22	AA18306	Human FVII mutant
20	119	62.3	406	22	AA18306	Human FVII mutant
21	119	62.3	406	22	AA18306	Human FVII mutant
22	119	62.3	406	22	AA18306	Human FVII mutant
23	119	62.3	406	22	AA18306	Human FVII mutant
24	119	62.3	406	22	AA18306	Wild-type human b1
25	119	62.3	406	22	AA18306	Mutant blood coagu
26	119	62.3	406	22	AA18306	Mutant blood coagu
27	119	62.3	406	22	AA18306	Mutant blood coagu
28	119	62.3	406	22	AA18306	Mutant blood coagu
29	119	62.3	406	22	AA18306	Human coagulation
30	119	62.3	406	22	AA18306	Human coagulation
31	119	62.3	406	22	AA18306	Human coagulation
32	119	62.3	406	22	AA18306	Human coagulation
33	119	62.3	406	22	AA18306	Human coagulation
34	119	62.3	406	22	AA18306	Human coagulation
35	119	62.3	406	22	AA18306	Human coagulation
36	119	62.3	406	22	AA18306	Human coagulation
37	119	62.3	406	22	AA18306	Human coagulation
38	119	62.3	406	22	AA18306	Human coagulation
39	119	62.3	406	22	AA18306	Human coagulation
40	119	62.3	406	22	AA18306	Human coagulation
41	119	62.3	406	22	AA18306	Human coagulation
42	119	62.3	406	22	AA18306	Human coagulation
43	119	62.3	406	22	AA18306	Human coagulation
44	119	62.3	406	22	AA18306	Human coagulation
45	119	62.3	406	22	AA18306	Human coagulation

ALIGNMENTS

RESULT 1					
AA18306					
ID	AA18306	standard; peptide; 44 AA.			
XX					
AC	AA18306;				
XX					
DT	17-AUG-1999	(first entry)			
XX					
DE	Bovine factor VII GLA domain.				
XX					
KW	GLA domain; vitamin K-dependent protein; clotting disorder;				
XX	therapy.				
OS	Bos taurus.				
XX					
FH	Key	Location/Qualifiers			
FT	Misc-difference 1.44	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"			
FT					
XX					
PN	MO9920767-A1.				
XX					
PD	29-APR-1999.				
XX					
PF	20-OCT-1998;	98WO-US22152.			
XX					
PR	23-OCT-1997;	97US-0955636.			
XX					
PA	(MINU) UNIV MINNESOTA.				
XX					
PI	Nelaeuten GL;				
XX					
DR	WPI; 1999-288309/24.				

XX vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure; Page 15; 86pp; English.
 CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 SQ Sequence 44 AA;
 Query Match 80.6%; Score 154; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 1,7e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 ANGFLXXLRNGSLKRXCRXXLCSPFXAXFIFRNXXRTQFWVS 44
 Db 1 ANGFLXXLRPGSLKRXCRXXLCSPFXAXHIFRNXXRTQFWVS 44
 RESULT 2
 AAB36396
 ID AAB36396 standard; peptide: 44 AA.
 AC AAB36396;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.
 XX
 KM Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KM factor X; prothrombin; enhanced membrane binding affinity;
 KM clot formation; thrombolytic; haemostatic; bleeding disorder;
 KM thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KM liver disease.
 KM
 XX
 OS Bos taurus.
 XX
 PN WO20006753-A2.
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US11416.
 XX
 PR 29-APR-1999; 99US-0302239.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsestuen GL;
 XX
 DR WPI; 2001-007226/01.
 XX
 XX Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprises modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity -
 XX
 PS Disclosure; Page 12; 81pp; English.
 CC The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified
 CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type bovine factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.
 CC
 SQ Sequence 44 AA;
 Query Match 80.6%; Score 154; DB 22; Length 44;
 Best Local Similarity 95.5%; Pred. No. 1,7e-18;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 ANGFLXXLRNGSLKRXCRXXLCSPFXAXFIFRNXXRTQFWVS 44
 Db 1 ANGFLXXLRPGSLKRXCRXXLCSPFXAXHIFRNXXRTQFWVS 44
 RESULT 3
 AAY18312
 ID AAY18312 standard; peptide: 44 AA.
 AC AAY18312;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KM therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Aaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 FT
 FT
 PN WO9920767-A1.
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsestuen GL;
 XX
 DR WPI; 1999-288309/24.
 XX
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 PT
 XX
 PS Disclosure; Page 80; 86pp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 SQ Sequence 44 AA;
 Query Match 67.0%; Score 128; DB 20; Length 44;
 Best Local Similarity 77.3%; Pred. No. 4e-14;
 Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLXRXCRXXLCSPFXAXFI FRNXXRTROPFWSY 44
 Db 1 ANAFLLXXLRPGSLXRXCKXXQCSFXAXFI FKDAAXRTKLFWISY 44

RESULT 4
 ID AAY18311

AAV18311 standard; peptide; 44 AA.

AC AAY18311;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.

KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder; therapy.

OS Homo sapiens.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 1..44 /note="Xaa= gamma-carboxyglutamic acid, or glutamic acid"

FT acid"

PN MO9920767-A1.

XX 29-APR-1999.

PF 20-OCT-1998; 98WO-US22152.

PR 23-OCT-1997; 97US-0955636.

PA (MINU) UNIV MINNESOTA.

PI Nelsestuen GL;

XX WPI; 1999-288309/24.

XX vitamin K-dependent polypeptide with modified gamma-carboxyglutamic

PT acid domain; useful for treating clotting disorders

PS Disclosure; Page 80; 86pp; English.

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)

CC domain. The invention relates to a vitamin K-dependent polypeptide

CC comprising a modified GLA domain containing an amino acid substitution

CC which enhances membrane binding of the modified polypeptide as compared

CC to the native polypeptide. The polypeptide is used to treat a clotting

CC disorder by decreasing or increasing clot formation. Modification of the

CC GLA domain results in a protein which has enhanced membrane binding

CC affinity as compared to the native protein.

CC

CC

CC

CC

CC

CC

DE Modified GLA domain of vitamin K-dependent protein.
 XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
 KM therapy.

OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 1..44 /note="Xaa= gamma-carboxyglutamic acid, or glutamic

FT acid"

PN MO9920767-A1.

XX 29-APR-1999.

PF 20-OCT-1998; 98WO-US22152.

PR 23-OCT-1997; 97US-0955636.

PA (MINU) UNIV MINNESOTA.

PI Nelsestuen GL;

XX WPI; 1999-288309/24.

XX vitamin K-dependent polypeptide with modified gamma-carboxyglutamic

PT acid domain; useful for treating clotting disorders

PS Disclosure; Page 80; 86pp; English.

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)

CC domain. The invention relates to a vitamin K-dependent polypeptide

CC comprising a modified GLA domain containing an amino acid substitution

CC which enhances membrane binding of the modified polypeptide as compared

CC to the native polypeptide. The polypeptide is used to treat a clotting

CC disorder by decreasing or increasing clot formation. Modification of the

CC GLA domain results in a protein which has enhanced membrane binding

CC affinity as compared to the native protein.

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

RESULT 6
 ID AAY18302

AAV18302 standard; peptide; 44 AA.

AC AAY18302;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.

KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder; therapy.

OS Homo sapiens.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 1..44 /note="Xaa= gamma-carboxyglutamic acid, or glutamic

FT acid"

FT

PN WO9920767-A1.
 XX 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsestuen GL;
 XX
 DR WPI; 1999-288309/24.
 XX
 PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 XX acid domain, useful for treating clotting disorders
 PS
 PS Claim 11; Page 81; 86pp; English.
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 XX
 SQ Sequence 44 AA;
 Query Match 62.3%; Score 119; DB 20; Length 44;
 Best Local Similarity 75.0%; Pred. No. 1,3e-12;
 Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 Oy 1 ANGFLXLRNGSLXRCXRLCSFXAXFIPRNXXRTQFWVS Y 44
 1 ANAFLXLRPGSLXRCXRCXQCSFXAXRIFDAXRRLFWIS Y 44
 Db
 RESULT 7
 ID AAY18305 standard; peptide; 44 AA.
 XX
 AC AAY18305;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Human factor VII GLA domain.
 XX
 KW GLA domain; vitamin K-dependent protein; clotting disorder;
 KM therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 XX acid"
 XX
 PN WO9920767-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsestuen GL;
 XX
 DR WPI; 1999-288309/24.
 XX

PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 XX acid domain, useful for treating clotting disorders
 XX
 PS Disclosure; Page 15; 86pp; English.
 CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 CC
 XX
 SQ Sequence 44 AA;
 Query Match 62.3%; Score 119; DB 20; Length 44;
 Best Local Similarity 75.0%; Pred. No. 1,3e-12;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 ANGFLXLRNGSLXRCXRLCSFXAXFIPRNXXRTQFWVS Y 44
 1 ANAFLXLRPGSLXRCXRCXQCSFXAXRIFDAXRRLFWIS Y 44
 Db
 RESULT 8
 ID AAB36395 standard; peptide; 44 AA.
 XX
 AC AAB36395;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX
 KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KW factor X; prothrombin; enhanced membrane binding affinity;
 KW clot formation; thrombolytic; haemostatic; bleeding disorder;
 KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KW liver disease.
 XX
 OS Homo sapiens.
 XX
 PN WO20006753-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US11416.
 XX
 PR 29-APR-1999; 99US-0302239.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsestuen GL;
 XX
 DR WPI; 2001-007226/01.
 XX
 PT Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprises modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity -
 PS Disclosure; Page 12; 81pp; English.
 CC The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
 CC at least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation.
 CC (I) can have thrombolytic and haemostatic activities, and can be used
 CC as an inhibitor of clot formation. (I) is useful for decreasing clot
 CC formation in a mammal, a factor VII or factor IX containing a modified

CC GLA domain is useful for increasing clot formation and for treating a
 CC bleeding disorder, including thrombosis and clotting disorders such as
 CC haemophilia A, haemophilia B and liver disease. The present sequence
 CC represents a wild type human factor VII GLA domain sequence, given in
 CC the exemplification of the present invention.

SQ Sequence 44 AA;

Query Match 62.3%; Score 119; DB 22; Length 44;

Best Local Similarity 75.0%; Pred. No. 1,1e-12; Mismatches 6; Indels 0; Gaps 0;

1 ANGFLXXLRNGSLRXRCXXLCSEFXAFIIRNXXRTQFVWSY 44
 1 ANAFLEELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 9

AAB84870 AAB84870 standard; Protein; 401 AA.

XX AAB84870;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-31).

KM Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;

KW mutant; mutcin.

OS Homo sapiens.

OS Synthetic.

FT Key

FT Misc-difference 311..317

PN JP2001061479-A.

PD 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19463.

PT Mutant of blood coagulant factor VII, used for substitution therapy in

PT the treatment of hemophilia -

PS Claim 14; Page 20-21; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII

CC (FVII) or activated blood coagulant factor VII (FVIIa). The present

CC sequence is one such mutant FVII: VII-31. The mutants can be used as an

CC agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 401 AA;

Query Match 62.3%; Score 119; DB 22; Length 401;

Best Local Similarity 52.3%; Pred. No. 1,1e-11; Mismatches 5; Indels 0; Gaps 0;

1 ANGFLXXLRNGSLRXRCXXLCSEFXAFIIRNXXRTQFVWSY 44
 1 ANAFLEELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 10

AAB84871 AAB84871 standard; Protein; 401 AA.

XX AAB84871;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-39).

KM Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;

KW mutant; mutcin.

OS Homo sapiens.

OS Synthetic.

FT Key

FT Misc-difference 235..239

PN JP2001061479-A.

PD 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19464.

PT Mutant of blood coagulant factor VII, used for substitution therapy in

PT the treatment of hemophilia -

PS Claim 16; Page 23-24; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII

CC (FVII) or activated blood coagulant factor VII (FVIIa). The present

CC sequence is one such mutant FVII: VII-39. The mutants can be used as an

CC agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 401 AA;

Query Match 62.3%; Score 119; DB 22; Length 401;

Best Local Similarity 52.3%; Pred. No. 1,1e-11; Mismatches 5; Indels 0; Gaps 0;

1 ANGFLXXLRNGSLRXRCXXLCSEFXAFIIRNXXRTQFVWSY 44
 1 ANAFLEELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 11

AAR35764 AAR35764 standard; protein; 406 AA.

XX AAR35764;

DT 24-SEP-1993 (first entry)

DE Factor VII (VII).

KM P.; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;

KW Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;

XX exosite; catalytic activity.

OS Homo sapiens.

Key Location/Qualifiers
Region 1..152
/note= "Factor VII light chain"
Region 153..406
/note= "Factor VII heavy chain"
Peptide 374..388
/note= "exosite 1"
Peptide 290..310
/note= "exosite 2"
Peptide 290..310
/note= "pref. PC polypeptide; claim 2, page 136"
Peptide 374..388
/note= "pref. PC polypeptide; claim 2, page 136"
Peptide 289..304
/note= "pref. PC polypeptide; claim 4, page 137"
Peptide 290..304
/note= "pref. PC polypeptide; claim 4, page 137"
Peptide 245..266
/note= "claim 9, page 138-139 describes an antibody that reacts with Factor VII; fragments 289-304, 290-304, 290-310, 374-388 and 400-414 but not with fragment 245-266"
MO9309804-A.
27-MAY-1993.
18-NOV-1992; 92WO-US10242.
18-NOV-1991; 91US-0793989.
(SCRI) SCRIPPS RES INST.
Griffin JH, Meesters RM;
WPI; 1993-182244/22.
Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples
Disclosure; Page 133-135; 149pp; English.
The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-10) microm.
NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE LISTING.
Sequence 406 AA;
Query Match 62.3%; Score 119; DB 14; Length 406;
Best Local Similarity 52.3%; Pred. No. 1,1e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
1 ANGFLXLRNGSLXRXCRXLCSFXXAFIFRNXXRTROFWSY 44
1 ANAFLEURPGSLERCKEQCSFEARRTFYDAERTKLFWISY 44
RESULT 12
AAW14509
ID AAW14509 standard; protein; 406 AA.
AAW14509;
14-MAY-1997 (first entry)
Modified blood coagulation Factor VII (R290S).
Blood coagulation; factor 7; mutein; mutation; modification;

thrombocytopenia; von Willebrand's disease; plasma substitute.
Homo sapiens.
Synthetic.
Key
Modified-site
Location/Qualifiers
6
/label= OTHER
/note= "gamma-carboxylutamic acid"
7
/label= OTHER
/note= "gamma-carboxylutamic acid"
14
/label= OTHER
/note= "gamma-carboxylutamic acid"
16
/label= OTHER
/note= "gamma-carboxylutamic acid"
19
/label= OTHER
/note= "gamma-carboxylutamic acid"
20
/label= OTHER
/note= "gamma-carboxylutamic acid"
25
/label= OTHER
/note= "gamma-carboxylutamic acid"
26
/label= OTHER
/note= "gamma-carboxylutamic acid"
29
/label= OTHER
/note= "gamma-carboxylutamic acid"
32..33
/note= "gamma-carboxylutamic acid"
35
/label= OTHER
/note= "gamma-carboxylutamic acid"
38..39
/note= "gamma-carboxylutamic acid"
42..43
/note= "proteolytic site"
44..45
/note= "proteolytic site"
50..61
/note= "proteolytic site"
55..70
/label= OTHER
/note= "beta-hydroxy-aspartic acid"
72..81
/note= "beta-hydroxy-aspartic acid"
91..102
/note= "beta-hydroxy-aspartic acid"
98..112
/note= "beta-hydroxy-aspartic acid"
114..127
/note= "beta-hydroxy-aspartic acid"
135..162
/note= "beta-hydroxy-aspartic acid"
143..144
/note= "proteolytic site"
145
/note= "proteolytic site"
159..164
/note= "proteolytic site"
178..194
/note= "proteolytic site"
193
/note= "proteolytic site"
242
/note= "proteolytic site"
244
/note= "proteolytic site"
290..291
/note= "proteolytic site in unmodified factor VII"
290
/note= "proteolytic site in unmodified factor VII"
310..329
/note= "proteolytic site in unmodified factor VII"
315..316
/note= "proteolytic site in unmodified factor VII"

FT Modified-site 322 /note= "glycosylation site"
 FT Disulfide-bond 340..368
 FT Cleavage-site 341..342
 FT Cleavage-site /note= "proteolytic site"
 FT Cleavage-site 392..393 /note= "proteolytic site"
 FT Cleavage-site 396..397 /note= "proteolytic site"
 FT Cleavage-site 402..403 /note= "proteolytic site"
 FT /note= "proteolytic site"
 XX
 PN USS580560-A.
 XX
 PD 03-DEC-1996.
 XX
 PF 13-NOV-1989; 89US-0434149.
 XX
 PR 09-AUG-1993; 93US-0104509.
 PR 13-NOV-1989; 89US-0434149.
 PR 12-JUN-1992; 92US-0888248.
 PR 22-AUG-1994; 94US-0293778.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 PI Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
 DR WPI; 1997-033523/03.
 XX
 PT Mutated human factor VII or VIIa proteins - with amino acid
 PT substitutions to improve proteolytic stability
 XX
 PS Example 3; Page -: 28pp; English.
 XX
 CC Modified human factor VII or VIIa proteins are stabilised against
 CC proteolytic cleavage by substitution of one of the residues Lys32,
 CC Lys33, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
 CC Lys341 by an amino acid that provides a proteolytically more stable
 CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
 CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
 CC bleeding disorders such as thrombocytopenia and von Willebrand's
 CC disease. They are also suitable for addition to plasma substitutes.
 CC The present sequence is a specific example of a modified factor VII
 CC protein.
 CC
 XX
 SQ Sequence 406 AA;
 XX
 QY 1 ANGELXXLRNGSLRXCRRXXLCSPFXAEXIFRNXXRTROFVWSY 44
 Db 1 ANAFLEELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY 44
 XX
 RESULT 13
 ID AAM14510 standard; protein; 406 AA.
 XX
 AC AAM14510;
 XX
 DT 14-MAY-1997 (first entry)
 XX
 DE Modified blood coagulation Factor VII (R315S).
 XX
 KM Blood coagulation; factor 7; mutein; mutation; modification;
 KM thrombocytopenia; von Willebrand's disease; plasma substitute.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

FT Modified-site 6 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 7 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 14 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 16 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 19 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 20 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Disulfide-bond 17..22 /label= OTHER
 FT Modified-site 25 /note= "gamma-carboxyglutamic acid"
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 26 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 29 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Cleavage-site 32..33 /note= "gamma-carboxyglutamic acid"
 FT Modified-site 35 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Cleavage-site 38..39 /note= "gamma-carboxyglutamic acid"
 FT Cleavage-site 42..43 /note= "proteolytic site"
 FT Cleavage-site 44..45 /note= "proteolytic site"
 FT Disulfide-bond 50..61 /note= "proteolytic site"
 FT Disulfide-bond 55..70 /label= OTHER
 FT Modified-site 63 /label= "beta-hydroxy-aspartic acid"
 FT Disulfide-bond 72..81
 FT Disulfide-bond 91..102
 FT Disulfide-bond 98..112
 FT Disulfide-bond 114..127
 FT Disulfide-bond 135..162
 FT Cleavage-site 143..144 /note= "proteolytic site"
 FT Modified-site 145 /note= "glycosylation site"
 FT Disulfide-bond 159..164
 FT Disulfide-bond 178..194
 FT Active-site 193
 FT Active-site 242
 FT Active-site 344
 FT Cleavage-site 290..291 /note= "proteolytic site"
 FT Disulfide-bond 310..329 /note= "proteolytic site"
 FT Cleavage-site 315..316 /note= "proteolytic site in unmodified factor VII"
 FT Misc-difference 315 /note= "native Arg315 has been substituted by Ser to provide a proteolytically more stable peptide bond"
 FT Modified-site 322 /note= "glycosylation site"
 FT Disulfide-bond 340..368
 FT Cleavage-site 341..342 /note= "proteolytic site"
 FT Cleavage-site 392..393

```

FT      /note= "proteolytic site"
FT      396..397
FT      /note= "proteolytic site"
FT      402..403
FT      /note= "proteolytic site"
XX
PN      USS580560-A.
XX
PD      03-DEC-1996.
XX
PF      13-NOV-1989; 89US-0434149.
XX
PR      09-AUG-1993; 93US-0104509.
PR      13-NOV-1989; 89US-0434149.
PR      12-JUN-1992; 92US-0898248.
PR      22-AUG-1994; 94US-0293778.
XX
PA      (NOVO ) NOVO-NORDISK AS.
XX
PI      Bjorn SE, Nicolaissen EM, Wiberg FC, Woodbury R;
XX
DR      WPI; 1997-033523/03.
XX
PT      Mutated human factor VII or VIIa proteins - with amino acid
XX      substitutions to improve proteolytic stability
XX
PS      Example 4; Page -; 28pp; English.
XX
CC      Modified human factor VII or VIIa proteins are stabilised against
CC      proteolytic cleavage by substitution of one of the residues Lys32,
CC      Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
CC      Lys341 by an amino acid that provides a proteolytically more stable
CC      peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
CC      Gly, Thr, Ala or Ser. The modified proteins are useful for treating
CC      bleeding disorders such as thrombocytopenia and von Willebrand's
CC      disease. They are also suitable for addition to plasma substitutes.
CC      The present sequence is a specific example of a modified factor VII
CC      protein.
XX
SQ      Sequence 406 AA;

Query Match 62.3%; Score 119; DB 18; Length 406;
Best Local Similarity 52.3%; Pred. No. 1,1e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY      1 ANGFLXLRLNGSLRXRCXPLCSFXAXFIPRNXXRTROFWVSY 44
      |||||
DB      1 ANAFLELRPGSLRECKEQCSEFAREIFXDARTLFWISY 44

RESULT 14
AAU77745
ID      AAU77745 standard; protein; 406 AA.
XX
AC      AAU77745;
XX
DT      05-JUN-2002 (first entry)
XX
DE      Human factor VIIa active site mutant.
XX
KW      Factor VIIa; human; shock heat treatment; protein stability;
KW      protein manufacture; protein conformation; mutant; muten.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
XX
Key      Location/Qualifiers
FH      193
FT      /note= "Member of the factor VIIa catalytic triad"
FT      242
FT      /note= "Member of the factor VIIa catalytic triad"
FT      344
FT      /note= "Member of the factor VIIa catalytic triad"

```

```

FT      Misc-difference 344
FT      /label= Gly, Met, Thr
FT      /note= "Preferably Ala. wild type Ser"
XX
XX      WO200177141-A1.
XX
XX      18-OCT-2001.
XX
XX      06-APR-2001; 2001WO-DK00234.
XX
XX      06-APR-2000; 2000DK-0000573.
XX      17-APR-2000; 2000US-197650P.
XX
XX      (NOVO ) NOVO NORDISK AS.
XX
XX      Matchless F;
XX
XX      WPI; 2001-657162/75.
XX
XX      Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX      involves a shock heat treatment -
XX
XX      Disclosure; Page -; 22pp; English.
XX
CC      The invention describes a method of stabilising a polypeptide involving
CC      shock heat treatment of the polypeptide. The method is useful in a
CC      pharmaceutical composition, in the industrial or large scale method of
CC      manufacturing a polypeptide, also as a unit operation during preparation,
CC      purification, recovery and/or formulation of polypeptides. The shock heat
CC      treatment improves the protein stability without substantial loss of
CC      biological activity. The method can be applied to change polypeptide
CC      conformation in a very fast and non-invasive manner. The polypeptide
CC      formed is stable. The method is also useful for decreasing the
CC      association of the polypeptide. This sequence represents a modified
CC      human factor VIIa protein, mutated at the catalytic site, described
CC      in the invention.
CC
CC      Note: This sequence does not appear in the specification but has
CC      been obtained using information given in the invention.
XX
SQ      Sequence 406 AA;

Query Match 62.3%; Score 119; DB 22; Length 406;
Best Local Similarity 52.3%; Pred. No. 1,1e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY      1 ANGFLXLRLNGSLRXRCXPLCSFXAXFIPRNXXRTROFWVSY 44
      |||||
DB      1 ANAFLELRPGSLRECKEQCSEFAREIFXDARTLFWISY 44

RESULT 15
AAM52171
ID      AAM52171 standard; Protein; 406 AA.
XX
AC      AAM52171;
XX
DT      07-FEB-2002 (first entry)
XX
DE      Human FVII SEQ ID NO 1.
XX
KW      Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW      cardiac; hepatocytic; cerebroprotective; haemophilia; liver disease;
KW      myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
OS      Homo sapiens.
XX
XX
Key      Location/Qualifiers
FH      6
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxylutamic acid"
FT      7
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxylutamic acid"

```

FT Misc-difference 14
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 16
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 19
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 20
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 25
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 26
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 29
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 35
 /label= Glu, OTHER
 /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Modified-site 52
 /note= "O-glycosylated"
 FT
 FT Modified-site 60
 /note= "O-glycosylated"
 FT
 FT Modified-site 145
 /note= "N-glycosylated"
 FT
 FT Cleavage-site 152..153
 /note= "proteolytic cleavage site converting FVII zymogen
 to an activated form, comprising two chains
 linked by a single disulphide bridge"
 FT
 FT Modified-site 322
 /note= "N-glycosylated"
 FT
 FT
 PN W0200158935-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 12-FEB-2001, 2001WO-DK00094.
 XX
 PR 11-FEB-2000, 2000DK-0000218.
 PR 18-OCT-2000, 2000DK-0001558.
 XX
 PA (MAXY-) MAXYGEN ABS.
 XX
 PI Andersen KV, Pedersen AH, Bornaes C;
 XX
 DR WPI: 2001-581807/65.
 DR N-PDB; AAI99982.
 XX
 XX
 PT New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -
 XX
 PS Claim 1; Page 81-83; 89pp; English.
 XX
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAW52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a

CC number of advantages over currently available such as longer duration
 CC between injections.
 XX
 SQ Sequence 406 AA;
 Query Match 62.3%; Score 119; DB 22; Length 406;
 Best Local Similarity 75.0%; Pred. No. 1,1e-11;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLLXXLRNGSLXRXCRXXLCSPXXAFXIFRNXXRTRPFWSY 44
 DB 1 ANAFLLXXLRPGLXRXCKXXQCSFXXRXIFKDAKTKLFWISY 44

Search completed: March 19, 2003, 14:51:16
 Job time : 31.4375 secs

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GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds
(without alignments)
145.545 Million cell updates/sec

Title: 10ASN28PHE_4
Perfect score: 191
Sequence: 1 ANGFLXLLNGSLRXCRX.....XXAFXIFRXRXRPFWSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

PIR 73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	77.0	407	1 KFB07	coagulation factor
2	127	66.5	443	2 I46932	coagulation factor
3	119	62.3	466	1 KFH07	coagulation factor
4	103	53.9	461	1 JX0210	protein C (activat
5	102	53.4	461	1 S18994	protein C (activat
6	93	48.7	466	1 KXBO	protein C (activat
7	92	48.2	482	1 EXRT	coagulation factor
8	92	48.2	488	1 EXHU	coagulation factor
9	90	47.1	461	1 KXHU	protein C (activat
10	87	45.5	492	1 EXBO	coagulation factor
11	86	45.0	622	1 TBHU	thrombin (EC 3.4.2
12	85	44.5	416	1 KFB0	coagulation factor
13	85	44.5	461	1 KFHU	coagulation factor
14	83	43.5	617	2 S10511	thrombin (EC 3.4.2
15	83	43.5	618	2 A35827	thrombin (EC 3.4.2
16	80	41.9	452	1 A30351	coagulation factor
17	80	41.9	459	2 J00419	coagulation factor
18	79	41.4	475	1 EXCH	coagulation factor
19	77	40.3	625	1 TBBO	thrombin (EC 3.4.2
20	72	37.7	642	2 S53433	plasma protein S p
21	68	35.6	675	1 KXBO	plasma protein S p
22	67	35.1	642	2 S53434	plasma protein S p
23	67	35.1	646	2 S38819	plasma protein S p
24	67	35.1	676	1 KXHU	plasma protein S p
25	65	34.0	675	1 KXRT	plasma protein S p
26	64	33.5	422	1 KXHU	plasma protein Z p
27	60	31.4	396	1 KXBO	plasma protein Z p
28	58	30.4	675	1 KXMS	plasma protein S p
29	56	29.3	678	2 B48089	growth arrest-spec

30	55	28.8	673	2 A48089	growth arrest-spec
31	53	27.7	674	2 I55476	growth potentialin
32	52	27.2	605	1 MWLEB	E1 protein - bovin
33	52	27.2	620	1 MWLB2	E1 protein - bovin
34	49	25.7	1217	2 T21403	hypothetical prote
35	48	25.1	413	1 VHVNIH	nucleoprotein - in
36	46.5	24.3	594	2 D84859	probable MAP kinase
37	46.5	24.3	603	2 C96575	probable MAP kinase
38	45.5	23.8	576	2 G96763	probable MAP kinase
39	45	23.6	448	2 T18710	hypothetical prote
40	45	23.6	687	2 T08528	probable DNA topoi
41	43.5	22.8	105	2 S09766	hypothetical prote
42	43.5	22.8	304	2 AF2942	5-dehydro-4-deoxyg
43	43.5	22.8	304	2 D98340	5-dehydro-4-deoxyg
44	43.5	22.8	2133	2 T42763	coagulation factor
45	43	22.5	440	2 C83368	probable MRS trans

ALIGNMENTS

RESULT 1

KFB07 coagulation factor VIIa (EC 3.4.21.21) - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999

C/Accession: A31979; C02074

R/Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A/Title: Bovine factor VII. Its purification and complete amino acid sequence.

A/Reference number: A31979; PMID:89008362; PMID:3049594

A/Accession: A31979

A/Molecule type: protein

A/Residues: 1-407 <TRK>

R/McMullen, B.A.; Fujikawa, K.; Kiesel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX in the presence of calcium and tissue factor

A/Reference number: A44556; PMID:89213929; PMID:3149637

A/Contents: annotation

A/Note: structure and location of covalently bound carboxylate

C/Function:

A/Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor

A/Pathway: blood coagulation extrinsic pathway

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate

F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>

F:1-44/Domain: Gla domain homology (fragment) <GLA>

F:50-81/Domain: BGF homology <EG1>

F:91-127/Domain: EGF homology <EG2>

F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F:153-387/Domain: trypsin homology <TRY>

F:6-7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:52/Binding site: carboxylate (Ser) (covalent) #status experimental

F:145,203/Binding site: carboxylate (Asn) (covalent) #status experimental

F:152-153/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental

F:193,242,344/Active site: His, Asp, Ser #status predicted

F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 77.0%; Score 147; DB 1; Length 407;

Best Local Similarity 68.2%; Pred. No. 4,1e-18;

Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
Qy      1  ANGFLXLRNGSLKRCXKXLCSPFXAXFIFRNXXRTQFWVSY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1  ANGFLLELLPGLSRECKEELCSFEAREHIFRNERTQFWVSY 44

RESULT 2
146932
Coagulation factor VII - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C/Accession: 146932
R/Brother: A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A/Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A/Reference number: 146932; MUID:93190306; PMID:8383365
A/Accession: 146932
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-443 <BRO>
A/Cross-references: GB:S56300; NID:g266294; PID:g266295
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F/24-83/Domain: Gla domain homology <GLA>
F/89-120/Domain: EGF homology <EG1>
F/130-166/Domain: EGF homology <EG2>
F/192-425/Domain: trypsin homology <TRY>

Query Match      66.5%; Score 127; DB 2; Length 443;
Best Local Similarity 52.3%; Pred. No. 1,6e-14;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy      1  ANGFLXLRNGSLKRCXKXLCSPFXAXFIFRNXXRTQFWVSY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      40 ANSFLLELRPGSLRECKEELCSFEAREHVFQSTERTKQFWVSY 83

RESULT 3
KFH07
Coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
C/Accession: A28322; A23819; A31186; B31186; S63524
R/O'Hare, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.V.; Hagen, F.S.; Murt
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A/Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A/Reference number: A28322; MUID:87260948; PMID:3037537
A/Accession: A28322
A/Molecule type: DNA
A/Residues: 1-466 <OHA>
A/Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
R/Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A/Title: Characterization of a cDNA coding for human factor VII.
A/Reference number: A23819; MUID:86205965; PMID:3486420
A/Accession: A23819
A/Molecule type: mRNA
A/Residues: 1-466 <HAG>
A/Cross-references: GB:M13232; NID:g182799; PIDN:AAA8040.1; PID:g182801
R/Thim, L.; Bioern, S.; Christensen, M.; Nicolaissen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A/Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A/Reference number: A90539; MUID:89088153; PMID:3264725
A/Accession: A31186
A/Molecule type: protein
A/Residues: 61-212 <THI>
A/Accession: B31186
A/Molecule type: protein
A/Residues: 213-466 <TH2>
R/Bioern, S.; Foster, D.C.; Thim, L.; Wilberg, F.C.; Christensen, M.; Komiyama, Y.; Peder
J. Biol. Chem. 266, 11051-11057, 1991
A/Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A/Reference number: A40529; MUID:91250411; PMID:1904059
A/Contents: annotation; carbohydrate binding sites
R/Persson, E.; Petersen, L.C.
```

```
Eur. J. Biochem. 234, 293-300, 1995
A/Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy
A/Reference number: S63524; MUID:96096752; PMID:8529655
A/Accession: S63524
A/Molecule type: protein
A/Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C/Genetics:
A/Gene: GDB:F7
A/Cross-references: GDB:119697; OMIM:227500
A/Map position: 13q34-13q34
A/Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C/Function:
A/Description: catalyzes the proteolytic activation of coagulation factor X in the preser
coagulation factor IX in the presence of calcium and tissue factor
A/Pathway: blood coagulation extrinsic pathway
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-60/Domain: propeptide #status predicted <PRO>
F/45-104/Domain: Gla domain homology <GLA>
F/61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F/110-141/Domain: EGF homology <EG1>
F/151-187/Domain: EGF homology <EG2>
F/213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F/213-447/Domain: trypsin homology <TRY>
F/66-67;74;76;79;80;85;86;89;96/Modified site: gamma-carboxylglutamic acid (Glu) #status e
F/77-82;110-121;115-130;132-141;151-162;158-172;174-187;195-322;219-224;238-254;370-389;4
F/112;120/Binding site: carboxylate (Ser) (covalent) #status experimental
F/122/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F/205;382/Binding site: carboxylate (Asn) (covalent) #status experimental
F/212-213/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F/253;302;404/Active site: His, Asp, Ser #status predicted
F/350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match      62.3%; Score 119; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 4,4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy      1  ANGFLXLRNGSLKRCXKXLCSPFXAXFIFRNXXRTQFWVSY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61 ANAFLEELRPGSLRECKEELCSFEAREHIFKDAERTLQFWVSY 104

RESULT 4
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N/Alternate names: vitamin K-dependent serine proteinase
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C/Accession: JX0210
R/Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A/Title: Isolation and characterization of a mouse protein C cDNA.
A/Reference number: JX0210; MUID:92316897; PMID:1618739
A/Accession: JX0210
A/Molecule type: mRNA
A/Residues: 1-461 <TRD>
A/Cross-references: GB:D10445; NID:g220385; PIDN:BAA01235.1; PID:g220386
A/Experimental source: liver
C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg
B.
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F/1-33/Domain: signal sequence #status predicted <SIG>
F/27-85/Domain: Gla domain homology <GLA>
F/34-41/Domain: propeptide #status predicted <PRO>
F/42-196;199-461/Product: protein C #status predicted <PRC>
F/42-196/Domain: light chain #status predicted <PC1>
F/91-130/Domain: EGF homology <EG1>
F/139-174/Domain: EGF homology <EG2>
F/199-461/Domain: heavy chain #status predicted <PCH>
F/199-211/Domain: activation peptide #status predicted <ACT>
F/212-461/Product: vitamin K-dependent serine proteinase #status predicted <VTR>
```

F:212-445/Domain: trypsin homology <TRY>
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat
 F:214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 53.9%; Score 103; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 3e-10;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLRXCRXXLCSPXXAFXIFRNXXRTQFWVSF 44
 Db 42 ANSFLEMRPGSLERECMEICDFEEAOEIFQVVEDTLAWIKY 85

RESULT 5
 S18994
 protein C (activated) (EC 3.4.21.69) precursor - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
 C:Accession: S18994; S24312
 R:Okatufj, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
 A:Description: The EMBL Data Library, February 1992
 A:Description: The CDNA cloning and mRNA expression of rat protein C.
 A:Reference number: S18994

A:Accession: S18994
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <OKA>

A:Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
 R:Okatufj, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
 Biochim. Biophys. Acta 1131, 329-332, 1992

A:Title: The CDNA cloning and mRNA expression of rat protein C.
 A:Reference number: S24312; MUID:92329550; PMID:1627650
 A:Accession: S24312
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-461 <OKA>
 A:Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine protease

F:1-35/Domain: signal sequence #status predicted <SIG>
 F:27-85/Domain: Gla domain homology <GLA>
 F:33-42/Domain: propeptide #status predicted <PRO>
 F:43-461/Product: protein C #status predicted <PRC>

F:91-130/Domain: EGF homology <EG1>
 F:139-174/Domain: EGF homology <EG2>
 F:213-445/Domain: trypsin homology <TRY>
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat
 F:215,299,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 53.4%; Score 102; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 4.6e-10;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLRXCRXXLCSPXXAFXIFRNXXRTQFWVSF 44
 Db 42 ANSFLEMRPGSLERECMEICDFEEAOEIFQVVEDTLAWIKY 85

RESULT 6
 KXBO
 protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)

N:Alternate names: autoprothrombin IIA; plasma protein C
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
 C:Accession: A26250; A18385; A18386; A00928
 R:Long, G.L.; Balagaje, R.M.; Macgillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984

A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.

A:Reference number: A26250; MUID:85014826; PMID:6091100
 A:Accession: A26250
 A:Molecule type: mRNA

A:Residues: 1-456 <LON>
 R:Fernlund, P.; Stenflo, J.
 J. Biol. Chem. 257, 12170-12179, 1982

A:Title: Amino acid sequence of the light chain of bovine protein C.
 A:Reference number: A18385; MUID:83007325; PMID:6896876
 A:Accession: A18385

A:Molecule type: protein
 A:Residues: 40-194 <PER>
 A:Note: 82-Lys was also found
 R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
 Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983

A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
 A:Reference number: A19316; MUID:83169769; PMID:6572939
 A:Contents: annotation; revision to residue 110
 R:Stenflo, J.; Fernlund, P.
 J. Biol. Chem. 257, 12180-12190, 1982

A:Title: Amino acid sequence of the heavy chain of bovine protein C.
 A:Reference number: A18386; MUID:83007326; PMID:6896877
 A:Accession: A18386

A:Molecule type: protein
 A:Residues: 197-454, 'pv' <STB>
 R:Esmon, N.L.; DeBault, L.E.; Esmon, C.T.
 J. Biol. Chem. 258, 5548-5553, 1983

A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless p
 A:Reference number: A37541; MUID:83213513; PMID:604092
 A:Contents: annotation; activation; calcium binding
 R:Johnson, A.E.; Esmon, N.L.; Lave, T.M.; Esmon, C.T.
 J. Biol. Chem. 258, 5554-5560, 1983

A:Title: Structural changes required for activation of protein C are induced by Ca2+ bind
 A:Reference number: A37542; MUID:83213514; PMID:606503
 A:Contents: annotation; activation; calcium binding
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg

s.
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c)
 bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stero

C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding;

F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
 F:24-83/Domain: Gla domain homology <GLA>
 F:30-39/Domain: propeptide #status predicted <PRO>
 F:40-194/Product: protein C light chain #status experimental <LCH>

F:98-128/Domain: EGF homology <EG1>
 F:137-172/Domain: EGF homology <EG2>
 F:197-456/Product: protein C heavy chain #status experimental <HCH>
 F:197-210/Domain: activation peptide #status experimental <APT>

F:211-440/Domain: trypsin homology <TRY>
 F:45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:119-128,137-148,144-157,159-187,190-318,237-253,368-382,393-421/Disulfide bonds: #stat
 F:136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:352,298,397/Active site: His, Asp, Ser #status predicted
 F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 48.7%; Score 93; DB 1; Length 456;
 Best Local Similarity 43.2%; Pred. No. 1.8e-08;
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLRXCRXXLCSPXXAFXIFRNXXRTQFWVSF 44
 Db 40 ANSFLEBLRGVNERCESEVCEFEAREEIFQVTEDTMAFWFSF 83

RESULT 7
 EXRT
 coagulation factor Xa (EC 3.4.21.6) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

Gene 84, 517-519, 1989
 A>Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
 A:Reference number: I54051; MUID:90128239; PMID:2612918
 A:Accession: I54051
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23 <RES>
 A:Cross-references: GB:M33297; NID:918360; PIDN:AA52636.1; PID:9553330
 R:Padmanabhan, K.; Padmanabhan, K.P.; Tullinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Biol.
 J. Mol. Biol. 232, 947-966, 1993
 A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
 A:Reference number: A49458; MUID:93360277; PMID:8355279
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms
 C:Comment: The two chains held together by one disulfide bond are formed from a single-C
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
 C:Genetics:
 A:Gene: GDB:F10
 A:Cross-references: GDB:119890; OMIM:227600
 A:Map position: 13q34-13q34
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
 A>Note: deficiency of this factor causes Stuart disease
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-23/Domain: signal sequence #status predicted <PRO>
 F:1-40/Domain: propeptide #status predicted <SIG>
 F:25-84/Domain: Gla domain homology <Gla>
 F:91-179/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:183-234/Domain: activation peptide #status experimental <APT>
 F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
 F:235-462/Domain: trypsin homology <TRY>
 F:46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat
 F:57-62/Disulfide bonds: #status predicted
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:199,211/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 48.2%; Score 92; DB 1; Length 488;
 Best Local Similarity 36.4%; Pred. No. 2.9e-08;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRXCRXXLCSPFXAFIFRNXXRTROFVSY 44
 Db 41 ANSFLEEMKXGHLRECEMETCTSYEARREVEDSDKTNEFNKY 84

RESULT 9

KXHU
 Protein C (activated) (EC 3.4.21.69) precursor - human
 N:Alternate names: autoproteobin IIA; plasma protein C
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
 C:Accession: A22331; A25426; A21781; A23789; A00927
 R:Foster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A>Title: The nucleotide sequence of the gene for human protein C.
 A:Reference number: A22331; MUID:85270390; PMID:2991887
 A:Accession: A22331
 A:Molecule type: DNA
 A:Residues: 1-461 <FOS1>
 A:Cross-references: GB:M1228; NID:9190333; PIDN:AAA60166.1; PID:9190334
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A>Title: Evolution and organization of the human protein C gene.
 A:Reference number: A25426; MUID:86120978; PMID:3511471

A:Accession: A25426
 A:Molecule type: DNA
 A:Residues: 1-445, 'L', 446-461 <PLU>
 A:Cross-references: GB:M12712; NID:9190330; PIDN:AAA60165.1; PID:9190332
 R:Foster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A>Title: Characterization of a cDNA coding for human protein C.
 A:Reference number: A21781; MUID:84272714; PMID:6589623
 A:Accession: A21781
 A:Molecule type: mRNA
 A:Residues: 'Q', 107-461 <FOS2>
 A:Cross-references: GB:K02059; NID:9190322; PIDN:AAA60164.1; PID:9190323
 R:Beckmann, R.J.; Schmidt, R.J.; Sauter, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5233-5247, 1985
 A>Title: The structure and evolution of a 461 amino acid human protein C precursor and it
 A:Reference number: A23789; MUID:85269639; PMID:2991859
 A:Accession: A23789
 A:Molecule type: mRNA
 A:Residues: 1-461 <BEC>
 A:Cross-references: GB:X02750; NID:935689; PIDN:CAA26528.1; PID:9763120
 R:Wietlich, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A>Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me
 A:Reference number: A44605; MUID:90293094; PMID:1694179
 A:Contents: annotation; carboxylate binding sites; activation peptide
 A>Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
 R:Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A>Title: O-linked fucose is present in the first epidermal growth factor domain of factor
 A:Reference number: A44606; MUID:92184750; PMID:1544894
 A:Contents: annotation; beta-hydroxyaspartic acid
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine protease that in
 ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also fi
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction.
 C:Genetics:
 A:Gene: GDB:PROC
 A:Cross-references: GDB:120317; OMIM:176860
 A:Map position: 2q13-2q21
 A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding;
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:27-86/Domain: Gla domain homology <Gla>
 F:33-42/Domain: propeptide #status predicted <PRO>
 F:43-197/Product: protein C light chain #status predicted <LCH>
 F:92-131/Domain: EGF homology <EG1>
 F:140-175/Domain: EGF homology <EG2>
 F:200-461/Product: protein C heavy chain #status predicted <APT>
 F:200-211/Domain: activation peptide #status experimental <ACT>
 F:212-445/Domain: trypsin homology <TRY>
 F:48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxylglutamic acid (Glu) #status expe
 F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D
 F:106-111/Disulfide bonds: #status predicted
 F:110/Binding site: carboxylate (Thr) (covalent) #status absent
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:139,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
 F:253,299,402/Active site: His, Asp, Ser #status predicted
 F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 47.1%; Score 90; DB 1; Length 461;
 Best Local Similarity 46.3%; Pred. No. 6.2e-08;
 Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRXCRXXLCSPFXAFIFRNXXRTROFV 41
 Db 43 ANSFLEIRHSSLERECIERICDFEAKETIFQVNDTLATW 83

RESULT 10

EXBO
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N:Alternate names: Stuart factor
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
 C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
 C:Pung, M.R.; Campbell, R.M.; Macgillivray, T.A.
 Nucleic Acids Res. 12, 4481-4492, 1984
 A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
 A:Reference number: A22867; MUID:84247315; PMID:6330671
 A:Accession: A22867
 A:Molecule type: mRNA
 A:Residues: 1-487 <FNU>
 A:Cross-references: GB:X00673; NID:9192; PIDN:CAA25286.1; PID:9193
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
 Biochemistry 19, 659-667, 1980
 A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A:Reference number: A14997; MUID:80130563; PMID:6766735
 A:Accession: A14997
 A:Molecule type: protein
 A:Residues: 41-102, 'N', 104-180 <ENF>
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; MUID:83308813; PMID:6688526
 A:Contents: annotation; revision to residue 103
 R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
 A:Reference number: A12030; MUID:76053069; PMID:1059093
 A:Accession: A12030
 A:Molecule type: protein
 A:Residues: 183-282,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GRFG', 446-492 <I
 A:Note: carboxylate binding sites and disulfide bonds were determined
 R:Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oellin, A.K.; Stenflo, J.
 J. Biol. Chem. 264, 16897-16904, 1989
 A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
 A:Reference number: A34412; MUID:89380326; PMID:2789221
 A:Accession: A34412
 A:Molecule type: protein
 A:Residues: 85-126 <PER>
 A:Note: beta-hydroxyaspartic acid site
 R:Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A:Reference number: S39414; MUID:94062825; PMID:8243461
 A:Accession: S39414
 A:Molecule type: protein
 A:Residues: 183-196,199-209,216-233 <INO>
 A:Note: carboxylate binding sites
 R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
 Biochemistry 11, 4899-4903, 1972
 A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammal
 A:Reference number: A12453; MUID:70553314; PMID:4264286
 A:Contents: annotation; active site
 R:Fujikawa, K.; Titani, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
 A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to
 A:Reference number: A13504; MUID:76053121; PMID:1059122
 A:Contents: annotation; activation
 R:Suigo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
 J. Biol. Chem. 259, 5705-5710, 1984
 A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
 A:Reference number: A38024; MUID:84185716; PMID:6546930
 A:Contents: annotation; calcium binding
 R:Morita, T.; Jackson, C.M.
 J. Biol. Chem. 261, 4008-4014, 1986
 A:Reference number: A38025; MUID:86140210; PMID:3949800
 A:Contents: annotation; sulfate binding
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C:Comment: The two chains are formed from a single-chain precursor by the excision of tw
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
 activation.
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
 C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C:Genetics:
 A:Gene: F10
 A:Map position: 13q34
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-40/Domain: propeptide #status predicted <PRO>
 F:41-180/Domain: Gla domain homology <Gla>
 F:90-122/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:183-233/Domain: activation peptide #status experimental <APR>
 F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
 F:234-461/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #st
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status p
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F:208,485/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:218/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:233-234/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #statu
 F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental
 F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 45.5%; Score 87; DB 1; Length 492;
 Best Local Similarity 36.4%; Pred. No. 2,2e-07;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
 Oy 1 ANGFLXLRNGSLKRXCRXXLCSPFXAFPIFRNXXRTGQFVSVY 44
 Db 41 ANSFLEVKQNLRECELEBACSLSEAREVEDAQTDFEFSKY 84

RESULT 11
 TBHU
 thrombin (BC 3.4.21.5) precursor [validated] - human
 N:Alternate names: coagulation factor II
 N:Contains: prothrombin
 C:Species: Homo sapiens (man)
 C:Date: 30-Nov-1980 #sequence_revision 22-Jul-1994 #text_change 08-Dec-2000
 C:Accession: A29351; A00914; B00914; A37549; A37550; I51952
 R:Deegen, S.J.F.; Davie, E.W.
 Biochemistry 26, 6165-6177, 1987
 A:Title: Nucleotide sequence of the gene for human prothrombin.
 A:Reference number: A29351; MUID:88077877; PMID:2825773
 A:Accession: A29351
 A:Molecule type: DNA
 A:Residues: 1-622 <DEG>
 A:Cross-references: GB:M17262; GB:M33691; NID:9558069; PIDN:MAC63054.1; PID:G339641
 R:Deegen, S.J.F.; Macgillivray, R.T.A.; Davie, E.W.
 Biochemistry 22, 2087-2097, 1983
 A:Title: Characterization of the complementary deoxyribonucleic acid and gene coding for
 A:Reference number: A00914; MUID:83231469; PMID:6305407
 A:Accession: A00914
 A:Molecule type: mRNA
 A:Residues: 8-163, 'N', 165-622 <DE2>
 A:Cross-references: GB:V00585; GB:J00307; NID:937128; PIDN:CAA23842.1; PID:G1335344
 A:Accession: B00914
 A:Molecule type: DNA
 A:Residues: 188-311 <DE3>
 R:Walz, D.A.; Hewett-Emmett, D.; Seegers, W.H.
 Proc. Natl. Acad. Sci. U.S.A. 74, 1968-1972, 1977
 A:Reference number: A37549; MUID:77193964; PMID:2266717
 A:Accession: A37549
 A:Molecule type: protein
 A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'WV', 196-308, '
 R:Butkowski, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.
 J. Biol. Chem. 255, 4942-4957, 1977
 A:Title: Primary structure of human prothrombin 2 and alpha-chrombin.

A:Reference number: A37550; PMID:77207112; PMID:873923
A:Accession: A37550
A:Molecule type: protein
A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
R:Rabbit, M.J.; Blahall, A.; Furie, B.; Furie, B.C.
J. Biol. Chem. 261, 13210-13215, 1986
A:Reference number: A37551; PMID:87008532; PMID:3759958
A:Contents: annotation; activation cleavages
R:MacGillivray, R.T.; Irwin, D.M.; Guinco, E.R.; Stone, J.C.
Ann. N.Y. Acad. Sci. 485, 73-79, 1986
A:Title: Recombinant genetic approaches to functional mapping of thrombin.
A:Reference number: I51952; PMID:87182874; PMID:3471151
A:Accession: I51952
A:Molecule type: mRNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-2, 'R', 5-100 <RES>
A:Cross-references: GB:M3031; NID:q190723; PIND:AAA60220.1; PID:q190724
C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
C:Comment: can be removed either by factor Xa or thrombin; the cleavage into light and heavy chain
ter 314-Arg, are released in natural blood clotting.
C:Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
C:Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
ent interaction with the negatively charged phospholipid membrane surface.
C:Comment: The prothrombin precursor is synthesized in the liver.
C:Genetics:
A:Gene: GDB:F2
A:Cross-references: GDB:119894; OMIM:176930
A:Map position: 11p11-11q12
A:introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: signal sequence #status predicted <PRO>
F:28-87/Domain: Gla domain homology <Gla>
F:44-622/Produce: prothrombin peptide #status experimental <MAT>
F:44-327/Domain: activation peptide #status experimental <APT>
F:108-186/Domain: kringle homology <KR1>
F:213-291/Domain: kringle homology <KR2>
F:328-363/Produce: thrombin light chain #status experimental <LCH>
F:364-622/Produce: thrombin heavy chain #status experimental <HCH>
F:364-613/Domain: trypsin homology <TRY>
F:49-50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:60-65,90-103,108-168,129-169,187-201,213-291,234-274,262-286/Disulfide bonds: #status
F:121,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:336-482,536-550,564-594/Disulfide bonds: #status predicted
F:391-407/Disulfide bonds: #status experimental
F:406,462/Active site: His, Asp #status predicted
F:416/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:568/Active site: Ser #status experimental

Query Match 45.0%; Score 86; DB 1; Length 622;
Best Local Similarity 38.6%; Pred. No. 4.2e-07;
Matches 17; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

QY 1 ANGEFLXLRNGSLXRCXXLCSPFXAFXIFRNXXRRQFWVS 44
Db 44 ANTFLEVRGNLRECBVETCTSTEEAFEALESSTADIVFWAKT 87

RESULT 12
KFBH
coagulation factor IXa (EC 3.4.21.22) precursor - bovine
N:Alternate names: Christmas factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence, revision 03-Aug-1984 #text_change 16-Jul-1999
C:Accession: A14757; B20274; I45891; A00923
R:Katsuyama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neuwath, H.; Davie, E.W.; Ti
Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa
A:Reference number: A14757; PMID:80056619; PMID:291916
A:Accession: A14757
A:Molecule type: protein

A:Residues: 1-63, 'T', 65-416 <MAT>
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coe
A:Reference number: A20274; PMID:83308813; PMID:6688526
A:Accession: B20274
A:Molecule type: protein
A:Residues: 59-63, 'X', 65-69 <MCW>
R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
Nature 299, 178-180, 1982
A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
A:Reference number: I45891; PMID:82272386; PMID:6287289
A:Accession: I45891
A:Molecule type: mRNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 52-139 <CHO>
A:Cross-references: GB:J00007; NID:q163053; PIND:AAA0520.1; PID:q163054
R:Rase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.
J. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
A:Reference number: A44556; PMID:89213999; PMID:3149637
A:Contents: annotation
A:Note: structure and location of a carbohydrate covalently bound to Ser
C:Comment: Factor IX is activated by factor Xa, which excises the activation peptide pro
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamu
F:1-146/Produce: coagulation factor IXa light chain #status experimental <ALC>
F:1-45/Domain: Gla domain homology (fragment) <Gla>
F:51-82/Domain: EGF homology <EG1>
F:88-124/Domain: EGF homology <EG2>
F:147-181/Domain: activation peptide #status experimental <APT>
F:182-416/Produce: coagulation factor IXa heavy chain #status experimental <AHC>
F:182-409/Domain: trypsin homology <TRY>
F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,123-220,207-223,337-351,362-390/Disulfide
F:53/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:54/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:158,168,177,261/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 44.5%; Score 85; DB 1; Length 416;
Best Local Similarity 37.2%; Pred. No. 4.3e-07;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRNGSLXRCXXLCSPFXAFXIFRNXXRRQFWVS 44
Db 3 SGKLEFRGNLRECBVETCTSTEEAFEALESSTADIVFWAKT 45

RESULT 13
KFBH
coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
N:Alternate names: antihemophilic factor B; Christmas factor
C:Species: Homo sapiens (man)
C:Date: 17-Dec-1982 #sequence, revision 30-Jun-1987 #text_change 15-Sep-2000
C:Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20;
R:Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
Biochemistry 24, 3736-3750, 1985
A:Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
A:Reference number: A00922; PMID:86000558; PMID:2994716
A:Accession: A00922
A:Molecule type: DNA
A:Residues: 1-461 <YOS>
A:Cross-references: GB:K02402; NID:q182612; PIND:AA59620.1; PID:q182613
R:Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giamelli, F.; Gould, K.; Huddleston, J.A.; Bro
EMBO J. 3, 1053-1060, 1984
A:Title: The gene structure of human anti-haemophilic factor IX.
A:Reference number: A37570; PMID:84236100; PMID:6329734

A:Accession: A37570
 A:Molecule type: DNA
 A:Residues: 1-461 <ANS>
 A:Cross-references: GB:K02048
 R:Reitema, P.H.; Bering, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
 Blood 72, 1074-1076, 1988
 A:Title: The putative factor IX gene promoter in hemophilia B Leyden.
 A:Reference number: A30511; MUID:88327116; PMID:3416065
 A:Accession: A30511
 A:Molecule type: DNA
 A:Residues: 8-24 <RE>
 A:Cross-references: EMBL:X55008; NID:G311288; PIDN:CA838245.2; PID:G4469253
 R:Koebel, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
 Am. J. Hum. Genet. 45, 448-457, 1989
 A:Title: Functionally important regions of the factor IX gene have a low rate of polymor
 A:Reference number: A32989; MUID:89371752; PMID:2773937
 A:Accession: A32989
 A:Molecule type: DNA
 A:Note: not compared with conceptual translation
 A:Residues: 30-92 <KOE>
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
 A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
 A:Reference number: A22673; MUID:85190593; PMID:3857619
 A:Accession: A22673
 A:Molecule type: mRNA
 A:Residues: 1-193, 'T', 195-461 <MC>
 A:Cross-references: GB:M11309; NID:G180552; PIDN:AA52023.1; PID:G180553
 A:Note: the authors translated the codon ACA for residue 29 as Tyr
 R:Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findel, A.; Tolero
 Nucleic Acids Res. 11, 2325-2335, 1983
 A:Title: Isolation and characterization of a human factor IX cDNA: identification of Tag I
 A:Reference number: A37546; MUID:84300526; PMID:6089357
 A:Accession: A37546
 A:Molecule type: Protein
 A:Residues: 38-193, 'T', 195-326 <JAG>
 A:Cross-references: GB:M35672
 R:Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
 A:Title: Isolation and characterization of a cDNA coding for human factor IX.
 A:Reference number: A30623; MUID:81065193; PMID:6959130
 A:Accession: A30623
 A:Molecule type: mRNA
 A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',
 A:Cross-references: GB:U00136; NID:G182608; PIDN:AA98726.1; PID:G182609
 R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
 Vox Sang. 58, 21-29, 1990
 A:Title: Development of an immunofluorescence process for factor IX purification.
 A:Reference number: A60486; MUID:90194857; PMID:2316207
 A:Accession: A60486
 A:Molecule type: Protein
 A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
 R:McMullen, B.A.; Fujikawa, K.; Kistler, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; MUID:83308813; PMID:6688526
 A:Accession: A20274
 A:Molecule type: Protein
 A:Residues: 105-109, 'X', 111-115 <MC>
 R:Balland, A.; Faure, T.; Carvalho, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall
 Eur. J. Biochem. 172, 565-572, 1988
 A:Title: Characterisation of two differently processed forms of human recombinant factor
 A:Reference number: S02527; MUID:88166735; PMID:3280312
 A:Accession: S02527

A:Molecule type: protein
 A:Residues: 23-63 <BAL>
 A:Note: processed forms expressed in recombinant system
 R:Julia, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Neulien, I
 EMBO J. 9, 3295-3301, 1990
 A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice and
 A:Reference number: S12058; MUID:91006024; PMID:2209546
 A:Accession: S12058
 A:Molecule type: mRNA; protein
 A:Residues: 1-68 <JAL>
 A:Note: processed forms expressed in recombinant system
 R:Handford, P.A.; Baron, M.; Mayhew, M.; Willie, A.; Beealey, T.; Brownlee, G.G.; Campe
 EMBO J. 9, 475-480, 1990
 A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
 A:Reference number: S12377; MUID:90151623; PMID:2406129
 A:Accession: S12377
 A:Molecule type: Protein
 A:Residues: 92-130 <HAN>
 A:Note: NMR detection of calcium binding by domain expressed in recombinant system
 R:de la Salle, C.; Charantier, J.L.; Baes, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
 Thromb. Haemost. 70, 370-371, 1993
 A:Title: A deletion located in the 3' non translated part of the factor IX gene responsi
 A:Reference number: S19612; MUID:94054330; PMID:8236150
 A:Accession: S19612
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 444-461 <RES>
 A:Cross-references: GB:S66752; NID:G439773; PIDN:AA828588.1; PID:G439774
 R:Stoffet, E.S.; Koebel, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A:Title: Genomic amplification with transcript sequencing.
 A:Reference number: S19529; MUID:88127096; PMID:3340835
 A:Accession: S19529
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 290-359 <RE2>
 A:Cross-references: GB:M19063; NID:G182622; PIDN:AA52456.1; PID:G182623
 R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimomishi, Y.; Nishimura, H.; Iw
 Biochemistry 33, 5167-5171, 1994
 A:Title: Activation peptide of human factor IX has oligosaccharide O-glycosidically link
 A:Reference number: A54255; MUID:94227047; PMID:8172892
 A:Accession: A54255
 A:Molecule type: Protein
 A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrate
 R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A:Title: Activation of human factor IX (Christmas factor).
 A:Reference number: A18483; MUID:78194509; PMID:659613
 A:Contents: annotation; activation; active site; carbohydrate binding
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
 A:Reference number: A37569
 A:Contents: annotation
 A:Note: 194-Thr was also found
 R:Morita, T.; Isaacs, B.S.; Emon, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5696-5704, 1984
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
 A:Reference number: A37543; MUID:8185715; PMID:6425296
 A:Contents: annotation; calcium binding
 R:Morita, T.; Isaacs, B.S.; Emon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A:Reference number: A37544
 A:Contents: annotation; calcium binding; correction
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation c
 A:Reference number: A37545; MUID:86189947; PMID:3009023
 A:Contents: annotation; signal sequence cleavage site
 R:Stuhli, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
 J. Biol. Chem. 264, 21257-21265, 1989
 A:Title: Blood clotting factor IX (Bw) Nsgova: substitution of arginine 180 by tryptophan
 A:Reference number: A30622; MUID:90078225; PMID:2592373

A/Contents: annotation; sequence of mutant B(M) Nagoya
 A/Note: carboxylation, glycosylation, and cleavage sites
 R/Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownie
 submitted to the Brookhaven Protein Data Bank, November 1991
 A/Reference number: A51252; PDB:1IXA
 A/Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A/Note: recombinant form expressed in yeast
 C/Comment: Factor IX is activated by Factor Xla, which excises the activation peptide p
 C/Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
 C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc
 C/Genetics:
 A/Gene: GDB:F9
 A/Cross-references: GDB:119900; OMIM:306900
 A/Map position: Xq27.1-Xq27.2
 A/Intons: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 C/Function:
 A/Description: catalyzes the proteolytic activation of coagulation factor X in the prese
 A/Pathway: blood coagulation intrinsic pathway
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut
 F1-28/Domain: signal sequence #status predicted <SIG>
 F1-29/Domain: signal sequence #status predicted <PPT>
 F1-31-91/Domain: Gla domain homology <GLA>
 F1-97-128/Domain: coagulation factor IXa light chain #status experimental <ALC>
 F1-134-170/Domain: EGF homology <EG2>
 F1-92-226/Domain: activation peptide #status experimental <ACT>
 F1-227-461/Domain: coagulation factor IXa heavy chain #status experimental <AHC>
 F1-227-454/Domain: trypsin homology <TRY>
 F1-53-54-66-67-72-73-76-79-82-88/Modified site: gamma-carboxyglutamic acid (Glu) #
 F1-64-69-97-108-102-117-119-128-134-145-141-155-157-170-178-335-252-268-382-396-407-435/D
 F1-99/Binding site: carboxylate (Ser) (covalent) #status experimental
 F1-110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F1-91-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental
 F1-203-213/Binding site: carboxylate (Asn) (covalent) #status experimental
 F1-205-215/Binding site: carboxylate (Thr) (covalent) #status experimental
 F1-226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

Query Match 44.5%; Score 85; DB 1; Length 461;
 Best Local Similarity 39.5%; Pred. No. 4.8e-07;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

2 NGFLXLRNGSLKRCXKXLCSEFXKAFIRNXXRTQFWVSY 44
 Db 49 SGKLEPVGKGLERECMEKCSFEAREVFPENTERITTEFMKQY 91

RESULT 14
 S10511
 thrombin (EC 3.4.21.5) precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 07-May-1993 #sequence revision 07-May-1993 #text_change 03-May-2002
 C/Accession: S10511; A60576; B42696
 R/Dhanich, M.; Monard, D.
 Nucleic Acids Res. 18, 4251, 1990
 A/Title: cDNA sequence of rat prothrombin.
 A/Reference number: S10511; MUID:90332426; PMID:2377469
 A/Accession: S10511
 A/Molecule type: mRNA
 A/Residues: 1-617 <DH>
 A/Cross-references: EMBL:X52835; NID:956969; PIDN:CAA37017.1; PID:956970
 R/Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
 Endocrinology 126, 167-175, 1990
 A/Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
 A/Reference number: A60576; MUID:90091942; PMID:2293980
 A/Accession: A60576
 A/Molecule type: protein
 A/Residues: 44-58 <HN>
 A/Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute
 R/Banfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A/Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
 A/Reference number: A42696; MUID:92212913; PMID:1557383

A/Accession: B42696
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 383-617, 'E', <BAN>
 A/Cross-references: GB:M81397
 C/Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C/Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
 F1-24/Domain: signal sequence #status predicted <SIG>
 F1-25-43/Domain: propeptide #status predicted <PRO>
 F1-28-88/Domain: Gla domain homology <GLA>
 F1-44-617/Product: prothrombin #status experimental <PMAT>
 F1-109-187/Domain: kringle homology <KR1>
 F1-215-292/Domain: kringle homology <KR2>
 F1-360-609/Domain: trypsin homology <TRY>
 F1-50-51-58-60-63-64-69-70-73-76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F1-61-66-91-104-109-187-130-170-158-182-215-292-236-276-264-287-332-478-387-403-532-546,5
 F1-402,458,564/Active site: His, Asp, Ser #status predicted

Query Match 43.5%; Score 83; DB 2; Length 617;
 Best Local Similarity 39.5%; Pred. No. 1.4e-06;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

2 NGFLXLRNGSLKRCXKXLCSEFXKAFIRNXXRTQFWVSY 44
 Db 46 SGFLERKGNLRECEVCEQSYEAFALESQDITDVFVAKY 88

RESULT 15
 A35827
 thrombin (EC 3.4.21.5) precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text_change 03-May-2002
 C/Accession: A35827; A42696; G12081
 R/Degen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A.;
 DNA Cell Biol. 9, 487-498, 1990
 A/Title: Characterization of the cDNA coding for mouse prothrombin and localization of
 A/Reference number: A35827; MUID:91025551; PMID:2222810
 A/Accession: A35827
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-618 <DE>
 A/Cross-references: GB:X52308; NID:953813; PIDN:CAA36548.1; PID:953814
 A/Experimental source: strain C57BL/6
 A/Note: the data were obtained from females resulting from the cross of M. domesticus and
 R/Banfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A/Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
 A/Reference number: A42696; MUID:92212913; PMID:1557383
 A/Accession: A42696
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 384-618, 'E', <BAN>
 A/Cross-references: GB:M81394
 C/Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C/Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
 F1-24/Domain: signal sequence #status predicted <PRO>
 F1-25-43/Domain: propeptide #status predicted <PRO>
 F1-28-88/Domain: Gla domain homology <GLA>
 F1-44-618/Product: prothrombin B #status predicted <MAT>
 F1-109-187/Domain: kringle homology <KR1>
 F1-215-293/Domain: kringle homology <KR2>
 F1-361-610/Domain: trypsin homology <TRY>
 F1-50-51-58-60-63-64-69-70-73-76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F1-61-66-91-104-109-187-130-170-158-182-215-293-236-276-264-288-333-479-388-404-533-547,5
 F1-403,459,565/Active site: His, Asp, Ser #status predicted

Query Match 43.5%; Score 83; DB 2; Length 618;
 Best Local Similarity 39.5%; Pred. No. 1.4e-06;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

2 NGFLXLRNGSLKRCXKXLCSEFXKAFIRNXXRTQFWVSY 44
 Db 46 SGFLERKGNLRECEVCEQSYEAFALESQDITDVFVAKY 88

Search completed: March 19, 2003, 15:01:02
Job time : 30.125 secs

...

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds
(without alignments)
328.082 Million cell updates/sec

Title: 10ASN28PHE_4

Perfect score: 191
Sequence: 1 ANGFLXKLNGSLKRCRX.....XXAFIFRNXXRTQFWVS Y 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	77.0	407	FA7_BOVIN	P22457 Bos taurus
2	127	66.5	444	FA7_RABIT	P8139 cyctolagus
3	119	62.3	466	FA7_HUMAN	P08709 homo sapien
4	105	55.0	218	TMG1_HUMAN	O14668 homo sapien
5	103	53.9	461	PRTC_MOUSE	P35587 mus musculu
6	102	53.4	446	FA7_MOUSE	P70375 mus musculu
7	102	53.4	461	PRTC_RAT	Q9bzd7 homo sapien
8	98	51.3	231	TMG3_HUMAN	O9glb2 sus scrofa
9	98	51.3	459	PRTC_PIG	O19045 cyctolagus
10	96	50.3	490	FA10_RABIT	P00745 Bos taurus
11	93	48.7	456	PRTC_BOVIN	P00745 Bos taurus
12	92	48.2	488	FA10_HUMAN	P04070 homo sapien
13	90	47.1	461	PRTC_HUMAN	P00743 Bos taurus
14	87	45.5	492	FA10_BOVIN	P00734 homo sapien
15	86	45.0	622	THRB_HUMAN	P00744 Bos taurus
16	85	44.5	416	FA9_BOVIN	P00740 homo sapien
17	85	44.5	461	FA9_HUMAN	P18297 rattus norv
18	83	43.5	617	THRB_RAT	P19221 mus musculu
19	83	43.5	618	THRB_MOUSE	O28661 cyctolagus
20	81	42.4	458	PRTC_RABIT	P09540 canis famli
21	80	41.9	452	FA9_CANFA	P16299 mus musculu
22	80	41.9	459	FA9_MOUSE	P25135 gallus gall
23	79	41.4	475	FA10_CHICK	P00735 Bos taurus
24	77	40.3	625	THRB_BOVIN	P07224 Bos taurus
25	68	35.6	675	PRTC_BOVIN	O14669 homo sapien
26	67	35.1	202	TMG2_HUMAN	P98126 homo sapien
27	67	35.1	226	TMG4_HUMAN	P98118 cyctolagus
28	67	35.1	646	PRTC_RABIT	O28520 macaca mula
29	67	35.1	649	PRTC_MACMU	P07225 homo sapien
30	67	35.1	676	PRTC_HUMAN	P81428 tropidichis
31	65	34.0	376	FA10_TROCA	P53813 rattus norv
32	65	34.0	675	PRTC_RAT	P22891 homo sapien
33	64	33.5	400	PRTC_HUMAN	

34	60	31.4	396	1	PRTC_BOVIN	P00744 Bos taurus
35	58	30.4	675	1	PRTC_MOUSE	Q08761 mus musculu
36	52	27.2	604	1	VE1_BPV2	P1298 bovine papl
37	52	27.2	605	1	VE1_BPV1	P03116 bovine papl
38	48	25.1	413	1	NCAP_HINV	P19691 infectious
39	45	23.6	818	1	CDB1_HUMAN	O95F53 homo sapien
40	43.5	22.8	105	1	UL03_HCMVA	P16775 human cytom
41	43.5	22.8	2133	1	FA8_PIG	P12263 sus scrofa
42	43	22.5	350	1	VOD1_DROME	Q9w4p5 drosophila
43	42	22.0	320	1	GSHB_BUCAL	P57612 buchiera ap
44	42	22.0	473	1	FP2_MYGA	Q25464 mytilus gal
45	42	22.0	1275	1	RFBC_MYXXA	Q50864 myxococcus

ALIGNMENTS

RESULT 1	ID	FA7_BOVIN	STANDARD;	PRT;	407 AA.
AC	P22457;				
DT	01-AUG-1991 (Rel. 19, Last sequence update)				
DT	01-AUG-1991 (Rel. 19, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Coagulation factor VII (BC 3.4.21.21) (Serum prothrombin conversion accelerator).				
DE	accelerator).				
GN	F7.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_Taxid=9913;				
PN	[1]				
RP	SEQUENCE				
RX	MEDLINE=89008362; PubMed=3049594;				
RA	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,				
RA	Iwanaga S.;				
RT	"Bovine factor VII. Its purification and complete amino acid				
RT	sequence.";				
RL	J. Biol. Chem. 263:14868-14877(1988).				
RN	[2]				
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.				
RX	MEDLINE=89213999; PubMed=3149637;				
RA	Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,				
RA	Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;				
RT	"A new trisaccharide sugar chain linked to a serine residue in bovine				
RT	blood coagulation factors VII and IX.";				
RL	J. Biochem. 104:867-868(1988).				
RN	[3]				
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.				
RX	MEDLINE=91344709; PubMed=2129367;				
RA	Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;				
RT	"A new trisaccharide sugar chain linked to a serine residue in the				
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";				
RL	Adv. Exp. Med. Biol. 281:121-131(1990).				
CC	-I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWMOGEN FORM. FACTOR VII IS				
CC	CONVERTED TO FACTOR VIIA BY FACTOR XA. FACTOR XIIA, FACTOR IXA, OR				
CC	THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR				
CC	AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA				
CC	BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO				
CC	FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR IX TO				
CC	-I- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -Ile bond in factor X to				
CC	form factor Xa.				
CC	-I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED				
CC	BY A DISULFIDE BOND.				
CC	-I- TISSUE SPECIFICITY: PLASMA.				
CC	-I- PM: THE VITAMIN K-DEPENDENT. ENZYMAIC CARBOXYLATION OF SOME				
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND				
CC	CALCIUM.				
CC	-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.				
CC	-I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.				
DR	PIR; A31979; A31979.				
DR	HSSP; P08709; 1BF9.				

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DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR01881; EGF_Ca.
DR InterPro; IPR01438; EGF_II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR0010; EGF_BLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00669; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR HydroLase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KM Layer; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
FT DOMAIN 153 407 FACTOR VII HEAVY CHAIN.
FT ACT_SITE 193 193 GLA-RICH.
FT ACT_SITE 242 242 EGF-LIKE 1. CALCIUM-BINDING (POTENTIAL).
FT BINDING 338 338 EGF-LIKE 2.
FT DISULFID 17 22 SERINE PROTEASE.
FT DISULFID 50 61 CLEAVAGE (BY FACTOR XA, FACTOR XIa,
FT DISULFID 55 70 FACTOR IXa, OR THROMBIN).
FT DISULFID 72 81 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 98 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 135 262 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 178 194 BY SIMILARITY.
FT DISULFID 310 329 BY SIMILARITY.
FT DISULFID 340 368 BY SIMILARITY.
FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 52 52 O-LINKED (GLC. . .).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;

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OY 1 ANGFLLXLRNGSLKRXCRXXLCSFXXAFYIRNXXKRTQFWNSY 44
DB 1 ANGFLEILLPSGLRECREELCSFEAAEIRFRNERTQFWNSY 44

RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII."
RL Thromb. Res. Suppl. 69:231-238 (1993).
RP [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIa BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg--Ile bond in factor X to
CC form factor Xa.
CC -I- SUBUNIT: HEMERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -I- TISSUE SPECIFICITY: PLASMA.
CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77477; BAB3326.1; -.
DR HSSP; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.

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Query March 77.0%; Score 147; DB 1; Length 407;
Best Local Similarity 60.2%; Pred. No. 1, 1e-16;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00001; EGF-like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TYP_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydroxylase; Serine protease; Blood coagulation: Zymogen; Glycoprotein;
KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
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FT DISULFID 217 233
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FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABCFE5427F8 CRC64;

Query Match 66.5%; Score 127; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 4.4e-15;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
QY 1 ANGELXXLRNGSLKRXCRXXLCSEFXAFXIFRNKXRTQRFWVS 44
Db 40 ANSLLEELRPSGLRBECKEELCSFEAREVQSTERTKQFWITY 83

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DT 01-JAN-1988 (rel. 06, last sequence update)
DT 15-JUN-2002 (rel. 41, last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Eptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davis E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.-U.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Thim L., Wlberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RL directed mutagenesis of serine 52 to alanine.";
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903; Winkler F.K., Guha A.,
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RL Nature 380:41-46(1996).

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RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950;
 RA Muranyi A., Finn B.E., Gipeert G.P., Forsen S., Stenflo J.,
 RA Drakeberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male";
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patrachini P., Gemmati D., Derosa V., Pinotti M.,
 RA Roderigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patrachini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kembell-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lunney H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94264305; PubMed=8204879;
 RA Chasing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohnwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CNC) for Arg (247) (CGC) in the
 RT catalytic domain.";

RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Ardin A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [19]
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostilhevsky M.,
 RA Zaitov R., Seligsohn U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Galdes R., Aguilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PM: THE VITAMIN K-DEPENDENT. ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -1- PHARMACEUTICAL: Available under the names Nistasee or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in
 CC Query Match 62.3%; Score 119; DB 1; Length 466;
 CC Best Local Similarity 52.3%; Pred. No. 1,3e-13;
 CC Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
 QY 1 ANGFLXLRNGSLKRXCRXXLCSFXAXFIRNXXRTQGFVVS 44
 DB 61 ANAFLEELRPGSLRBECKECSFEAREIRFDARTLFWISY 104
 RESULT 4
 TMG1 HUMAN STANDARD; PRT; 218 AA.
 AC 014668;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
 DE rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
 DE 1)
 GN PRG1 OR TMG1 OR PRG1.
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
gamma-carboxyglutamic acid proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
modifications of glutamic acid by a vitamin K-dependent gamma-
carboxylase.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF009242; AAB67070.1; -.
DR HSSP; P00740; ICFH.
DR Genew; HGNC:9469; PRRG1.
DR MIM; 604428; -.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20 POTENTIAL.
FT CHAIN 1 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT FT 21 218 PROTEIN 1.
FT FT 21 83 EXTRACELLULAR (POTENTIAL).
FT FT 84 106 POTENTIAL.
FT FT 107 218 CYTOPLASMIC (POTENTIAL).
FT FT 24 61 GLA-RICH.
FT FT 131 135 POLY-PRO.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;
Query Match 55.0%; Score 105; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 1.9e-11;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
OY 1 ANGFLXXLRGSLKRCXKXLCSPFXAFXIPRNXXRTQFVVS 44
DB 21 ANGFFETIRGQNIREFCKEFTFEAREAPENNEKTEFWSTY 64

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RT "Isolation and characterization of a mouse protein C cDNA.";
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX MEDLINE=94318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
RT "A comparative study of partial primary structures of the catalytic
region of mammalian protein C.";
RL Br. J. Haematol. 86:590-600(1994).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
SITE IS NECESSARY FOR THE RECOGNITION OF THE
THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; D10445; BAA01235.1; -.
DR EMBL; AF034569; AAC33795.1; -.
DR EMBL; DA3755; BAA07812.1; -.
DR PIR; JX0210; JX0210.
DR HSSP; P04070; IFCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF-like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PR00068; EGF_2.
DR Pfam; PR00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_1like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_Pc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.

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DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
 FT SIGNAL 1 33
 FT PROPEP 34 41
 FT CHAIN 42 196
 FT CHAIN 199 461
 FT PEPTIDE 199 461
 FT SITE 212 213
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 213 461
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 253 253
 FT ACT_SITE 299 299
 FT ACT_SITE 402 402
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 319
 FT DISULFID 238 254
 FT DISULFID 373 387
 FT DISULFID 398 426
 FT CARBOHYD 214 214
 FT CARBOHYD 290 290
 FT CARBOHYD 355 355
 FT CONFLICT 328 328
 FT CONFLICT 393 393
 FT SEQUENCE 461 AA; 51945 MM; 53FAAD08B194D6E CRC64;
 Query March 53.9%; Score 103; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 9.1e-11;
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

DT 01-NOV-1997 (Rel. 35, last annotation update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 DE conversion accelerator).
 GN F7 OR CF7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9127167; PubMed=8972017;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood
 RT coagulation factor VII gene.";
 RL Thromb. Haemost. 76:957-964 (1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; U66079; AAC33796.1; -.
 DR HSSP; P08709; 1BP9.
 DR MEROPS; S01.215; -.
 DR MGD; MGI:109325; F7.
 DR InterPro; IPR00152; Aex hydroxy1.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR00742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYOTRYPsin.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_1like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00069; GLA; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;

KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 24
 FT PROPEP 25 41
 FT CHAIN 42 193
 FT CHAIN 194 446
 FT CHAIN 47 76
 FT CHAIN 87 123
 FT CHAIN 128 169
 FT CHAIN 194 446
 FT SITE 193 194
 FT ACT SITE 234 234
 FT ACT SITE 283 283
 FT ACT SITE 385 385
 FT BINDING 379 379
 FT BINDING 58 63
 FT BINDING 91 102
 FT BINDING 96 111
 FT BINDING 113 122
 FT BINDING 132 143
 FT BINDING 139 153
 FT BINDING 155 168
 FT BINDING 176 303
 FT BINDING 200 205
 FT BINDING 219 235
 FT BINDING 351 370
 FT BINDING 381 409
 FT BINDING 47 47
 FT BINDING 48 48
 FT BINDING 55 55
 FT BINDING 57 57
 FT BINDING 60 60
 FT BINDING 61 61
 FT BINDING 66 66
 FT BINDING 67 67
 FT BINDING 70 70
 FT BINDING 76 76
 FT BINDING 104 104
 FT BINDING 186 186
 FT BINDING 244 244
 FT BINDING 446 AA; 50276 MW; 251284A45C96E CRC64;
 SQ SEQUENCE

Query Match 53.4%; Score 102; DB 1; Length 446;
 Best Local Similarity 47.7%; Pred. No. 1,3e-10;
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXLYLRNGSLKRXCRXXLCSPFXAXIFRNXXRTQFVSY 44
 DB 42 ANSLLELMFGSLERECNEQCSPFEAREIFKSPERTKQFWIVY 85

RESULT 7
 PRTC RAT STANDARD; PRT; 461 AA.
 AC P11394;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Auto)prothrombin IIA (Anticoagulant protein C) (Blood coagulation factor XIV).
 GN PROC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=92329550; PubMed=1627650;
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
 RT "The cDNA cloning and mRNA expression of rat protein C.";
 RL Biochim. Biophys. Acta 1131:329-332(1992).

CC - FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC - CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIA.
 CC - SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC - PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC - MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC - SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC
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 CC
 CC -----
 CC EMBL; X64336; CAA45617.1; -
 CC PIR; S18994; S18994.
 CC PIR; S24312; S24312.
 CC HSSP; P04070; 1PCU.
 CC
 CC MEROPS; S01.218; -
 CC InterPro; IPR000152; Asx_hydroxyl.
 CC InterPro; IPR001314; Chymotrypsin.
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR001881; EGF Ca.
 CC InterPro; IPR002383; GLA_blood.
 CC InterPro; IPR001254; Ser_protease_Try.
 CC InterPro; IPR000294; VitK_dep_GLA.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00089; trypsin; 1.
 CC Pfam; PF00594; gla; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00179; EGF_Ca; 1.
 CC SMART; SM00001; EGF-like; 1.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; TRYP_SPC; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS01187; EGF_Ca; 1.
 CC PROSITE; PS00011; GLU CARBOXYLATION; 1.
 CC PROSITE; PS00240; TRYPsin DOM; 1.
 CC PROSITE; PS00134; TRYPsin_HIS; 1.
 CC PROSITE; PS00135; TRYPsin_SER; 1.
 CC Blood coagulation; Glycoprotein; Serine protease;
 CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 CC EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 CC
 CC SIGNAL 1 32
 CC PROPEP 33 41
 CC CHAIN 42 196
 CC CHAIN 199 461
 CC PEPTIDE 199 212
 CC SITE 212 213
 CC SITE 96 131
 CC DOMAIN 135 175
 CC DOMAIN 213 461
 CC MOD_RES 47 47
 CC MOD_RES 48 48
 CC MOD_RES 48 48

BY SIMILARITY.
 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
 ACTIVATION PEPTIDE (BY SIMILARITY).
 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 EGF-LIKE 1.
 EGF-LIKE 2.
 SERINE PROTEASE.
 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
 GAMMA-CARBOXYGLUTAMIC ACID

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FT MOD_RES 55 55 (BY SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 57 57 (BY SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 60 60 (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 61 61 (BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 (BY SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 67 67 (BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 70 70 (BY SIMILARITY).
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 254 112 CHARGE RELAY SYSTEM.
FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 255 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDACD5 CRC64;

Query Match 53.4%; Score 102; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 1.4e-10;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRNGSLRXCRXXLCSPFXAFIPFNXXRTQFVWSY 44
Db 42 ANSFLEEVNAGSLREKMEIEICDFEADQEIFQVEDTLAFWKY 85

RESULT 8
TMG3_HUMAN STANDARD; PRT; 231 AA.
AC Q9BZD7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=spinal cord;
RX MEDLINE=21117044; PubMed=1171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- P.M.: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC -----
DR EMBL; AF326350; AA00955.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 20 231 PROTEIN 3
FT DOMAIN 79 101 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 102 231 POTENTIAL.
FT DOMAIN 23 60 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 60 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25648 MW; 8A373E4848490D81 CRC64;

Query Match 51.3%; Score 98; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 3.6e-10;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRNGSLRXCRXXLCSPFXAFIPFNXXRTQFVWSY 44
Db 20 ANSFLEEVNAGSLREKMEIEICDFEADQEIFQVEDTLAFWKY 63

RESULT 9
PRTC_PIG STANDARD; PRT; 459 AA.
AC Q9GUP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCB1_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
RA Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
RT protein modeling of membrane binding sites and comparative anatomy of
RT domains.";
RL Cell. Mol. Life Sci. 58:148-159(2001).
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- P.M.: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -----
```

CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the
 CC thrombin-thrombomodulin complex.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: AF191307; AAC28380.1; -.
 CC HSSP: P04070; 1PCU.
 CC MEROPS: S01.218; -.
 CC InterPro: IPR000152; Abx_hydroxyl.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR001881; EGF Ca.
 CC InterPro: IPR002383; GLA_blood.
 CC InterPro: IPR001254; Ser_protease_Try.
 CC InterPro: IPR000294; VitK_dep_GLA.
 CC Pfam: PF00008; EGF_2.
 CC Pfam: PF00089; trypsin; 1.
 CC Pfam: PF00584; glaf; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00001; GLABLOOD.
 CC SMART: SM00001; EGF like; 2.
 CC SMART: SM00069; GLA; 1.
 CC SMART: SM00020; Tryp_Spc; 1.
 CC PROSITE: PS00010; ASX_HYDROXYL; 1.
 CC PROSITE: PS00022; EGF_1; 1.
 CC PROSITE: PS01186; EGF_2; 2.
 CC PROSITE: PS01187; EGF CA; 1.
 CC PROSITE: PS00011; GLU CARBOXYLATION; 1.
 CC PROSITE: PS02040; TRYPSIN DOM; 1.
 CC PROSITE: PS00135; TRYPSIN HIS; 1.
 CC PROSITE: PS00135; TRYPSIN SER; 1.
 CC Blood coagulation; Glycoprotein; Serine protease;
 CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 CC EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 CC SIGNAL: 1 18
 CC PROPEP 19 41
 CC CHAIN 42 459
 CC CHAIN 42 196
 CC CHAIN 199 459
 CC PEPTIDE. 199 213
 CC SITE 213 214
 CC DOMAIN 96 131
 CC DOMAIN 135 175
 CC DOMAIN 214 459
 CC MOD_RES 47 47
 CC MOD_RES 48 48
 CC MOD_RES 55 55
 CC MOD_RES 57 57
 CC MOD_RES 60 60
 CC MOD_RES 61 61
 CC MOD_RES 66 66
 CC MOD_RES 67 67
 CC MOD_RES 67 67

FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 255 255
 FT ACT_SITE 301 301
 FT ACT_SITE 400 400
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 321
 FT DISULFID 240 256
 FT DISULFID 371 385
 FT DISULFID 396 424
 FT CARBOHYD 138 138
 FT CARBOHYD 292 292
 FT CARBOHYD 353 353
 SO SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 51.3%; Score 98; DB 1; Length 459;
 Best Local Similarity 45.5%; Pred. No. 7; 2e-10;
 Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;
 QY 1 ANGFLXLLRNGSLXKCRXKLCSPXAXFXFRNXXRRQWVSY 44
 DB 42 ANSFLBELRPSSLSRECKERTCDPEARELIFONTENTMAWSKY 85
 RESULT 10
 PA10_RABIT STANDARD; PRT; 490 AA.
 AC 019045;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OK NCBI_TaxID=9986;
 RN [1]
 RP MEDLINE=97256311; PubMed=9101642;
 RA Pendurthi U.R., Anderson K.D., James H.L.;
 RL "Characterization of a full-length cDNA for rabbit factor X.",
 CC Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
 CC (BY SIMILARITY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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RL J. Biol. Chem. 258:5548-5553 (1983).
 [6]
 RN PROCESSING, AND CALCIUM-BINDING DATA.
 RP MEDLINE=83213514; Pubmed=6406503;
 RX Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
 RA "structural changes required for activation of protein C are induced
 RT by Ca2+ binding to a high affinity site that does not contain gamma-
 RT carboxyglutamic acid."
 RL J. Biol. Chem. 258:5554-5560 (1983).
 CC -1 FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1 CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIA.
 CC -1 SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1 TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1 PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1 MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1 SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: K02435; AAA30685.1; -.
 DR PIR: A00928; KXBO.
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218; -.
 DR InterPro: IPR000152; Aex_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; trypsin_1.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; TRYP_SPC_1.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS00240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KM Blood coagulation; Glycoprotein; Serine protease;
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT NON_TER 1
 FT SIGNAL 1
 FT PROPEP 30
 FT CHAIN 40
 FT CHAIN 197
 FT PEPTIDE 197
 FT DOMAIN 94
 FT DOMAIN 133
 FT DOMAIN 211

FT MOD_RES 45
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 FT MOD_RES 68
 FT MOD_RES 74
 FT MOD_RES 110
 FT ACT_SITE 252
 FT ACT_SITE 298
 FT ACT_SITE 397
 FT DISULFID 56
 FT DISULFID 89
 FT DISULFID 98
 FT DISULFID 102
 FT DISULFID 119
 FT DISULFID 137
 FT DISULFID 144
 FT DISULFID 159
 FT DISULFID 180
 FT DISULFID 237
 FT DISULFID 368
 FT DISULFID 393
 FT CARBOHYD 136
 FT CARBOHYD 289
 FT CARBOHYD 350
 FT CARBOHYD 366
 FT VARIANT 82
 FT CONFLICT 455
 SQ SEQUENCE 456 AA; 51407 MW; CAA6833F894C209 CRC64;
 Query Match 48.7%; Score 93; DB 1; Length 456;
 Best Local Similarity 43.2%; Pred. No. 5,6e-09;
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
 QY 1 ANGFLXLRNGSLKRXCRXXLCSFXYAFKFRMXXRFRQFWGVY 44
 DB 40 ANSFLELRPGNVERECSEVCEFEARELIFONTEDTMAWSEFY 83
 ID FA10_HUMAN STANDARD; PRT; 488 AA.
 AC P00742; Q14340;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91216473; Pubmed=1902434;
 RA Messler T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
 RT human coagulation factor X."
 RL Gene 99:291-294 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87026600; Pubmed=3768336;
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RL Biochemistry 25:5098-5102 (1986).
 RN [3]

RP SEQUENCE OF 13-488 FROM N.A.
RX MEDLINE=65216545; PubMed=25882420.
RA Fung W.R., Hay C.W., McGillivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human
RL blood coagulation factor X.";
RN Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
[4]
RP SEQUENCE OF 19-488 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86221713; PubMed=3011603;
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
RT "Isolation and characterization of human blood-coagulation factor X
RL cDNA.";
RN Gene 41:311-314(1986).
[5]
RP SEQUENCE OF 41-179.
RX MEDLINE=89257207; PubMed=6681167;
RA Mcullen B.A., Fujikawa K., Kistiel W., Sasagawa T., Howald W.N.,
RA Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
RT coagulation factor X: evidence for identification of residue 63 as
RL beta-hydroxyaspartic acid.";
RN Biochemistry 22:2875-2884(1983).
[6]
RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=84222026; PubMed=6587384;
RA Leytus S.P., Chung D.W., Kistiel W., Kuzachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
[7]
RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RL moieties in the activation of factor X.";
RN Eur. J. Biochem. 218:153-163(1993).
[8]
RP SEQUENCE OF 1-23 FROM N.A.
RX MEDLINE=90128299; PubMed=2612918;
RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hameeshahnam K., Lyman G.;
RT "Cloning and characterization of the 5' end (exon I) of the gene
RL encoding human factor X.";
RN Gene 84:517-519(1989).
[9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=93360277; PubMed=8355279;
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;
RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
RL J. Mol. Biol. 223:947-966(1993).
[10]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=98283982; PubMed=9618463;
RA Kanata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
RT "Structural basis for chemical inhibition of human blood coagulation
RL factor Xa.";
RN Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
[11]
RP FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC CATALYTIC ACTIVITY: Preferential cleavage: Arg-[Thr and then
CC Arg-]-Ile bonds in prothrombin to form thrombin.
CC -1 SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC - BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OTHER
CC MORE DISULFIDE BONDS.
CC TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1 PM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1 PM: N- AND O-GLYCOSYLATED.
CC -1 PM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE

```

CC      INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 51.
CC      -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC      -----
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CC      entities requires a license agreement (See http://www.embnet.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL, K03194; AAA52490.1; -.
DR      EMBL, M57285; AAA52421.1; -.
DR      EMBL, L29433; AAA52764.1; -.
DR      EMBL, L00390; AAA52764.1; JOINED.
DR      EMBL, L00391; AAA52764.1; JOINED.
DR      EMBL, L00392; AAA52764.1; JOINED.
DR      EMBL, L00393; AAA52764.1; JOINED.
DR      EMBL, L00394; AAA52764.1; JOINED.
DR      EMBL, L00395; AAA52764.1; JOINED.
DR      EMBL, L00396; AAA52764.1; JOINED.
DR      EMBL, M22613; AAA51984.1; -.
DR      EMBL, K01866; AAA52486.1; -.
DR      EMBL, M33297; AAA52636.1; -.
DR      PIR, A20924; EXHU.
DR      PIR, A25853; A25853.
DR      PIR, A24478; A24478.
DR      PDB, 1HCG; 08-MAY-95.
DR      PDB, 1FAX; 29-OCT-97.
DR      PDB, 1EXY; 17-JUN-98.
DR      PDB, 1XKA; 23-MAR-99.
DR      PDB, 1XKB; 23-MAR-99.
DR      MEROPS, S01.216; -.
DR      GlycoSiteDB; P00742; -.
DR      Genew; HGNC:3528; P10.
DR      MIM, 134530; -.
DR      MIM, 227600; -.
DR      InterPro; IPR000152; Aex_hydroxyl.
DR      InterPro; IPR001314; Chymotrypsin.
DR      InterPro; IPR000561; EGF-like.
DR      InterPro; IPR000742; EGF_2.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR002383; GLA_Blood.
DR      InterPro; IPR001254; Ser_protease_Try.
DR      InterPro; IPR000294; VitK_dep_GLA.
DR      Pfam; PF00068; EGF_2.
DR      Pfam; PF00089; Trypsin_1.
DR      Pfam; PF00594; gla; 1.
DR      PRINTS; PRO0722; CHYMOTRYPSIN.
DR      PRINTS; PRO0001; GLABLOOD.
DR      SMART; SM00017; EGF_Ca; 1.
DR      SMART; SM00001; EGF_like; 1.
DR      SMART; SM00069; GLA; 1.
DR      SMART; SM00020; TRYD_SPC; 1.
DR      PROSITE; PS00010; ASX_HYDROXYL; 1.
DR      PROSITE; PS00022; EGF_1; 1.
DR      PROSITE; PS01186; EGF_2; 2.
DR      PROSITE; PS01187; EGF_CA; 1.
DR      PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR      PROSITE; PS50240; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; 1.
DR      PROSITE; PS00135; TRYPSIN_SER; 1.
KW      Glycoprotein. Hydrolase. Serine protease. Plasma. Blood coagulation;
KW      Gamma-carboxyglutamic acid. Hydroxylation; Calcium-binding; Vitamin K;
KW      Signal; Zymogen; EGF-like domain. Repeat; 3d-structure.
FT      SIGNAL 1 31
FT      PROPEP 32 40
FT      CHAIN 41 179 FACTOR X LIGHT CHAIN.
FT      CHAIN 183 488 FACTOR X HEAVY CHAIN.
FT      PROPEP 183 234 ACTIVATION PEPTIDE.
FT      CHAIN 235 488 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT      DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

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FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 235 488 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT MOD_RES 199 199 O-LINKED (GLNAC. . .)
FT CARBOHYD 211 211 O-LINKED (GLNAC. . .)
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .)
FT CARBOHYD 231 231 /FTID=CAR_000012.
FT CARBOHYD 231 231 /FTID=CAR_000013.
FT ACT_SITE 276 276 /FTID=CAR_000013.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110 CHARGE RELAY SYSTEM.
FT DISULFID 112 121 CHARGE RELAY SYSTEM.
FT DISULFID 129 140 CHARGE RELAY SYSTEM.

Query Match 48.4%; Score 92; DB 1; Length 488;
Best Local Similarity 36.4%; Pred. No. 9e-09;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANGLXXLRNGSLKRCRXKCSFXAFXRNRXRRQFVSVY 44
Db 41 ANSFLPEMKKHLEKCEMETCTSYEARVEPDSDKTFEWNKY 84

RESULT 13
PRIC_HUMAN STANDARD; PRT; 461 AA.
AC P04070; Q16001; Q15190; Q15189;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (Ec 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=65270390; Pubmed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RT "The nucleotide sequence of the gene for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
RN 2
RP SEQUENCE FROM N.A.
RX MEDLINE=65269639; Pubmed=2991859;
RA Beckmann R.J., Schmidt R.J., Santerre R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs.";
RL Nucleic Acids Res. 13:5233-5247(1985).
RN 3
RP SEQUENCE FROM N.A.
RX MEDLINE=86120978; Pubmed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
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RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN 5
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=84272714; Pubmed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN 6
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; Pubmed=1694179;
RA Mjelich J.P., Broze G.J. Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN 7
RP HYDROXYLATION.
RX MEDLINE=92184750; Pubmed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN 8
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; Pubmed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN 9
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; Pubmed=9003757;
RA Mather T., Oganesyan V., Hof P., Huber R., Foundling S., Esmen C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN 10
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; Pubmed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
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RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN 11
RP VARIANT CYS-444.
RX MEDLINE=87204221; Pubmed=2437584;
RA Romeo G., Hassan H.J., Staampfli S., Roncuzzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
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RT mutations in the protein C gene.";
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RN 12
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=90098906; Pubmed=2602169;
RA Grundy C.B., Chitloie A., Talbot S., Bevan D., Kakkar V.V.,
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RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
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RN 13
RP VARIANT CYS-272.
RX MEDLINE=91329836; Pubmed=1868249;
RA Reitsma P.H., Poort S.R., Allart C.F., Briet E., Bertina R.M.;
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 RN [14]
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 RX MEDLINE=92190481; PubMed=1347706;
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
 RA Rainville I.R., Long G.L.;
 RT "Protein C deficiency: symptomatic type II protein C deficiency
 RT associated with two GLA domain mutations.";
 RL Blood 79:1456-1465(1992).
 RN [15]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RT a missense mutation.";
 RL Blood 80:126-133(1992).
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 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RT causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [17]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schliman S., Tengborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RT gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [18]
 RP VARIANT GLN-220.
 RX MEDLINE=92350852; PubMed=1301959;
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 RA Gaudrille S., Toulin P., Fiesinger J.N., Goossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
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 RT electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [19]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yamamoto K., Matsumita T., Sugitani I., Takamatsu J., Iwasaki E.,
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 RT "Homozygous protein C deficiency: identification of a novel missense
 RT mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
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 RP VARIANTS TRP-38, CYS-42, HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE=93313192; PubMed=8324221;
 RA Gaudrille S., Alhenc-Gelas M., Gausem P., Allaud M.-F., Dupuy E.,
 RA Juhani-Vague I., Alach M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RT gene in patients presenting with defective protein C anticoagulant
 RT activity.";
 RL Blood 82:159-168(1993).
 RN [21]
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND
 RP V-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poor S.R., Fabinger-Fasching I., Mannhalter C., Reitema P.H.,
 RA Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RT with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [22]
 RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A Glu domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 RT causing type 2 protein C deficiency and recurrent venous

RT thrombosis.";
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [23]
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; W-340 AND Y-426.
 RX MEDLINE=94122329; PubMed=8292730;
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
 RA Koopman M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with
 RT symptomatic type I protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).
 RN [24]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Patrachini P., Gemmati D., Castaman G., Rodeghiero F.,
 RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RL Br. J. Haematol. 84:285-289(1993).
 RN [25]
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
 Query Match 47.1%; Score 90; DB 1; Length 461;
 Best Local Similarity 46.3%; Pred. No. 1.9e-08;
 Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
 Oy 1 ANGFLXLRNGSLKRXCRXXLCSEFXAXFIRNXXRTQFM 41
 Db 43 ANSFLELRHSLRECEIEICDFEEAKEIFQNVDDTLAFW 83
 RESULT 14
 FA10_BOVIN STANDARD; PRT; 492 AA.
 ID FA10_BOVIN
 AC P00743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OK NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-487 FROM N.A.
 RX MEDLINE=84247315; PubMed=6330671;
 RA Fung M.R., Campbell R.M., McGilivray R.T.A.;
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
 RT containing a prepro leader sequence.";
 RL Nucleic Acids Res. 12:4481-4492(1984).
 RN [2]
 RP SEQUENCE OF 41-180.
 RX MEDLINE=80130563; PubMed=6766735;
 RA Entfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
 RA Titani K.;
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
 RT factor).";
 RL Biochemistry 19:659-667(1980).
 RN [3]
 RP REVISION TO 103.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kisiel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens.";
 RL Biochem. Biophys. Res. Commun. 115:8-14(1993).
 RN [4]
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Titani K., Fujikawa K., Entfield D.L., Ericsson L.H., Walsh K.A.,
 RA Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 RT chain.";

Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 [5]
 RN SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RP MEDLINE=94062825; PubMed=8243461;
 RX Inoue K., Morita T.;
 RA "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE=73053314; PubMed=4264286;
 RA Titani K., Hermanson M.A., Fujikawa K., Ericsson J.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 RL Biochemistry 11:4899-4903(1972).
 RN [7]
 RP PROCESSING.
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Titani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN [8]
 RP CALCULUM-BINDING DATA.
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN [9]
 RP SULFATION.
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN [10]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=91084483; PubMed=2261466;
 RA Seldner M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the C2(+)-free form of
 RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN [11]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92329412; PubMed=627540;
 RA Ullner M., Seldner M., Persson E., Stenflo J., Drakenberg T.,
 RA Teleman O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN [12]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1527084;
 RA Seldner M., Seldner M., Ullner M., Persson E., Teleman O.,
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 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
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 RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96367194; PubMed=8794734;
 RA Sunnehaugen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Tremella J.;
 RT "The relative orientation of Glu and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";

Biochemistry 35:11547-11559(1996).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC CATALYTIC ACTIVITY: Preferential cleavage: Arg|-Thr and then
 CC Arg|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; X00673; CAA35286.1; -.
 CC PIR; A00925; EXBO.
 CC PDB; IAPD; 31-JAN-94.
 CC PDB; 1CCF; 31-MAY-94.
 CC PDB; 1WHE; 15-MAY-97.
 CC PDB; 1WHE; 15-MAY-97.
 CC MEROPS; S01.216; -.
 CC DR GlycosultedB; P00743; -.
 CC DR InterPro; IPR000152; Asx_hydroxyl.
 CC DR InterPro; IPR001314; Chymotrypsin.
 CC DR InterPro; IPR000561; EGF-like.
 CC DR InterPro; IPR000742; EGF_2.
 CC DR InterPro; IPR001881; EGF-Ca.
 CC DR InterPro; IPR002383; GLA_blood.
 CC DR InterPro; IPR001254; Ser_protease_Try.
 CC DR InterPro; IPR000294; VitK_dep_GLA.
 CC DR Pfam; PR00008; EGF_2.
 CC DR Pfam; PR00089; trypsin; 1.
 CC DR Pfam; PR00594; gla; 1.
 CC DR PRINTS; PR00722; CHYMOTRYPSIN.
 CC DR PRINTS; PR00001; GLABLOOD.
 CC DR SMART; SM00179; EGF_CA; 1.
 CC DR SMART; SM00001; EGF_like; 1.
 CC DR SMART; SM00069; GLA; 1.
 CC DR SMART; SM00020; TRYP_SPC; 1.
 CC DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC DR PROSITE; PS00022; EGF_1; 1.
 CC DR PROSITE; PS01186; EGF_2; 2.
 CC DR PROSITE; PS01187; EGF_CA; 1.
 CC DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 CC DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC DR PROSITE; PS00135; TRYPSIN_SER; 1.
 CC KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 CC KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 CC FT SIGNAL 1 23
 CC FT PROPEP 24 40
 CC FT CHAIN 41 180
 CC FT CHAIN 183 492
 CC FT PROPEP 183 233
 CC FT CHAIN 234 492
 CC FT PROPEP 476 492
 CC FT DOMAIN 86 122
 CC FACTOR X LIGHT CHAIN.
 CC FACTOR X HEAVY CHAIN.
 CC ACTIVATION PEPTIDE.
 CC ACTIVATED FACTOR XA, HEAVY CHAIN
 CC MAY BE REMOVED BUT IS NOT NECESSARY FOR
 CC ACTIVATION.
 CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

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FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 234 492 SERINE PROTEASE.
FT ACT_SITE 275 425 CHARGE RELAY SYSTEM.
FT ACT_SITE 321 321 CHARGE RELAY SYSTEM.
FT ACT_SITE 418 418 CHARGE RELAY SYSTEM.
FT MOD_RSS 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RSS 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RSS 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RSS 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RSS 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RSS 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RSS 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RSS 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

Query Match 45.5%; Score 87; DB 1; Length 492;
Best Local Similarity 36.4%; Pred. No. 7.2e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRNGSLRXCRXXLCSPKXAFIFRNXXRTQFWTSY 44
Db 41 ANSFLEEVKQGLERECLEACSLSEAREVPDAEQTDEFSKY 84

RESULT 15
THRB_HUMAN STANDARD; PRT; 622 AA.
AC P00734;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RX MEDLINE=88077877; PubMed=2825773;
RA Degen S.J.F., Davie E.W.;
RT "Nucleotide sequence of the gene for human prothrombin.";
RL Biochemistry 26:6165-6177(1987).
RN [2]
RX MEDLINE=83231469; PubMed=6305407;
RA Degen S.J.F., McGillivray R.T.A., Davie E.W.;
RT "Characterization of the complementary deoxyribonucleic acid and gene coding for human prothrombin.";
RL Biochemistry 22:2087-2097(1983).
RN [3]
RX MEDLINE=83231469; PubMed=6305407;
RA Degen S.J.F., McGillivray R.T.A., Davie E.W.;
RT "Characterization of the complementary deoxyribonucleic acid and gene coding for human prothrombin.";
RL Biochemistry 22:2087-2097(1983).
RN [4]
RX MEDLINE=77193964; PubMed=266717;
RA Walz D.A., Hewett-Evmet D., Seegers W.H.;
RT "Amino acid sequence of human prothrombin fragments 1 and 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
RN [5]
RX MEDLINE=87008532; PubMed=3759958;
RA Rabiet M.-J., Blaehill A., Furie B., Furie B.C.;
RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin activation in human plasma.";
RL J. Biol. Chem. 261:13210-13215(1986).
RN [6]
RX MEDLINE=87008532; PubMed=3759958;
RA Rabiet M.-J., Blaehill A., Furie B., Furie B.C.;
RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin activation in human plasma.";
RL J. Biol. Chem. 261:13210-13215(1986).
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RN [7]
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=90059942; PubMed=2583108;
RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
RT "The refined 1.9 A crystal structure of human alpha-thrombin: interaction with D-Phe-Pro-Arg chloromethylketone and significance of the Tyr-Pro-Tip insertion segment.";
RL EMBO J. 8:3467-3475(1989).
RN [8]
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=90327074; PubMed=2374926;
RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R., Roltsch C., Fenton J.W. II;
RT "The structure of a complex of recombinant hirudin and human alpha-thrombin.";
RL Science 249:277-280(1990).
RN [9]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94350942; PubMed=8071320;
RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D., Correa P.E., Fenton J.W. II, Tulinsky A.;
RT "Crystallographic structure of human gamma-thrombin.";
RL J. Biol. Chem. 269:22000-22006(1994).
RN [10]
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=97357286; PubMed=9214615;
RA van de Loch A., Bode W., Huber R., le Bonniec B.F., Stone S.R., Esmon C.T., Stubbs M.T.;
RT "The thrombin E192Q-BPTI complex reveals gross structural rearrangements: implications for the interaction with antithrombin and thrombomodulin.";
RL EMBO J. 16:2977-2984(1997).
RN [11]
RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
RX MEDLINE=99162521; PubMed=10051558;
RA Guinto E.R., Caccia S., Rose T., Fuetterer K., Waksman G., di Cera E.;
RT "Unexpected crucial role of residue 225 in serine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
RN [12]
RX MEDLINE=87033739; PubMed=3771562;
RA Rabiet M.-J., Furie B.C., Furie B.;
RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine for arginine at residue 273.";
RL J. Biol. Chem. 261:15045-15048(1986).
RN [13]
RX MEDLINE=95313001; PubMed=7792730;
RA Degen S.J.F., McDowell S.A., Sparks L.M., Scharer I.;
RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by substitution of Glu-466 by Ala.";
RL Thromb. Haemost. 73:203-209(1995).
RN [14]
RX MEDLINE=93043342; PubMed=1421398;
RA Morishita E., Saito W., Kumabashiri I., Asekura H., Matsumoto T., Yamaguchi K.;
RT "Prothrombin Himi: a compound heterozygote for two dysfunctional prothrombin molecules (Met-337-->Thr and Arg-388-->His).";
RL Blood 80:2275-2280(1992).
RN [15]
RX MEDLINE=95169898; PubMed=7865694;
RA James H.L., Kim D.J., Zheng D.-Q., Girolami A.;
RT "Prothrombin Padua I: incomplete activation due to an amino acid substitution at a factor Xa cleavage site.";
RL Blood Coagul. Fibrinolysis 5:841-844(1994).
RN [16]
RX MEDLINE=89207504; PubMed=3242619;
RA Henriksen R.A., Mann K.G.;
RT "Identification of the primary structural defect in the dysprothrombin thrombin Quick I: substitution of cysteine for arginine-382.";
```

RL Biochemistry 27:9160-9165(1988).
 RN (17)
 RP VARIANT QUICK-2.
 RX MEDLINE=89247398; PubMed=2719946;
 RA Henriksen R.A., Mann K.G.;
 RT "Substitution of valine for glycine-558 in the congenital dysfibrinogen
 thrombin Quick II alters primary substrate specificity.";
 RL Biochemistry 28:2078-2082(1989).
 RN (18)
 RP VARIANT SALAKTA.
 RX MEDLINE=92378975; PubMed=1354985;
 RA Miyata T., Aruga R., Uneyama H., Bezeaud A., Guillin M.-C.,
 RA Iwanaga S.;
 RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
 reduces the fibrinogen clotting activity and the esterase activity.";
 RL Biochemistry 31:7457-7462(1992).
 RN (19)
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=87185407; PubMed=3567158;
 RA Miyata T., Morita T., Inomoto T., Kawachi S., Shirakami A.,
 RA Iwanaga S.;
 RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
 that impairs the fibrinogen clotting activity of derived thrombin
 Tokushima.";
 RL Biochemistry 26:1117-1122(1987).
 RN (20)
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=87101511; PubMed=3801671;
 RA Inomoto T., Shirakami A., Kawachi S., Shigekiyo T., Saito S.,
 RA Miyoshi K., Morita T., Iwanaga S.;
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
 derived from a variant of human prothrombin.";
 RL Blood 69:565-569(1987).
 RN (21)
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=92256895; PubMed=1349838;
 RA Iwahana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,
 RA Itakura M.;
 RT "Detection of a single base substitution of the gene for prothrombin
 Tokushima. The application of PCR-SSCP for the genetic and molecular
 analysis of dysprothrombinemia.";
 RL Int. J. Hematol. 55:93-100(1992).
 RN (22)
 RP VARIANT TYPE-3.
 RX MEDLINE=83204687; PubMed=6405779;
 RA Board P.G., Shaw D.C.;
 RT "Determination of the amino acid substitution in human prothrombin
 type 3 (157 Glu leads to Lys) and the localization of a third
 thrombin cleavage site.";
 RL Br. J. Haematol. 54:245-254(1983).
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C,
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
 fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER. FOUND IN PLASMA.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 OF PROTHROMBIN TO THROMBIN.
 CC -1- DISEASE: DEFECTS IN F2 ARE THE CAUSE OF VARIOUS FORMS OF
 DYSPROTHROMBINEMIA.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS. FACTOR XA REMOVES
 THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 THROMBIN.
 CC -1- MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION

CC PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN
 CC NATURAL BLOOD CLOTTING.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO, DOES
 Query Match 45.0%; Score 86; DB 1; Length 622;
 Best Local Similarity 38.6%; Pred. No. 1.4e-07;
 Matches 17; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLXRXCRXXLCSFXXAFXFRNXXTRQFWSY 44
 DB 44 ANTFLEVRKGNLRRCVETCTSYEAFFEALESSTATDVFWAKY 87

Search completed: March 19, 2003, 14:53:00
 Job time : 6.625 secs

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GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10ASN28PHE_4
Perfect score: 191
Sequence: 1 ANGFLXLLRNGSLXRCRX.....XXAFKIFRNXXRTPFWSV 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	62.3	701	4 Q96PQ8	Q96PQ8 homo sapien
2	103	53.9	460	11 Q91WN8	Q91WN8 mus musculu
3	102	53.4	446	11 Q61109	Q61109 mus musculu
4	97	50.8	460	11 Q99PC6	Q99PC6 mus musculu
5	95	49.7	456	6 Q91TR0	Q91TR0 canis fami1
6	92	48.2	482	11 Q63207	Q63207 rattus norv
7	89	46.6	481	11 Q54740	Q54740 mus musculu
8	89	46.6	481	11 Q99J32	Q99J32 mus musculu
9	89	46.6	481	11 Q88947	Q88947 mus musculu
10	86	45.0	100	4 Q15253	Q15253 homo sapien
11	86	45.0	608	13 Q9PTW7	Q9PTW7 struthio ca
12	85	44.5	49	6 Q95ME8	Q95ME8 bos taurus
13	85	44.5	456	4 Q14316	Q14316 homo sapien
14	85	44.5	461	6 Q95ND7	Q95ND7 pan troglod
15	85	44.5	461	6 Q95ND6	Q95ND6 pan troglod
16	85	44.5	469	6 Q9GMD9	Q9GMD9 ornithorhyn

17	78	40.8	138	6 Q28994	Q28994 sus scrofa
18	78	40.8	433	13 Q90YK1	Q90YK1 brachydanto
19	74	38.7	607	13 Q91001	Q91001 gallus gall
20	72	37.7	648	6 Q29094	Q29094 sus scrofa
21	71	37.2	399	11 Q9COW3	Q9COW3 mus musculu
22	68.5	35.9	542	5 Q8TE13	Q8TE13 halocynthia
23	67	35.1	179	4 Q8TAS3	Q8TAS3 homo sapien
24	67	35.1	198	11 Q8TAS3	Q8TAS3 homo sapien
25	67	35.1	650	4 Q9NSD0	Q9NSD0 homo sapien
26	67	35.1	650	4 Q16519	Q16519 homo sapien
27	57	29.8	25	11 Q9QVH6	Q9QVH6 rattus sp.
28	56	29.3	678	11 Q14393	Q14393 homo sapien
29	55	28.8	673	11 Q61592	Q61592 mus musculu
30	55	28.8	674	11 Q99K57	Q99K57 mus musculu
31	53	27.7	98	13 P82807	P82807 notechis sc
32	53	27.7	674	11 Q63772	Q63772 rattus sp.
33	52	27.2	249	5 Q9VYS0	Q9VYS0 drosophila
34	51	26.7	130	12 Q9DUB8	Q9DUB8 tt virus. o
35	50	26.2	184	10 Q9LVF1	Q9LVF1 arabidopsis
36	49	25.7	1217	5 Q9XV62	Q9XV62 caenorhabdi
37	48	25.1	472	13 Q98SU5	Q98SU5 gaetereoste
38	48	25.1	613	13 Q98SU5	Q98SU5 gaetereoste
39	48	25.1	910	13 Q98SU7	Q98SU7 gaetereoste
40	47.5	24.9	575	10 Q94E17	Q94E17 oryza sativ
41	47.5	24.9	608	10 Q9XF36	Q9XF36 medicago sa
42	46.5	24.3	196	10 Q04284	Q04284 selaginella
43	46.5	24.3	567	10 Q8W4J2	Q8W4J2 arabidopsis
44	46.5	24.3	603	10 Q9LPG7	Q9LPG7 arabidopsis
45	46.5	24.3	606	10 Q9SUG9	Q9SUG9 arabidopsis

ALIGNMENTS

RESULT 1

Q96PQ8 PRELIMINARY; PRT; 701 AA.

ID Q96PQ8

AC Q96PQ8; 01-DIC-2001 (TEMBLrel. 19, Created)

DT 01-DIC-2001 (TEMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)

DE Factor VII active site mutant immunocoujugate.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NC NCB1_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21477448; PubMed=11593034;

RA Hu Z., Garen A.;

RT "Targeting tissue factor on tumor vascular endothelial cells and tumor

RT cells for immunotherapy in mouse models of prostatic cancer.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).

DR EMBL; AF272774; AAKS8686.1; -

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VltK_dep_GLA.

DR Pfam; PRF00008; EGF_2.

DR Pfam; PRF00594; G1a; 1.

DR Pfam; PRF00047; Ig; 2.

DR Pfam; PRF00089; trypsin; 1.

DR SMART; SM00181; EGF; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01186; EGF_2; UNKNOWN_1.

DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

DR PROSITE; PSS0240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94ACCEB42CC992F CRC64;

Query Match 62.3%; Score 119; DB 4; Length 701;
Best Local Similarity 52.3%; Pred. No. 4.4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRXCRXXLCSFXXAFIPRNXXRTQFWVS 44
Db 61 ANAFLEELRPGSLERECKEBOCSFEAREITFDARTKLFWISY 104

RESULT 2

091NM8

ID 091NM8 PRELIMINARY; PRT; 460 AA.

AC 091NM8;

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Similar to protein C.

GN PROC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RA Strauberg R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC013896; AAH13896.1; -.

DR MGD; MGI:97771; Proc.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001254; Ser_protease_Try.

DR Pfam; PF000294; VltK_dep_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00089; trypsin; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01186; EGF_2; UNKNOWN_2.

DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.

DR PROSITE; PS02440; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.

KM Hydrolase; Serine protease.

SQ SEQUENCE 460 AA; 51818 MW; 0117F26B6FCC274 CRC64;

Query Match 53.9%; Score 103; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 2.5e-10;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRXCRXXLCSFXXAFIPRNXXRTQFWVS 44
Db 42 ANSLLEELWPGSLERECKEBOCSFEAREITKSPRTKQFWIV 85

RESULT 3

061109

ID 061109 PRELIMINARY; PRT; 446 AA.

AC 061109;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Coagulation factor VII.

GN F7 OR FVII.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RX MEDLINE=96276538; PubMed=8701412;

RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,

RA Castellino F.J.;

RT "Characterization of a cDNA encoding murine coagulation factor VII.";

RT Thomb. Haemost. 75:481-487(1996).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

CC TRYPSIN FAMILY

CC EMBL; U44795; AAC52570.1; -.

DR HSSP; P08709; 1PAK.

DR MEROPS; S01.215; -.

DR MGD; MGI:109325; F7.

DR InterPro; IPR002086; Aldehyde dehydr.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR001064; Crystallin.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR002383; GLA_plood.

DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR00294; VltK_dep_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 1.

DR SMART; SM00001; EGF_like; 1.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; TRYP_SPC; 1.

DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.

DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

DR PROSITE; PS00225; CRYSTALLIN_BETGAMMA; UNKNOWN_1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS02440; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;

KM Serine protease.

SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 53.4%; Score 102; DB 11; Length 446;
Best Local Similarity 47.7%; Pred. No. 3.6e-10;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRNGSLKRXCRXXLCSFXXAFIPRNXXRTQFWVS 44
Db 42 ANSLLEELWPGSLERECKEBOCSFEAREITKSPRTKQFWIV 85

RESULT 4

099PC6

ID 099PC6 PRELIMINARY; PRT; 460 AA.

AC 099PC6;

DT 01-JUN-2001 (TRENBLrel. 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Anticoagulant protein C.

GN PROC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL;

RA Kozf I.;

RT "Complete sequence of UC72A01.";
RU Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF318182; AAK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGJ:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;
Query Match 50.8%; Score 97; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 3.1e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
QY 1 ANGFLXXLRNGSLKRXCRXXLCSPFXAFLPRNXXRTQRFVSY 44
DB 42 ANSLFLEMRPOSLEKRCMEICDLEBAQEIFQVNDTLAYWIKY 85
RESULT 5
Q9TRRO PRELIMINARY; PRT; 456 AA.
AC Q9TRRO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Protein C precursor.
OS PROC.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matie U., Brunberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene.";
RL Mamm. Genome 10:135-139 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99371952; Pubmed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms.";
RL Anim. Genet. 30:237-238 (1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

DR EMBL; AJ001979; CAA05126.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL 1 42
FT CHAIN 43 192
FT CHAIN 193 194
FT CHAIN 195 456
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;
Query Match 49.7%; Score 95; DB 6; Length 456;
Best Local Similarity 43.2%; Pred. No. 7e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
QY 1 ANGFLXXLRNGSLKRXCRXXLCSPFXAFLPRNXXRTQRFVSY 44
DB 43 ANSLFLEMRPOSLEKRCMEICDLEBAQEIFQVNDTLAYWIKY 86
RESULT 6
Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; Pubmed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73 (1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; X79807; CAA56202.1; -.
DR HSSP; P00742; 1YXA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00059; GLA; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 48.2%; Score 92; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 2.6e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLKRCXKXLCSEFXKXAFIRNXXRTQFWVSY 44
Db 41 ANSFEEFKGNLERECWEICSEYEVREIFEDDEKTKYWTXY 84

RESULT 7

OS04740 PRELIMINARY; PRT; 481 AA.
ID OS04740
AC OS04740; 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR F10.
OS Mus musculus (Mouse).
OC Plasmid; B12; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98454993; PubMed=9783672;
RA Heldmann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
DR EMBL; AJ222677; CAA10933.1; -.
DR HSSP; P00742; IYKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00059; GLA; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481
SQ SEQUENCE 481 AA; 53986 MW; CF702DB5EF9D97AE CRC64;

Query Match 46.6%; Score 89; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 9.2e-08;
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXLRNGSLKRCXKXLCSEFXKXAFIRNXXRTQFWVSY 44
Db 41 ANSFEEFKGNLERECWEICSEYEVREIFEDDEKTKYWTXY 84

RESULT 8

Q99L32 PRELIMINARY; PRT; 481 AA.
ID Q99L32
AC Q99L32; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
DR EMBL; BC003877; AA03877.1; -.
DR HSSP; P00742; IYKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_1.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00059; GLA; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF_CA.1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88B96C8A0B7E7F CRC64;
Query Match 46.6%; Score 89; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 9.2e-08;
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
Qy 1 ANGFLXXLRNGSLRXCRXXLCSPFXAXFIFRNXXRTROFWVSY 44
Db 41 ANSFEEFKKGNLERECMEICSYEVRREIFEDDKTKETWTKY 84
RESULT 9
088947 PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE=8347933; Pubmed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
factor X";
RT Thromb. Haemost. 80:87-91 (1998).
RL
RN
RN
RP SEQUENCE FROM N.A.
RC STRAIN=129SJ;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of the Murine Factor X Gene";
RT Thromb. Haemost. 0:0-0 (2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC36345.1; -;
DR EMBL; AF211347; AAF22980.1; -;
DR HSSP; P00742; 1KKA.
DR MEROPS; S01.216; -;
DR MGD; MGI:103107; F10.
DR Interpro; IPR000152; Asx_hydroxyl.
DR Interpro; IPR001314; Chymotrypsin.
DR Interpro; IPR000561; EGF-like.
DR Interpro; IPR000742; EGF_2.
DR Interpro; IPR001881; EGF_Ca.
DR Interpro; IPR002383; GLA_blood.
DR Interpro; IPR001254; Ser_protease_Try.
DR Interpro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA.1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF_CA.1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5E9D271E CRC64;
Query Match 46.6%; Score 89; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 9.2e-08;
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
Qy 1 ANGFLXXLRNGSLRXCRXXLCSPFXAXFIFRNXXRTROFWVSY 44
Db 41 ANSFEEFKKGNLERECMEICSYEVRREIFEDDKTKETWTKY 84
RESULT 10
015253 PRELIMINARY; PRT; 100 AA.
ID 015253
AC 015253;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thrombin precursor (Fragment).
GN F2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; Pubmed=3471151;
RA MacGillivray R.T., Irwin D.M., Guinco E.R., Stone J.C.;
RT "Recombinant genetic approaches to functional mapping of thrombin.";
RL Ann. N. Y. Acad. Sci. 485:73-79 (1986).
DR EMBL; M33031; AAA60220.1; -;
DR HSSP; P00735; 2PFI.
DR Interpro; IPR002383; GLA_blood.
DR Interpro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW SIGNAL.
FT SIGNAL 1 43
FT CHAIN 44 >100
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 11302 MW; FD0E5D0174E1F6FE CRC64;
Query Match 45.0%; Score 86; DB 4; Length 100;
Best Local Similarity 38.6%; Pred. No. 6.9e-08;
Matches 17; Conservative 4; Mismatches 23; Indels 0; Gaps 0;
Qy 1 ANGFLXXLRNGSLRXCRXXLCSPFXAXFIFRNXXRTROFWVSY 44
Db 44 ANTLFEBVRKGNLERECVEETCSYBAFEALBSTADVWAKY 87
RESULT 11
09PTW7 PRELIMINARY; PRT; 608 AA.
ID 09PTW7
AC 09PTW7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Prothomdin.
GN OSPT.
OS Struthio camelus (Ostrich).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
OC Struthio.
OX NCBI_Taxid=8601;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20579470; PubMed=1137455;
RA Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.;
RT "Participation and characterization of ostrich prothrombin.";
RL Int. J. Biochem. Cell Biol. 32:1151-1159(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AB028871; BAA89046.1; -.
DR HSSP: P00734; IUVS.
DR MEROPS: S01.217; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Ser. protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00051; Kringle_2.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PRODOM: PD000395; Kringle_2.
DR SMART: SM00069; GLA_1.
DR SMART: SM00130; KR_2.
DR SMART: SM00020; Tryp_Spc_1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS50070; KRINGLE_2; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolyase: Serine protease.
SQ SEQUENCE 608 AA; 69392 MW; 11B974B9AE54EA2 CRC64;

Query Match 45.0%; Score 86; DB 13; Length 608;
Best Local Similarity 35.7%; Pred. No. 4.1e-07;
Matches 15; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 3 GFLXLRNGSLRXRCRXLYLCSFXAFIFRNXXRTROFWVSY 44
Db 47 GFLEEMLGNLERECLEICIEEFALEASTARTEEFWSKY 88

RESULT 12
Q95ME8 PRELIMINARY; PRT; 49 AA.
AC Q95ME8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizlata M.N., Amaral E.J.;
RT "Partial sequence of bovine F9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF394598; AAK7556.1; -.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla_1.
DR PROSITE: PS00011; GLU CARBOXYLATION; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 49 AA; 6023 MW; DISC6DE9CBA4A14 CRC64;
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Query Match 44.5%; Score 85; DB 6; Length 49;
Best Local Similarity 37.2%; Pred. No. 5.2e-08;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXLRNGSLRXRCRXLYLCSFXAFIFRNXXRTROFWVSY 44
Db 6 SGKLEEFVRGNLERECKSEKSFEEARREVFENTETTEFWQY 48

RESULT 13
Q14316 PRELIMINARY; PRT; 456 AA.
AC Q14316;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1999 (TREMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, Christmas
DE disease, HAEMOPHILIA B)) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemsma A.,
RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AL033403; CAA21954.1; -.
DR EMBL: X55008; CAB38245.2; -.
DR HSSP: P00740; ICFH.
DR MEROPS: S01.214; -.
DR InterPro: IPR000152; Aex hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR00742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR001254; Ser. protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBLLOOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA_1.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; Tryp_Spc_1.
DR PROSITE: PS00010; ASX hydroxyl; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA_1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E214 CRC64;

Query Match 44.5%; Score 85; DB 4; Length 456;
Best Local Similarity 39.5%; Pred. No. 4.7e-07;
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Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXLRNGSLXRCXRLCSFXXAFIIPNXXRTROFWVS 44
Db 44 SGKLEEFVQGNLERECMEKCSFEAREVFNTERTEFTFWKQY 86

RESULT 14

Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxId=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_Protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydroxylase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 44.5%; Score 85; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 4.8e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXLRNGSLXRCXRLCSFXXAFIIPNXXRTROFWVS 44
Db 49 SGKLEEFVQGNLERECMEKCSFEAREVFNTERTEFTFWKQY 91

RESULT 15

Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN
OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxId=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; -.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_Protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydroxylase; Serine protease.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 44.5%; Score 85; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 4.8e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXLRNGSLXRCXRLCSFXXAFIIPNXXRTROFWVS 44
Db 49 SGKLEEFVQGNLERECMEKCSFEAREVFNTERTEFTFWKQY 91

Search completed: March 19, 2003, 15:13:42
Job time : 47.3125 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10ASN28PHE_4
Perfect score: 191
Sequence: 1 ANGFLXXLRNGSLRXCRXX.....XXAFXIFRNXXRTQFWVSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154	80.6	44	3	US-08-955-636-4
2	128	67.0	44	3	US-08-955-636-28
3	122	63.9	44	3	US-08-955-636-27
4	121	63.4	44	3	US-08-955-636-26
5	119	62.3	44	3	US-08-955-636-3
6	119	62.3	44	3	US-08-955-636-30
7	119	62.3	406	1	US-08-293-778-24
8	119	62.3	406	1	US-08-295-411-5
9	119	62.3	406	5	US-08-955-471-5
10	119	62.3	406	5	PCT-US93-10242-5
11	119	62.3	444	1	US-08-475-845-2
12	119	62.3	444	2	US-08-327-590-2
13	119	62.3	444	2	US-08-660-289-2
14	119	62.3	444	2	US-08-537-807-2
15	119	62.3	444	2	US-08-871-003-2
16	119	62.3	444	2	US-08-464-333-2
17	119	62.3	444	4	US-08-189-607-2
18	119	62.3	444	4	US-09-378-907-2
19	119	62.3	444	5	PCT-US94-05779-2
20	119	62.3	466	1	US-07-882-0202A-4
21	119	62.3	466	1	US-08-021-615A-4
22	119	62.3	466	1	US-08-321-777-4
23	119	62.3	466	4	US-09-009-217-14
24	119	62.3	466	4	US-09-009-656-14
25	119	62.3	466	5	PCT-US93-04493-4
26	115	60.2	44	3	US-08-955-636-29
27	105	55.0	41	1	US-08-229-280-4

28	97	50.8	139	1	US-08-330-978-2	Sequence 2, Appl1
29	97	50.8	139	1	US-08-474-042-2	Sequence 2, Appl1
30	97	50.8	139	1	US-08-484-558-2	Sequence 2, Appl1
31	97	50.8	139	1	US-08-774-592-2	Sequence 2, Appl1
32	97	50.8	437	1	US-08-487-037-2	Sequence 2, Appl1
33	97	50.8	437	1	US-08-487-037-3	Sequence 3, Appl1
34	97	50.8	488	1	US-08-487-037-1	Sequence 1, Appl1
35	96	50.3	44	3	US-08-955-636-23	Sequence 23, Appl1
36	93	48.7	44	3	US-08-955-636-2	Sequence 2, Appl1
37	93	48.7	44	3	US-08-955-636-25	Sequence 25, Appl1
38	92	48.2	448	1	US-08-295-411-3	Sequence 3, Appl1
39	92	48.2	448	2	US-08-955-471-3	Sequence 3, Appl1
40	92	48.2	448	5	PCT-US92-10068-1	Sequence 1, Appl1
41	92	48.2	448	5	PCT-US92-10242-3	Sequence 3, Appl1
42	90	47.1	41	1	US-08-229-280-5	Sequence 5, Appl1
43	90	47.1	42	2	US-08-745-254A-2	Sequence 2, Appl1
44	90	47.1	44	3	US-08-955-636-1	Sequence 1, Appl1
45	90	47.1	45	2	US-08-965-832-2	Sequence 2, Appl1

ALIGNMENTS

```
RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelssestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      80.6%; Score 154; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 6.6e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ANGFLXXLRNGSLRXCRXXLCFXAXFIFRNXXRTQFWVSY 44
Db       1 ANGFLXXLRNGSLRXCRXXLCFXAXHIFRNXXRTQFWVSY 44

RESULT 2
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelssestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28

Query Match 67.0%; Score 128; DB 3; Length 44;
Best Local Similarity 77.3%; Pred. No. 2,1e-15;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRNGSLXRCXRLCSFYXAFIFRNXXRTROFWVS 44
Db 1 ANAFLLXLRPGSLXRCXRCXQCSFYXAFIFDAXRTKLFWISY 44

RESULT 3

US-08-955-636-27
Sequence 27, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match 63.9%; Score 122; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 2,4e-14;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRNGSLXRCXRLCSFYXAFIFRNXXRTROFWVS 44
Db 1 ANAFLLXLRDGSXLRXCXQCSFYXARXIFDAXRTKLFWISY 44

RESULT 4

US-08-955-636-26
Sequence 26, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match 63.4%; Score 121; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3,5e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRNGSLXRCXRLCSFYXAFIFRNXXRTROFWVS 44
Db 1 ANAFLLXLRDGSXLRXCXQCSFYXARXIFDAXRTKLFWISY 44

RESULT 5

US-08-955-636-3
Sequence 3, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match 62.3%; Score 119; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7,8e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRNGSLXRCXRLCSFYXAFIFRNXXRTROFWVS 44
Db 1 ANAFLLXLRPGSLXRCXRCXQCSFYXARXIFDAXRTKLFWISY 44

RESULT 6

US-08-955-636-30
Sequence 30, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30

Query Match 62.3%; Score 119; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7,8e-14;
Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRNGSLXRCXRLCSFYXAFIFRNXXRTROFWVS 44
Db 1 ANAFLLXLRQGSXLRXCXQCSFYXARXIFDAXRTKLFWISY 44

RESULT 7

US-08-293-778-24
Sequence 24, Application US/08293778
Patent No. 5580560

ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: T5R1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5
Query Match 62.3%; Score 119; DB 2; Length 406;
Best Local Similarity 52.3%; Pred. No. 8e-13; Indels 0; Gaps 0;
Matches 23; Conservative 5; Mismatches 16;
Qy 1 ANGFLXLRLNGSLKRXCRXLCSPFXAXIFRNXXRTQFWVSY 44
Db 1 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 10
PCT-US92-10242-5
Sequence 5, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Messers, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242

FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5
Query Match 62.3%; Score 119; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 8e-13; Indels 0; Gaps 0;
Matches 23; Conservative 5; Mismatches 16;
Qy 1 ANGFLXLRLNGSLKRXCRXLCSPFXAXIFRNXXRTQFWVSY 44
Db 1 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 11
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5788965
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725

;; FILING DATE: 21-MAY-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA: 07/662,920
;; APPLICATION NUMBER: 07/662,920
;; FILING DATE: 28-FEB-1991
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-467-9600
;; TELEFAX: 415-543-5043
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 444 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-475-845-2

Query Match 62.3%; Score 119; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 8,8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPFXAFXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPSLERBECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 12
US-08-327-690-2
; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 444 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-327-690-2

Query Match 62.3%; Score 119; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 8,8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRNGSLRXCRXXLCSPFXAFXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPSLERBECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 13
US-08-660-289-2
; Sequence 2, Application US/08660289
; Patent No. 5833982

;; GENERAL INFORMATION:
;; APPLICANT: Berkner, Kathleen L.
;; APPLICANT: Petersen, Lars C.
;; APPLICANT: Hart, Charles E.
;; APPLICANT: Hedner, Ulla
;; APPLICANT: Bregengaard, Claus
;; TITLE OF INVENTION: Modified Factor VII
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourie and Crew
;; STREET: One Market Plaza, Stewart Street Tower
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: U.S.A.
;; ZIP: 94105-1492
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/660,289
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/475,845
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: 08/327,690
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/065,725
;; FILING DATE: 21-MAY-1993
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/662,920
;; FILING DATE: 28-FEB-1991
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 13952-8-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-467-9600
;; TELEFAX: 415-543-5043
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 444 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-660-289-2

Query Match 62.3%; Score 119; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 8.8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRNGSLXRCXKXLCSPFXAFIPFNXXRTROFVWSY 44
DB 39 ANAFLELRPGSLRECKEKCQCFEAREIFKDAERTYKLFWISY 82

RESULT 14
US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 62.3%; Score 119; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 8.8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRNGSLXRCXKXLCSPFXAFIPFNXXRTROFVWSY 44
DB 39 ANAFLELRPGSLRECKEKCQCFEAREIFKDAERTYKLFWISY 82

RESULT 15
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle

STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 62.3%; Score 119; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 8.8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRNGSLXRCXKXLCSPFXAFIPFNXXRTROFVWSY 44
DB 39 ANAFLELRPGSLRECKEKCQCFEAREIFKDAERTYKLFWISY 82

Search completed: March 19, 2003, 15:16:21
Job time: 9.75 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds
(without alignments)
280.876 Million cell updates/sec

Title: 10ASN28PHE_4
Perfect score: 191
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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9: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/prodata/2/pubpaa/US05_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
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13: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	119	62.3	406	9	US-10-109-498-1
2	90	47.1	419	9	US-10-182-263-1
3	90	47.1	419	9	US-10-182-263-3
4	90	47.1	419	9	US-10-182-263-4
5	90	47.1	419	9	US-10-182-263-5
6	90	47.1	419	9	US-09-978-917A-4
7	90	47.1	461	9	US-10-182-263-2
8	90	47.1	461	9	US-09-978-917A-2
9	89	46.6	419	9	US-10-182-263-6
10	85	44.5	415	10	US-09-118-748-2
11	85	44.5	461	9	US-10-132-829-5
12	85	44.5	461	9	US-09-884-901-3
13	67	35.1	96	9	US-09-759-1308-313
14	67	35.1	209	9	US-09-759-1308-312
15	67	35.1	226	9	US-09-759-1308-310
16	50	26.2	95	9	US-09-759-1308-356
17	50	26.2	208	9	US-09-759-1308-355
18	50	26.2	225	9	US-09-759-1308-353
19	40	20.9	197	9	US-10-076-622-516

20	40	20.9	197	12	US-10-007-805-516	Sequence 516, App
21	40	20.9	232	9	US-10-076-622-517	Sequence 517, App
22	40	20.9	232	12	US-10-007-805-517	Sequence 517, App
23	40	20.9	243	9	US-09-938-418-7	Sequence 7, Appl
24	40	20.9	243	9	US-10-045-992-4	Sequence 4, Appl
25	40	20.9	243	9	US-10-063-547-122	Sequence 122, App
26	40	20.9	243	9	US-10-174-590-366	Sequence 366, App
27	40	20.9	243	9	US-10-176-758-366	Sequence 366, App
28	40	20.9	243	9	US-10-063-616-122	Sequence 122, App
29	40	20.9	243	9	US-10-176-737-366	Sequence 366, App
30	40	20.9	243	9	US-10-063-502-122	Sequence 122, App
31	40	20.9	243	9	US-10-076-622-514	Sequence 514, App
32	40	20.9	243	9	US-10-173-706-366	Sequence 366, App
33	40	20.9	243	9	US-10-175-738-366	Sequence 366, App
34	40	20.9	243	9	US-10-175-752-366	Sequence 366, App
35	40	20.9	243	9	US-10-176-482-366	Sequence 366, App
36	40	20.9	243	9	US-10-176-757-366	Sequence 366, App
37	40	20.9	243	9	US-10-176-913-366	Sequence 366, App
38	40	20.9	243	9	US-10-180-552-366	Sequence 366, App
39	40	20.9	243	9	US-10-180-557-366	Sequence 366, App
40	40	20.9	243	9	US-10-173-700-366	Sequence 366, App
41	40	20.9	243	9	US-10-174-572-366	Sequence 366, App
42	40	20.9	243	9	US-10-174-579-366	Sequence 366, App
43	40	20.9	243	9	US-10-174-582-366	Sequence 366, App
44	40	20.9	243	9	US-10-174-588-366	Sequence 366, App
45	40	20.9	243	9	US-10-175-739-366	Sequence 366, App

ALIGNMENTS

RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OR INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286,200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match 62.3%; Score 119; DB 9; Length 406;
Best Local Similarity 75.0%; Pred. No. 1,1e-12;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLLXLLRPGSLRXKCRXXLCSFFXAFXIFRXXRTQFWVSY 44
DB 1 ANAFLLXLLRPGSLRXKCRXXQCSFFXAXRIFKDXARTKLFWISY 44

RESULT 2
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E

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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          47.1%; Score 90; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

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Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFQVDDTLAFW 41

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          47.1%; Score 90; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Cy 1 ANGFLXLRNGSLXRXCRXXLCSPXAXFIFPNXXRTQFW 41
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFQVDDTLAFW 41

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          47.1%; Score 90; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

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Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFQVDDTLAFW 41

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

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Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Cy 1 ANGFLXLRNGSLXRXCRXXLCSPXAXFIFPNXXRTQFW 41
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RESULT 6
US-09-978-917A-4
; Sequence 4, Application US/09978917A
; Publication No. US200300227299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219a310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match          47.1%; Score 90; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.1e-07;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.

3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds

(without alignments)
328.082 Million cell updates/sec

Title: 10GLN28GLU

Perfect score: 190
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	159	83.7	466	1	FA7_HUMAN
2	125	65.8	444	2	FA7_RABIT
3	115	60.5	407	1	FA7_BOVIN
4	114	60.0	446	1	FA7_MOUSE
5	102	53.7	461	1	PRTC_MOUSE
6	102	53.7	492	1	FA10_BOVIN
7	101	53.2	459	1	PRTC_PIG
8	101	53.2	461	1	PRTC_RAT
9	100	52.6	218	1	TMG1_HUMAN
10	99	52.1	488	1	FA10_HUMAN
11	93	48.9	231	1	TMG3_HUMAN
12	93	48.9	231	1	TMG3_HUMAN
13	92	48.4	475	1	FA10_CHICK
14	91	47.9	456	1	PRTC_BOVIN
15	85	44.7	458	1	PRTC_RABIT
16	85	44.7	461	1	PRTC_HUMAN
17	85	44.7	622	1	THRB_HUMAN
18	83	43.7	461	1	FAV_HUMAN
19	82	43.2	416	1	FAV_BOVIN
20	81	42.6	618	1	THRB_RAT
21	81	42.6	618	1	THRB_MOUSE
22	79	41.6	376	1	FA10_TROCA
23	76	40.0	202	1	TMG2_HUMAN
24	74	38.9	452	1	FAV_CANFA
25	74	38.9	452	1	FAV_MOUSE
26	69.5	36.6	226	1	TMG4_HUMAN
27	65	34.2	625	1	THRB_BOVIN
28	65	34.2	625	1	PRTC_MOUSE
29	65	34.2	676	1	PRTC_HUMAN
30	63	33.2	675	1	PRTC_BOVIN
31	61	32.1	646	1	PRTC_RABIT
32	61	32.1	646	1	PRTC_RAT
33	60	31.6	675	1	PRTC_RAT

34	56	29.5	400	1	PRTZ_HUMAN
35	53	27.9	675	1	PRTS_MOUSE
36	45	23.7	879	1	YN65_YEAST
37	44	23.2	413	1	NCAP_IHNV
38	43.5	22.9	322	1	YOL3_CARBL
39	42	22.1	263	1	PFLA_STRMU
40	41.5	21.8	271	1	MD12_YEAST
41	41.5	21.8	1290	1	BXB_CLOBO
42	40	21.1	341	1	MURB_PASMU
43	40	21.1	343	1	HMD_METMO
44	40	21.1	353	1	HMD_METTU
45	39.5	20.8	356	1	MURB_BUCAI

ALIGNMENTS

RESULT 1	ID	FA7_HUMAN	STANDARD	PRT	466 AA.
AC	P08709	014339			
DT	01-JAN-1988	(Rel. 06, Last sequence update)			
DT	01-JAN-1988	(Rel. 06, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).				
DN	F7.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=86205965; PubMed=3486420;				
RA	Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C., Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K., Davie B.W.;				
RT	"Characterization of a cDNA coding for human factor VII."				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87260948; PubMed=3037537;				
RA	O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y., Hagen F.S., Murray M.J.;				
RT	"Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein participating in blood coagulation."				
RL	Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).				
RN	[3]				
RP	SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.				
RA	Riederer M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;				
RT	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.				
RN	[4]				
RP	SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.				
RX	MEDLINE=89088153; PubMed=3264725;				
RA	Thim L., Bjorn S., Christensen M., Nicolaissen E.M., Lund-Hansen T., Pedersen A.H., Hedner U.;				
RT	"Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells."				
RL	Biochemistry 27:7785-7793(1988).				
RN	[5]				
RP	CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.				
RX	MEDLINE=91250411; PubMed=1904059;				
RA	Bjorn S., Foster D.C., Thim L., Wiberg F.C., Christensen M., Komiyama Y., Pedersen A.H., Kistiel W.;				
RT	"Human plasma and recombinant factor VII. Characterization of O-glycosylations at serine residues 52 and 60 and effects of site-directed mutagenesis of serine 52 to alanine."				
RL	J. Biol. Chem. 266:11051-11057(1991).				
RN	[6]				
RP	STRUCTURE OF CARBOHYDRATE ON SER-112.				
RX	MEDLINE=90062160; PubMed=2511201;				

RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [7]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91144709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903; Winkler F.K., Guha A.,
 RA Banner D.W., D'Arcy A., Chene C., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950;
 RA Murenki A., Finn B.E., Gispert G.P., Forssen S., Stenflo J.,
 RA Drenthberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Weade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patraccchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patraccchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kemball-Cook G., Marin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE=94264305; PubMed=8204879;
 RA Chahing S., Clarke B., Sridhara S.,
 RA Roberts S.R., Blatchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 85:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arblin A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [19]
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Isasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaitov R., Seligsohn U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANTS MLTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Gaidies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN [22]
 RP FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIa BY FACTOR XIa, FACTOR XIIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -1- PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match 83.7%; Score 159; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 1.4e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLELRPGSLRERCKEKEQCFEAREIFPDARTKLFWISY 44
Db 61 ANAFLELRPGSLRERCKEKEQCFEAREIFPDARTKLFWISY 104

RESULT 2
ID_FAT_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothens A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII."
RL Thromb. Res. Suppl. 69:231-236(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg|-Ile bond in factor X to form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; U77477; AAB37326.1; -.
CC HSSP; P08709; IFAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin_1.
DR Pfam; PF00594; glaf_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
FT DISULFID 198 203
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;

Query Match 65.8%; Score 125; DB 1; Length 444;
Best Local Similarity 54.5%; Pred. No. 1.6e-14;
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLELRPGSLRERCKEKEQCFEAREIFPDARTKLFWISY 44
Db 40 ANAFLELRPGSLRERCKEKEQCFEAREIFPDARTKLFWISY 83

RESULT 3

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FA7_BOVIN
ID FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion
DE accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
OX [1]
RX MEDLINE=89008362; PubMed=3049594;
RA Takaya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,
RA Iwanaga S.;
RT "Bovine factor VII. Its purification and complete amino acid
RT sequence."
RL J. Biol. Chem. 263:14868-14877(1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;
RT "A new triasaccharide sugar chain linked to a serine residue in bovine
RT blood coagulation factors VII and IX."
RL J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=9144709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new triasaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z."
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [4]
RP FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
RP CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
RP THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
RP AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
RP BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
RP FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAITC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC PIR: A31979; A31979.
DR HSPF, P08709; 1B99.
DR MEROPS, S01.215; -.
DR Interpro: IPR000152; Asx_hydroxyl.
DR Interpro: IPR001314; Chymotrypsin.
DR Interpro: IPR000561; EGF-like.
DR Interpro: IPR000742; EGF-2.
DR Interpro: IPR001881; EGF-Ga.
DR Interpro: IPR001438; EGF-11.
DR Interpro: IPR002383; GLA blood.
DR Interpro: IPR001254; Ser_protease_Try.
DR Interpro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.

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DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_SER; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152
FT CHAIN 153 407
FT DOMAIN 6 35
FT DOMAIN 46 82
FT DOMAIN 87 128
FT DOMAIN 153 407
FT SITE 152 153
FT ACT_SITE 193 193
FT ACT_SITE 242 242
FT ACT_SITE 344 344
FT BINDING 338 338
FT DISULFID 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 72 81
FT DISULFID 91 102
FT DISULFID 98 112
FT DISULFID 114 127
FT DISULFID 135 164
FT DISULFID 159 164
FT DISULFID 178 194
FT DISULFID 310 329
FT DISULFID 340 368
FT MOD_RES 6 6
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 35 35
FT MOD_RES 52 52
FT CARBOHYD 145 145
FT CARBOHYD 203 203
SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;

Query Match 60.5%; Score 115; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 8,6e-13;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKXCKXQCSFXXAXEXIFDXDKTKLFWISY 44
DB 1 ANGFLEELPGLSLERCRELCSEFEAHFIFRNEETRQFWISY 44

RESULT 4
FA7_MOUSE STANDARD; PRT; 446 AA.
ID FA7_MOUSE
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=97127167; PubMed=8972017;
 RT Idusogie E., Rosen E.D., Carmeliet P., Collen D., Caestelejo F.J.;
 RT "Nucleotide structure and characterization of the murine blood
 RT coagulation factor VII gene."
 RL Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 CC SIMILARITY)
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PPM: THE VITAMIN K-DEPENDENT. ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@ebi.ac.uk).

CC EMBL; U66079; AAC33796.1; -
 DR HSBP; P08709; 1BF9.
 DR MEROPS; S01.215; -
 DR MGD; MGI.109325; F7.
 DR InterPro: IPR000152; Aex_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR00742; EGF 2.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; Vltk_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Glaf; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KM EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 24
 FT PROPEP 25 41
 FT CHAIN 42 193
 FT DOMAIN 194 446
 FT DOMAIN 47 76
 FT DOMAIN 87 123
 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 128 169 EGF-LIKE 2.
 FT DOMAIN 194 446 SERINE PROTEASE.
 FT SITE 193 194 CLEAVAGE (BY FACTOR Xa, FACTOR XIa,
 FT ACT_SITE 234 234 FACTOR IXa, OR THROMBIN) (BY SIMILARITY).
 FT ACT_SITE 283 283 BY SIMILARITY.
 FT ACT_SITE 385 385 BY SIMILARITY.
 FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).
 FT DISULFID 58 63 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT DISULFID 96 111 BY SIMILARITY.
 FT DISULFID 113 122 BY SIMILARITY.
 FT DISULFID 132 143 BY SIMILARITY.
 FT DISULFID 139 153 BY SIMILARITY.
 FT DISULFID 155 168 BY SIMILARITY.
 FT DISULFID 176 203 BY SIMILARITY.
 FT DISULFID 200 203 BY SIMILARITY.
 FT DISULFID 219 235 BY SIMILARITY.
 FT DISULFID 351 370 BY SIMILARITY.
 FT DISULFID 381 409 BY SIMILARITY.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 104 104 GAMMA-CARBOXYGLUTAMIC ACID.
 FT CARBOHYD 186 186 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 244 244 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 446 AA; 50276 MW; 251254445C9C95E CRC64;

Query Match 60.0%; Score 114; DB 1; Length 446;
 Best Local Similarity 54.5%; Pred. No. 1,4e-12;
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAPLXLRGSLKRXCKXKQCSFKXAEIIFKDXARTLFFIISY 44
 Db 42 ANSLLELWPSLRECEQCSFEAREIFKSPERTQFWIIVY 85

RESULT 5
 ID PRTC_MOUSE STANDARD; PRT; 461 AA.
 AC P33587; O35498;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.65)
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RX MEDLINE=92316897; PubMed=1618739;
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
 RT "Isolation and characterization of a mouse protein C cDNA."
 RL J. Biochem. 111:491-495(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=98152576; PubMed=9493582;
 RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
 RA Caestelejo F.J.;
 RT "Nucleotide structure and characterization of the murine gene encoding

RT anticeagulant protein C.";
 RL Thromb. Haemost. 79:310-316(1998).
 RN [3]
 RP SEQUENCE OF 274-434 FROM N.A.
 RC STRAIN-BALB/c;
 RX MEDLINE=94318474; PubMed=8043441;
 RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
 RT "A comparative study of partial primary structures of the catalytic
 RT region of mammalian protein C.";
 RL Br. J. Haematol. 86:590-600(1994).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIa.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PMW: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; D10445; BAA01235.1; -.
 DR EMBL; AF034569; AAC33795.1; -.
 DR EMBL; D43755; BAA07812.1; -.
 DR PIR; JX0210; JX0210.
 DR HSSP; P04070; JX0210.
 DR MGDI; S01.218; -.
 DR MGD; MGI:97771; Proc.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; Vldc_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00089; clypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_Like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SIS; 1.
 DR Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.

FT	SIGNAL	1	33	BY SIMILARITY.
FT	PROPEP	34	41	BY SIMILARITY.
FT	CHAIN	42	196	PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT	CHAIN	199	461	PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT	PEPTIDE	199	212	ACTIVATION PEPTIDE (BY SIMILARITY).
FT	SITE	212	213	CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT	DOMAIN	96	131	EGF-LIKE 1.
FT	DOMAIN	135	175	EGF-LIKE 2.
FT	DOMAIN	213	461	SERINE PROTEASE.
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	48	48	(BY SIMILARITY).
FT	MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	57	57	(BY SIMILARITY).
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	61	61	(BY SIMILARITY).
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	67	67	(BY SIMILARITY).
FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	70	70	(BY SIMILARITY).
FT	MOD_RES	112	112	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	253	253	CHARGE RELAY SYSTEM.
FT	ACT_SITE	289	299	CHARGE RELAY SYSTEM.
FT	ACT_SITE	402	402	CHARGE RELAY SYSTEM.
FT	DISULFID	58	63	BY SIMILARITY.
FT	DISULFID	91	110	BY SIMILARITY.
FT	DISULFID	100	105	BY SIMILARITY.
FT	DISULFID	104	119	BY SIMILARITY.
FT	DISULFID	121	130	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	146	159	BY SIMILARITY.
FT	DISULFID	161	174	BY SIMILARITY.
FT	DISULFID	182	319	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	238	254	BY SIMILARITY.
FT	DISULFID	373	387	BY SIMILARITY.
FT	DISULFID	398	426	BY SIMILARITY.
FT	CARBOHYD	214	214	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	328	328	MISSING (IN REF. 2).
FT	CONFLICT	393	393	N -> D (IN REF. 2).
FT	SEQUENCE	461 AA;	51945 MW;	53FAAD085B194D6E CRC64;

Query Match 53.7%; Score 102; DB 1; Length 461;
 Best local Similarity 45.5%; Pred. No. 2e-10;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKCKXKQCSFFXAEKIFDAXTKLFWISY 44
 DB 42 ANSFLEMRPGLERECMEBICDFEAOBIFQVEDTLFAWIKY 85

RESULT 6
 FA10 BOVIN STANDARD; PRT; 492 AA.
 AC P00743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxId=9913;

[1]
 RP SEQUENCE OF 1-487 FROM N.A.
 RX MEDLINE=84247315; PubMed=6330671;
 RA Fung M.R., Campbell R.M., McGillicravy R.T.A.;
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
 RT containing a prepro leader sequence.";
 RL Nucleic Acids Res. 12:4481-4492(1984).
 RN [2]
 RP SEQUENCE OF 41-180.
 RX MEDLINE=80130563; PubMed=6766735;
 RA Entfeld D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
 RA Tlani K.;
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
 RT factor).";
 RL Biochemistry 19:659-667(1980).
 RN [3]
 RP REVISION TO 103.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kisiel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens";
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [4]
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Tlani K., Fujikawa K., Entfeld D.L., Ericsson L.H., Walsh K.A.,
 RA Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 RT chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 RN [5]
 RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE=73053314; PubMed=4264286;
 RA Tlani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 RT "Bovine factor X Ia (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 RL Biochemistry 11:4899-4903(1972).
 RN [7]
 RP PROCESSING.
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Tlani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN [8]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN [9]
 RP SUPPARTION
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN [10]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of

RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN [11]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Telemann O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN [12]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1527084;
 RA Selander-Sunnerhagen M., Ullner M., Persson E., Telemann O.,
 RA Stenflo J., Drakenberg T.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
 RL J. Biol. Chem. 267:19642-19649(1992).
 RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunnerhagen M., Olah G.A., Stenflo J., Foren S., Drakenberg T.,
 RA Trewhella J.;
 RT "The relative orientation of Gla and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";
 RL Biochemistry 35:11547-11559(1996).
 CC -I- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -I- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -I- PM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -I- PM: N- AND O-GLYCOSYLATED.
 CC -I- PM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -I- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC DR EMBL; X00673; CA25286.1; -.
 CC DR PIR; A00925; EXBO.
 CC DR PDB; JAPC; 31-JAN-94.
 CC DR PDB; 1CCF; 31-MAY-94.
 CC DR PDB; 1WHE; 15-MAY-97.
 CC DR PDB; 1WHF; 15-MAY-97.
 CC DR MEROPS; S01.216; -.
 CC DR GlycoSuiteDB; P00743; -.
 CC DR InterPro; IPR000152; Aex hydroxyl-
 CC DR InterPro; IPR001314; Chymotrypsin.
 CC DR InterPro; IPR000561; EGF-like.
 CC DR InterPro; IPR00742; EGF_2.
 CC DR InterPro; IPR001881; EGF_Ca.
 CC DR InterPro; IPR002383; Gla_Blood.
 CC DR InterPro; IPR001254; Ser protease_Try.
 CC DR InterPro; IPR000294; VitK_dep_GLA_

DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_Like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 KM Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KM Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 FT SIGNAL 1 23
 FT PROPEP 24 40
 FT CHAIN 41 180
 FT PROPEP 183 492
 FT CHAIN 234 492
 FT PROPEP 476 492
 FT DOMAIN 46 132
 FT DOMAIN 125 155
 FT ACT SITE 234 492
 FT ACT SITE 275 492
 FT ACT SITE 321 492
 FT ACT SITE 418 492
 FT MOD_RES 46 46
 FT MOD_RES 47 47
 FT MOD_RES 54 54
 FT MOD_RES 56 56
 FT MOD_RES 59 59
 FT MOD_RES 60 60
 FT MOD_RES 65 65
 FT MOD_RES 66 66
 Query Match 53.7%; Score 102; DB 1; Length 492;
 Best Local Similarity 43.2%; Pred. No. 2.1e-10;
 Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANFLXXLRGSLRXKXKXQCSFXAEXFKDAXRKLFWISY 44
 DB 41 ANSFLFVKGNIERBCELEACSLLEBARVEFDAEQTFDEFSKY 84

RESULT 7
 PRTC_PIG STANDARD; PRT; 459 AA.
 AC O9GLB2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation
 factor XIV).
 GN PROC.
 OS Sus acrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sui.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21121490; PubMed=11229814;
 RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
 Kim H.K.W.;

RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
 RT protein modeling of membrane binding sites and comparative anatomy of
 RT domains.";
 RL Cell. Mol. Life Sci. 58:148-159(2001).
 CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
 CC regulates blood coagulation by inactivating factors Va and VIII
 CC in the presence of calcium ions and phospholipids.
 CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIa.
 CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
 CC into a light chain and a heavy chain held together by a disulfide
 CC bond. The enzyme is then activated by thrombin, which cleaves a
 CC tetradecapeptide from the amino end of the heavy chain; this
 CC reaction, which occurs at the surface of endothelial cells, is
 CC strongly promoted by thrombomodulin.
 CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
 CC residues allows the modified protein to bind calcium.
 CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the Gla domain. This Gla-independent binding
 CC site is necessary for the recognition of the
 CC thrombin-thrombomodulin complex.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; AF191307; AAG28380.1; -.
 DR HSSP; P04070; 1PCU.
 DR MEROPS; S01.218; -.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF_Like.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00001; EGF_Like; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Blood coagulation; Glycoprotein; Serine protease;
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 41
 FT CHAIN 42 459
 FT CHAIN 42 196
 FT CHAIN 199 459
 FT PEPTIDE 199 213
 FT SITE 213 214
 SIMILARITY).
 ACTIVATION PEPTIDE (BY SIMILARITY).
 CLEAVAGE (BY THROMBIN) (BY
 SIMILARITY).

FT		DNAIN	96	131	EGF-LIKE 1.
FT		DNAIN	135	175	SERINE PROTEASE.
FT		DNAIN	214	459	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT		MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT		MOD_RES	48	48	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT		MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT		MOD_RES	57	57	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT		MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT		MOD_RES	61	61	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT		MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT		MOD_RES	67	67	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT		MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT		MOD_RES	112	112	HYDROXYLATION (BY SIMILARITY).
FT		ACT_SITE	255	255	CHARGE RELAY SYSTEM.
FT		ACT_SITE	301	301	CHARGE RELAY SYSTEM.
FT		ACT_SITE	400	400	CHARGE RELAY SYSTEM.
FT		DISULFID	58	63	BY SIMILARITY.
FT		DISULFID	91	110	BY SIMILARITY.
FT		DISULFID	100	105	BY SIMILARITY.
FT		DISULFID	104	119	BY SIMILARITY.
FT		DISULFID	121	130	BY SIMILARITY.
FT		DISULFID	139	150	BY SIMILARITY.
FT		DISULFID	146	159	BY SIMILARITY.
FT		DISULFID	161	174	INTERCHAIN (BY SIMILARITY).
FT		DISULFID	182	321	INTERCHAIN (BY SIMILARITY).
FT		DISULFID	240	256	BY SIMILARITY.
FT		DISULFID	371	385	BY SIMILARITY.
FT		DISULFID	396	424	BY SIMILARITY.
FT		CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT		CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT		CARBOHYD	353	353	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO		SEQUENCE	459 AA;	51866 MW;	8541AAC14CC16D09 CRC64;
<hr/>					
Query Match					
Best Local Similarity 53.2%; Score 101; DB 1; Length 459;					
Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;					
Oy	1	ANAPFLXLRQGSIXRCKXXCSPFXAEXIFPDAXRTKLFWSY	44		
Db	42	ANSFLEELRPSSLRECKEETCDPEBARFIPTONTNTMFMFSKY	85		
<hr/>					
RESULT 8					
PRTC RAT	ID	PRTC RAT	STANDARD;	PRT;	461 AA.
AC	P31394;				
DT	01-JUN-1993 (Rel. 26, Created)				
DT	01-JUN-1993 (Rel. 26, Last sequence update)				
DR	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Vitamin-K dependent protein C precursor (EC 3.4.21.69)				
DE	(Autoproteolytic cleavage product of blood coagulation factor XIV).				
GN	Rattus norvegicus (Rat).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxId=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Mistar; TISSUE=Liver;				
RX	MEDLINE=92329550; PubMed=1627650;				
RA	Kakutani T., Maekawa K., Nawa K., Matsumoto Y.;				
RL	"The cDNA cloning and mRNA expression of rat protein C";				
	Biochim. Biophys. Acta 1131:329-332(1992).				

CC	- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC	- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIia.
CC	- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.
CC	- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC	- PM: THE VITAMIN K-DEPENDENT ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC	- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
CC	- SIMILARITY: BELONGS TO PERTIDEASE FAMILY S1.
CC	- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC	-----
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CC	-----
DR	EMBL; X64336; CAA45617.1; -.
DR	PIR; S18994; S18994.
DR	PIR; S24312; S24312.
DR	HSSP; P04070; IPCU.
DR	MEROPS; S01.218; -.
DR	InterPro; IPRO00152; Asx_hydroxyl.
DR	InterPro; IPRO03114; Chymotrypsin.
DR	InterPro; IPRO00561; EGF-like.
DR	InterPro; IPRO01881; EGF_Ca.
DR	InterPro; IPRO02383; GLA_Blood.
DR	InterPro; IPRO01254; Ser_protease_Try.
DR	InterPro; IPRO00294; Vitk_dep_GLA.
DR	Pfam; PF00008; EGF_2.
DR	Pfam; PF00089; Trypsin_1.
DR	Pfam; PF00594; gla_1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PRINTS; PR00001; GLABLOOD.
DR	SMART; SM00179; EGF_CA_1.
DR	SMART; SM00001; EGF_Like_1.
DR	SMART; SM00069; GLA_1.
DR	SMART; SM00020; TRYp_Spc_1.
DR	PROSITE; PS00010; ASX_HYDROXYL_1.
DR	PROSITE; PS00022; EGF_1; 1.
DR	PROSITE; PS01186; EGF_2; 2.
DR	PROSITE; PS01187; EGF_CA_1.
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR	PROSITE; PS00240; TRYPsin_DOM_1.
DR	PROSITE; PS00134; TRYPSIN_HIS_1.
DR	PROSITE; PS00135; TRYPSIN_SER_1.
KM	Blood coagulation; Glycoprotein; Serine protease;
KM	Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW	EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT	SIGNAL 1 32
FT	PROPEP 33 41
FT	CHAIN 42 196
FT	CHAIN 199 461
FT	PEPTIDE 199 212
FT	SITE 212 213
FT	DOMAIN 96 131
FT	DOMAIN 135 175
FT	DOMAIN 213 461
FT	MOD_RES 47 47
FT	MOD_RES 48 48
FT	MOD_RES 48 48
FT	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT	PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT	ACTIVATION PEPTIDE (BY SIMILARITY).
FT	CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT	EGF-LIKE 1.
FT	EGF-LIKE 2.
FT	SERINE PROTEASE.
FT	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).

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FT FT MOD_RES 55 55 (BY SIMILARITY).
FT FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID
FT FT MOD_RES 60 60 (BY SIMILARITY).
FT FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT FT MOD_RES 61 61 (BY SIMILARITY).
FT FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT FT MOD_RES 67 67 (BY SIMILARITY).
FT FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT FT MOD_RES 70 70 (BY SIMILARITY).
FT FT MOD_RES 112 112 GAMMA-CARBOXYGLUTAMIC ACID
FT FT ACT_SITE 254 254 (BY SIMILARITY).
FT FT ACT_SITE 300 300 HYDROXYLATION (BY SIMILARITY).
FT FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT FT DISULFID 58 63 CHARGE RELAY SYSTEM.
FT FT DISULFID 91 110 BY SIMILARITY.
FT FT DISULFID 100 105 BY SIMILARITY.
FT FT DISULFID 121 119 BY SIMILARITY.
FT FT DISULFID 139 130 BY SIMILARITY.
FT FT DISULFID 146 150 BY SIMILARITY.
FT FT DISULFID 161 174 BY SIMILARITY.
FT FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT FT DISULFID 239 255 BY SIMILARITY.
FT FT DISULFID 373 387 BY SIMILARITY.
FT FT DISULFID 398 426 BY SIMILARITY.
FT FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDAD5 CRC64;
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Query Match 53.2%; Score 101; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 3e-10;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

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QY 1 ANAFLLXLRQGSIXRXCKXQCSFXXAEXIFPKDAXRTKLFWISY 44
DB 42 ANSFLFVRAGSLERECMEICDFEEAQIFQVEDTLAWIKY 85
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RESULT 9

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TWG1_HUMAN STANDARD; PRT; 218 AA.
ID TWG1_HUMAN
AC 014668;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxylglutamic acid protein 1 precursor (Proline-
DE rich Gla protein 1) (Proline-rich gamma-carboxylglutamic acid protein
DE 1).
GN PRRG1 OR TWG1 OR PRPG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCB1_TaxID=9606;
RN 1;
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxylglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC 1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC 1- PTM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC or send an email to license@isb-sib.ch).

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DR EMBL; AF009242; AAB67070.1; -.
DR HSP; P00740; ICFH.
DR Genew; HGNC:9469; PRGGL.
DR MIM; 604428; -.
DR InterPro; IPR002383; Gla blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KM Gamma-carboxylglutamic acid; vitamin K; transmembrane.
FT PROPEP 1 20 POTENTIAL.
FT CHAIN 21 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT FT 21 83 PROTEIN 1.
FT FT TRANSMEM 84 106 EXTRACELLULAR (POTENTIAL).
FT FT DOMAIN 107 218 POTENTIAL.
FT FT DOMAIN 107 218 CYTOPLASMIC (POTENTIAL).
FT FT DOMAIN 24 61 GLA-RICH.
FT FT DOMAIN 131 135 POLY-PRO.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;
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Query Match 52.6%; Score 100; DB 1; Length 218;
Best Local Similarity 40.9%; Pred. No. 2.2e-10;
Matches 18; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

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QY 1 ANAFLLXLRQGSIXRXCKXQCSFXXAEXIFPKDAXRTKLFWISY 44
DB 21 ANGFEEIIRQGNIERECMEICDFEEARFAPENNETKTFWISY 64
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RESULT 10
FA10_HUMAN STANDARD; PRT; 488 AA.
ID FA10_HUMAN
AC P00742; O14340;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCB1_TaxID=9606;
RN 1;
RX MEDLINE=91216473; PubMed=1902434;
RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RT human coagulation factor X."
RL Gene 99:291-294(1991).
RN 1;
RX MEDLINE=87026600; PubMed=3768336;
RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
RT organization is essentially identical with that of factor IX and
RT protein C."
RL Biochemistry 25:5098-5102(1986).
RN 3;
RX MEDLINE=85216545; PubMed=2582420;
RA Fung M.R., Hay C.W., McGallivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human
RT blood coagulation factor X."
RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
RN 4;
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RP SEQUENCE OF 19-488 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86221713; PubMed=3011603;
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
RT Isolation and characterization of human blood-coagulation factor X
RT cDNA.";
RL Gene 41:311-314(1986).
RN [5]
RP SEQUENCE OF 41-179.
RX MEDLINE=83257207; PubMed=6871167;
RA Mcullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howard W.N.,
RA Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
RT coagulation factor X: evidence for identification of residue 63 as
RT beta-hydroxyaspartic acid.";
RL Biochemistry 22:2875-2884(1983).
RN [6]
RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=84222026; PubMed=6587384;
RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
RN [7]
RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [8]
RP SEQUENCE OF 1-23 FROM N.A.
RX MEDLINE=90128299; PubMed=2612918;
RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hameshushannam K., Lyman G.;
RT "Cloning and characterization of the 5' end (exon 1) of the gene
RT encoding human factor X.";
RL Gene 84:517-519(1989).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=93360277; PubMed=8355279;
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
RA Padmanabhan K., Padmanabhan D.T., Gardin A.D., Kisiel W.;
RT Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
RL "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
RN J. Mol. Biol. 233:947-966(1993).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=98283982; PubMed=9618463;
RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
RT "Structural basis for chemical inhibition of human blood coagulation
RT factor Xa.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
RN [11]
RP FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
RC converts prothrombin to thrombin in the presence of factor Va,
RX calcium and phospholipid during blood clotting.
RA CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -PTM: N- AND O-GLYCOSYLATED
CC -PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -SIMILARITY: CONSTAINS 2 EGF-LIKE DOMAINS.
CC -----
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DR EMBL; M03194; AAA52490.1; -.  
DR EMBL; M57285; AAA52421.1; -.  
DR EMBL; L29433; AAA52764.1; -.  
DR EMBL; L00390; AAA52764.1; JOINED.  
DR EMBL; L00391; AAA52764.1; JOINED.  
DR EMBL; L00392; AAA52764.1; JOINED.  
DR EMBL; L00393; AAA52764.1; JOINED.  
DR EMBL; L00394; AAA52764.1; JOINED.  
DR EMBL; L00395; AAA52764.1; JOINED.  
DR EMBL; M22613; AAA51984.1; -.  
DR EMBL; M01886; AAA52486.1; -.  
DR EMBL; M33297; AAA52636.1; -.  
DR PIR; A00924; EXHU.  
DR PIR; A25853; A25853.  
DR PIR; A24478; A24478.  
DR PDB; 1HCG; 08-MAY-95.  
DR PDB; 1FAX; 29-OCT-97.  
DR PDB; 1EXY; 17-JUN-98.  
DR PDB; 1XKA; 23-MAR-99.  
DR PDB; 1XKB; 23-MAR-99.  
DR MEROPS; S01_216; -.  
DR GlycoSuiteDB; P00742; -.  
DR Genew; HGNC:3528; F10.  
DR MIM; 134530; -.  
DR MIM; 227600; -.  
DR InterPro; IPR000152; Aex_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF 2.  
DR InterPro; IPR001881; EGF_Ca.  
DR InterPro; IPR002383; GLA_Dlood.  
DR InterPro; IPR001254; Ser_protease_Try.  
DR InterPro; IPR002994; Vitk_dep_GLA.  
DR Pfam; PF00008; EGF 2.  
DR Pfam; PF00089; trypsin; 1.  
DR Pfam; PF00594; gla; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF_CA; 1.  
DR SMART; SM00001; EGF_Like; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp_Spc; 1.  
DR PROSITE; PS00010; ASX_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF 1; 1.  
DR PROSITE; PS01186; EGF 2; 2.  
DR PROSITE; PS01187; EGF_CA; 1.  
DR PROSITE; PS00011; GLUT_CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN_DOM; 1.  
DR PROSITE; PS00134; TRYP SIN HIS; 1.  
DR PROSITE; PS00135; TRYP SIN SER; 1.  
KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;  
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
KW Signal; Zymogen; EGF-like domain; Repeat; 3d-structure.  
FT SIGNAL; 1  
FT PROPEP; 32  
FT CHAIN; 41  
FT CHAIN; 183  
FT PROPEP; 183  
FT CHAIN; 235  
FT DOMAIN; 86  
FT DOMAIN; 125  
FT MOD_RES; 46  
FT MOD_RES; 47  
FT MOD_RES; 54  
FT MOD_RES; 56  
FT MOD_RES; 59  
FT MOD_RES; 59  
FACTOR X LIGHT CHAIN.  
FACTOR X HEAVY CHAIN.  
ACTIVATION PEPTIDE.  
ACTIVATED FACTOR KA. HEAVY CHAIN.  
EGF-LIKE 1. CALCIUM-BINDING (POTENTIAL).  
EGF-LIKE 2.  
SERINE PROTEASE.  
GAMMA-CARBOXYGLUTAMIC ACID.  
GAMMA-CARBOXYGLUTAMIC ACID.  
GAMMA-CARBOXYGLUTAMIC ACID.  
GAMMA-CARBOXYGLUTAMIC ACID.  
GAMMA-CARBOXYGLUTAMIC ACID.
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FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 221 221 /FTID=CAR_000012.
FT CARBOHYD 231 231 /FTID=CAR_000013.
FT ACT_SITE 276 276 CHARGE RELAY SYSTEM.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110
FT DISULFID 112 121
FT DISULFID 129 140
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Query Match 52.1%; Score 99; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 7.3e-10;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

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Oy 1 ANAFLLXRLQSLRXCKXQCSFXXAEXIFKDXRTKLFMISY 44
Db 41 ANSFLFMKKGHLEKRECMETCSYEAREVEFSDKTNEMWNY 84
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RESULT 11
FA10_RABIT STANDARD; PRT; 490 AA.
ID FA10_RABIT
AC 019045;
DT 15-DEC-1998 (rel. 37, Created)
DT 15-DEC-1998 (rel. 37, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCB1_TaxID=9986;
OX NCB1_TaxID=9986;
RP SEQUENCE FROM N.A.
RX MEDLINE=97256311; PubMed=9101642;
RA Rendurichi U.R.; Anderson K.D.; James H.L.;
RT "Characterization of a full-length cDNA for rabbit factor X.";
RL Thromb. Res. 85:503-514(1997).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg1-Thr and then
CC Arg1-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
CC (BY SIMILARITY).
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF003200; AAB62542.1; -.
DR HSRP; P00742; IHCG.
DR MEROPS; S01.216; -.
DR InterPro; IPR001512; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Src; 1.
DR PROSITE; PS00010; ASK_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat.
FT SIGNAL 1 20
FT PROPEP 21 40 BY SIMILARITY.
FT CHAIN 41 180 FACTOR X LIGHT CHAIN.
FT CHAIN 184 490 FACTOR X HEAVY CHAIN.
FT PROPEP 184 232 ACTIVATION PEPTIDE.
FT CHAIN 233 490 ACTIVATION FACTOR XA, HEAVY CHAIN.
FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 233 490 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT SIMILARITY).
FT MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 274 274 CHARGE RELAY SYSTEM.
FT ACT_SITE 320 320 CHARGE RELAY SYSTEM.
FT ACT_SITE 417 417 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 BY SIMILARITY.
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FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 149 BY SIMILARITY.
FT DISULFID 151 164 BY SIMILARITY.
FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 244 BY SIMILARITY.
FT DISULFID 259 275 BY SIMILARITY.
FT DISULFID 388 402 BY SIMILARITY.
FT DISULFID 413 441 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 490 AA; 53965 MM; 3A39FA85AF2A6D11 CRC64;

Query Match 52.1%; Score 99; DB 1; Length 490;
Best Local Similarity 40.9%; Pred. No. 7.3e-10;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFPLXLRQSLXKXCKXQCFXAXEIPFDAXRTKLFMTSY 44
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 41 ANSFLEELKGNLERECMEHCNSYEALVEFEDREKTNFPMKY 84

RESULT 12
TMG3 HUMAN STANDARD; PRT; 231 AA.
AC Q9BZD7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RA MEDLINE=21117044; PubMed=1171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC -----
CC EMBL; AF36350; AAK0955.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR002394; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KM Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 20 78 PROTEIN 3.
FT TRANSMEM 79 101 EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
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FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25848 MM; 8A373E4848490D81 CRC64;

Query Match 48.9%; Score 93; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 4e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFPLXLRQSLXKXCKXQCFXAXEIPFDAXRTKLFMTSY 44
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 ANSFLEELRQGTIERECMEHCISYEAVKEVFNKKTWFMKGY 63

RESULT 13
PA10 CHICK STANDARD; PRT; 475 AA.
ID PA10 CHICK
AC P25155;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor)
DE (virus activating protease) (VAP).
GN FX.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Chorioallantoic membrane;
RA MEDLINE=91257322; PubMed=2044767;
RA Suzuki H., Harada A., Hayashi Y., Wada K., Asaka J.-I., Gotch B.,
RA Ogasawara T., Nagai Y.;
RT "Primary structure of the virus activating protease from chick
RT embryo. Its identity with the blood clotting factor Xa.";
RL FEBS Lett. 283:281-285(1991).
RN [2]
RP SEQUENCE OF 41-55 AND 241-261.
RC TISSUE=Allantoic fluid;
RA MEDLINE=91065352; PubMed=2174359;
RA Gotch B., Ogasawara T., Toyoda T., Innocencio N.M., Hamaguchi M.,
RA Nagai Y.;
RT "An endoprotease homologous to the blood clotting factor X as a
RT determinant of viral tropism in chick embryo.";
RL EMO J. 9:4189-4195(1990).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,
CC AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING
CC SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
CC SAC.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; D00844; BAA00724.1; -.
DR PIR; S15838; S15838.
DR HSR; P00742; IHCG.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vtck_deg_Gla.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00063; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_HIS; 1.
DR Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat.
FT SIGNAL 1 20 OR 30; OR 31 (POTENTIAL).
FT PROPEP 21 40
FT CHAIN 41 180 FACTOR X LIGHT CHAIN.
FT CHAIN 186 475 FACTOR X HEAVY CHAIN.
FT PROPEP 186 241 ACTIVATION PEPTIDE.
FT CHAIN 242 475 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 125 168 EGF-LIKE 2.
FT DOMAIN 241 475 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 282 328 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 328 328 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 425 425 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.

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FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 152 BY SIMILARITY.
FT DISULFID 154 167 BY SIMILARITY.
FT DISULFID 175 348 INTERCHAIN (BY SIMILARITY).
FT DISULFID 247 252 BY SIMILARITY.
FT DISULFID 267 283 BY SIMILARITY.
FT DISULFID 366 410 BY SIMILARITY.
FT DISULFID 421 449 BY SIMILARITY.
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 475 AA; 53142 MW; 570BF84956C5C74D CRC64;

Query Match 48.4%; Score 92; DB 1; Length 475;
Best Local Similarity 38.6%; Pred. No. 1.3e-08;
Matches 17; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLLXRLRQSLRXKXCKXGCSFXXAEXIFPDVARKLFWISY 44
Db 41 ANSFLEMKQGNTERECNERCSKEARAFEDNEXTEFFNMIY 84

RESULT 14
PRTC_BOVIN STANDARD; PRT; 456 AA.
AC P00745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Autoproteolytic cleavage of protein C) (Blood coagulation
DE factor XIV) (Fragment).
GN PROC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014626; PubMed=6091100;
RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
RT "Cloning and sequencing of liver cDNA coding for bovine protein C";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
RN [2]
RP SEQUENCE OF 40-194.
RX MEDLINE=83007325; PubMed=6696876;
RA Fernlund P., Stenflo J.;
RT "Amino acid sequence of the light chain of bovine protein C";
RL J. Biol. Chem. 257:12170-12179(1982).
RN [3]
RP REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
RN [4]
RP SEQUENCE OF 197-456.
RX MEDLINE=83007326; PubMed=6696877;
RA Stenflo J., Fernlund P.;
RT "Amino acid sequence of the heavy chain of bovine protein C";
RL J. Biol. Chem. 257:12180-12190(1982).
RN [5]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Esmen N.L., Debaill L.E., Esmen C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
domainless protein C";
RL J. Biol. Chem. 258:5548-5553(1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;

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CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCULUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: U49933; AAA92956.1; -
 CC HSRP; P04070; 1PCU.
 DR HSRP; P04070; 1PCU.
 DR MEROPS; S01.218; -
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000284; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00594; gla; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00010; ASK_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Glycoprotein; Serine protease;
 DR Gamma-carboxylglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 27
 FT PROPEP 28 36
 FT CHAIN 37 458
 FT CHAIN 37 192
 FT CHAIN 195 458
 FT PEPTIDE 195 209
 FT SITE 209 210
 FT DOMAIN 91 126
 FT DOMAIN 130 170
 FT DOMAIN 210 458
 FT MOD_RES 42 42
 FT MOD_RES 43 43
 FT MOD_RES 50 50
 FT MOD_RES 52 52
 FT MOD_RES 55 55
 FT MOD_RES 56 56
 FT MOD_RES 61 61
 FT MOD_RES 62 62
 FT MOD_RES 65 65
 FT MOD_RES 107 107
 FT ACT_SITE 250 250
 FT ACT_SITE 296 296

FT ACT_SITE 399 399 CHARGE RELAY SYSTEM.
 FT DISULFID 53 58 BY SIMILARITY.
 FT DISULFID 86 105 BY SIMILARITY.
 FT DISULFID 95 100 BY SIMILARITY.
 FT DISULFID 99 114 BY SIMILARITY.
 FT DISULFID 116 125 BY SIMILARITY.
 FT DISULFID 134 145 BY SIMILARITY.
 FT DISULFID 141 154 BY SIMILARITY.
 FT DISULFID 156 169 BY SIMILARITY.
 FT DISULFID 177 316 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 235 251 BY SIMILARITY.
 FT DISULFID 370 384 BY SIMILARITY.
 FT DISULFID 395 423 BY SIMILARITY.
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 458 AA; 51087 MW; D75A5F99C8F29D7 CRC64;

Query Match 44.7%; Score 85; DB 1; Length 458;
 Best Local Similarity 40.9%; Pred. No. 2.1e-07;
 Matches 18; Conservative 3; Mismatches 23; Indels 0; Gaps 0;

QY 1 ANAPLXXLRQGSIXRXCXXQCSFXXAEXIFDAXRTRKLFWISY 44
 Db 37 ANSFLERLPPSLERECVEVCDLEBAKIFQSVDDTLAFWIKY 80

Search completed: March 19, 2003, 14:52:45
 Job time : 8.625 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: 10gln28gln
Sequence: 1 ANAFXXIXRQSLXKCKXX.....XXAEXIFDAXRTLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_proteic:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	159	83.7	701	4	Q96PQ8	Q96PQ8 homo sapien
2	114	60.0	446	11	Q61109	Q61109 mus musculu
3	102	53.7	460	11	Q91WN8	Q91WN8 mus musculu
4	96	50.5	460	11	Q99PC6	Q99PC6 mus musculu
5	93	48.9	482	11	Q63207	Q63207 rattus norv
6	92	48.4	456	6	Q9TTR0	Q9TTR0 canis famli
7	91	47.9	469	6	Q9GMD9	Q9GMD9 ornithorhyn
8	91	47.9	481	11	Q54740	Q54740 mus musculu
9	91	47.9	481	11	Q99L32	Q99L32 mus musculu
10	91	47.9	481	11	Q88947	Q88947 mus musculu
11	85	44.7	100	4	Q15253	Q15253 homo sapien
12	83	43.7	456	4	Q14316	Q14316 homo sapien
13	83	43.7	461	6	Q95ND7	Q95ND7 pan troglod
14	83	43.7	461	6	Q95ND6	Q95ND6 pan troglod
15	82	43.2	49	6	Q95ME8	Q95ME8 bos taurus
16	76	40.0	179	4	Q8TAS3	Q8TAS3 homo sapien

17	76	40.0	198	11	Q8R182	Q8R182 mus musculu
18	75	39.5	138	6	Q28994	Q28994 sus scrofa
19	70	36.8	433	13	Q90YK1	Q90YK1 brachydanio
20	70	36.8	648	6	Q29094	Q29094 sus scrofa
21	67	35.3	399	11	Q9COW3	Q9COW3 mus musculu
22	65	34.2	98	13	P82807	P82807 notechis sc
23	65	34.2	650	4	Q9NSD0	Q9NSD0 homo sapien
24	65	34.2	650	4	Q16519	Q16519 homo sapien
25	63	33.2	548	13	Q9PTW7	Q9PTW7 struthio ca
26	60.5	31.8	602	5	Q8T613	Q8T613 halocynthia
27	60	31.6	607	13	Q91001	Q91001 gallus gall
28	58.5	30.8	431	10	Q94EY5	Q94EY5 arabisdopsis
29	58.5	30.8	492	10	Q9SMU7	Q9SMU7 cicor artet
30	58.5	30.8	543	10	Q9MB23	Q9MB23 arabisdopsis
31	58.5	30.8	576	10	Q9C9U4	Q9C9U4 arabisdopsis
32	58.5	30.8	589	10	Q9LMS2	Q9LMS2 arabisdopsis
33	57.5	30.3	196	10	Q04284	Q04284 selaginella
34	56.5	29.7	459	10	Q9SE22	Q9SE22 oryza sativ
35	56	29.5	673	11	Q61592	Q61592 mus musculu
36	56	29.5	674	11	Q99K57	Q99K57 mus musculu
37	55.5	29.2	506	10	Q9SPF0	Q9SPF0 oryza sativ
38	55.5	29.2	506	10	Q9SE23	Q9SE23 oryza sativ
39	55.5	29.2	567	10	Q8W4J2	Q8W4J2 arabisdopsis
40	55	28.9	25	11	Q9QVH6	Q9QVH6 rattus sp.
41	54.5	28.7	510	10	Q9MB22	Q9MB22 arabisdopsis
42	54.5	28.7	619	10	Q9LV37	Q9LV37 arabisdopsis
43	54	28.4	674	11	Q63772	Q63772 rattus sp.
44	54	28.4	678	4	Q14393	Q14393 homo sapien
45	52.5	27.6	588	10	Q9LM33	Q9LM33 arabisdopsis

ALIGNMENTS

RESULT 1
ID Q96PQ8 PRELIMINARY; PRT; 701 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor VII active site mutant Immunofugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
..NCBI_Taxid=9606;
..RN (1)
..RP SEQUENCE FROM N.A.
..RX MEDLINE=21477448; PubMed=11593034;
..RA Hu Z., Garen A.;
..RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
..RT cells for immunotherapy in mouse models of prostatic cancer.";
..RT Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
..DR EMBL; AF272774; AAK58686.1; -.
..DR InterPro; IPR000152; Asx hydroxyl.
..DR InterPro; IPR000561; EGF-like.
..DR InterPro; IPR000742; EGF-2.
..DR InterPro; IPR001881; EGF-Ca.
..DR InterPro; IPR003006; IG_MHC.
..DR InterPro; IPR001254; Ser protease_Try.
..DR InterPro; IPR000294; VltK_dep_GLA.
..DR Pfam; PF00504; EGF_2.
..DR Pfam; PF00594; gla; 1.
..DR Pfam; PF00047; Ig; 2.
..DR Pfam; PF00089; trypsin; 1.
..DR SMART; SM00181; EGF_2.
..DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
..DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
..DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
..DR PROSITE; PS01187; EGF-Ca; UNKNOWN_1.
..DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
..DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
..DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
DR Hydrolase; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CBB42CC92F CRC64;

Query Match 83.7%; Score 159; DB 4; Length 701;
Best Local Similarity 72.7%; Pred. No. 1.1e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSIXRXCXXQCSFFXAEXIFKDXARTKLFWISY 44
DB 61 ANAFLEELRPGSLERCEKQCSFEERAEIFKDAERTKLFWISY 104

RESULT 2

061109 PRELIMINARY; PRT; 446 AA.

AC 061109;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=96276538; PubMed=8701412;
RA Iduogile E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.",
CC Thromb. Haemost. 75:481-487(1996).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

DR EMBL; U44795; AAC52570.1; -.
DR HSSP; P08709; IFAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_1ike; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 60.0%; Score 114; DB 11; Length 446;

Best Local Similarity 54.5%; Pred. No. 1.5e-12;
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSIXRXCXXQCSFFXAEXIFKDXARTKLFWISY 44
DB 42 ANSLEELWPGSLERCEKQCSFEERAEIFKSPENTKQFWIV 85

RESULT 3

091WN8 PRELIMINARY; PRT; 460 AA.

AC 091WN8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013896; AAH13896.1; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 0117F2E68FCC274 CRC64;

Query Match 53.7%; Score 102; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 2.6e-10;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSIXRXCXXQCSFFXAEXIFKDXARTKLFWISY 44
DB 42 ANSLEELWPGSLERCEKQCSFEERAEIFQVVEDTLAFWIKY 85

RESULT 4

099PC6 PRELIMINARY; PRT; 460 AA.

AC 099PC6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anticoagulant protein C.
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;

```
RT "Complete sequence of UC72A01."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY
DR EMBL; AF318182; AAK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MCD; MG1.97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00889; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase;
KM Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC2589D3ED16 CRC64;

Query Match 50.5%; Score 96; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 3.4e-09;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFPLXLRQGLXRXCKXQCSFYXAEIIFDAXRTKLFWISY 44
Db 42 ANSFLEMRPGSLERECMEICDLEBAQEIFQNVEDTLAFWKY 85

RESULT 5
Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Huseon S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase."
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; X79807; CAAS6202.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
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DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00889; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase;
KM Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 48.9%; Score 93; DB 11; Length 482;
Best Local Similarity 38.6%; Pred. No. 1.3e-08;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFPLXLRQGLXRXCKXQCSFYXAEIIFDAXRTKLFWISY 44
Db 41 ANSFEEIKKGNLERECVEICISFEARAEVFDENKTEIFWKKY 84

RESULT 6
Q9TTR0 PRELIMINARY; PRT; 456 AA.
AC Q9TTR0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein C precursor.
CN PROC.
OS Canis familiaris (Dog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
CC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene."
RL Mamm. Genome 10:135-139(1999).
CC [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms."
RL Anim. Genet. 30:237-238(1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AJ001979; CAAS0126.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
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DR	SMART; SMO0001; EGF_1like; 2.
DR	SMART; SMO00069; GLA; 1.
DR	SMART; SMO00020; TRYD_SPC; 1.
DR	PROSITE; PS000010; ASX_HYDROXYL; UNKNOWN_1.
DR	PROSITE; PS000022; EGF_1; UNKNOWN_1.
DR	PROSITE; PS01186; EGF_2; 2.
DR	PROSITE; PS01187; EGF_CA; 1.
DR	PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR	PROSITE; PS50240; TRYPsin_DOM; 1.
DR	PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
KW	_PROSITE; PS00135; TRYPsin_SER; 1.
KW	Hydrolase; Serine protease.
SQ	SEQUENCE 469 AA; 52196 MW; 4C6C230D0758FEA CRC64;
Oy	
Dn	1 ANAFLLRLGSLKRXCKXCSPFXAXEIKFDKARLYLFMISY 44 ::: :: :: :: :: 41 ANSFLLELKGNLERECNEFTCSYEAREVEDDDTKTFPMNII 84
RESULT 8	
ID	OS4740 PRELIMINARY; PRT; 481 AA.
AC	OS4740;
DT	01-JUN-1998 (TReMBLe); 06, Created)
DT	01-JUN-1998 (TReMBLe); 06, Last sequence update)
DT	01-JUN-2002 (TReMBLe); 21, Last annotation update)
DE	Coagulation factor X precursor (EC 3.4.21.6).
CN	F10 OR PA10.
OS	Mus musculus (Mouse).
OG	Plasmod BILUESCIPt.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutelea; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LIVER;
RX	MEDLINE=98454993; PubMed=9783672;
RA	Heidemann H.H., Kontermann R.E.;
RL	"Cloning and recombinant expression of mouse coagulation factor X.";
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
CC	EMBL; AJ222677; CAA10933.1; -. HSSP; P00742; IYKA.
DR	MEROPS; S01.216; -.
DR	MGD; MGI:103107; F10.
DR	InterPro; IPRO00152; Aex_hydroxyl.
DR	InterPro; IPRO01314; Chymotrypsin.
DR	InterPro; IPRO00561; EGF-like.
DR	InterPro; IPRO00742; EGF_2.
DR	InterPro; IPRO01881; EGF_CA.
DR	InterPro; IPRO02383; GLA_Dlood.
DR	InterPro; IPRO01254; Ser_protease_TRY.
DR	InterPro; IPRO00294; Vltk_dep_GLA.
Pfam	PFO0008; EGF_2.
Pfam	PFO0594; gla; 1.
Pfam	PFO0089; trypsin; 1.
PRINTS	PR00722; CHYMOTRYPSIN.
PRINTS	PR00001; GLABLOOD.
SMART	SMO0179; EGF_CA; 1.
SMART	SMO0001; EGF_like; 1.
SMART	SMO0069; GLA; 1.
SMART	SMO0020; tryd_spec; 1.
PROSITE	PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE	PS00022; EGF_1; UNKNOWN_1.
PROSITE	PS01186; EGF_2; 2.
PROSITE	PS01187; EGF_CA; 1.
PROSITE	PS00011; GLU CARBOXYLATION; 1.
PROSITE	PS50240; TRYPsin_DOM; 1.
PROSITE	PS00134; TRYPsin_HIS; UNKNOWN_1.
PROSITE	PS00011; GLU_CARBOXYLATION; 1.
PROSITE	PS50240; TRYPsin_DOM; 1.

DR PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmaid;
KM Repeat; Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481
SQ SEQUENCE 481 AA; 53986 MM; CF702D5E5F9D97AE CRC64;

Query Match 47.9%; Score 91; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 3e-08; Mismatches 20; Indels 0; Gaps 0;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Cy 1 ANAFIXLRGSLKRXKXKXCCFFXAXEIPFDARTKLFMISY 44
Db 41 ANSFEEFKGNLERECMEICSYEEVREIFEDDKTKYWTKY 84

RESULT 9
ID 099132 PRELIMINARY; PRT; 481 AA.
AC 099132.
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
DR EMBL; BC003877; AA03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease; Signal.
SQ SEQUENCE 481 AA; 54004 MM; BD88E96C8A0B7E7F CRC64;

Query Match 47.9%; Score 91; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 3e-08;

Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
Cy 1 ANAFIXLRGSLKRXKXKXCCFFXAXEIPFDARTKLFMISY 44
Db 41 ANSFEEFKGNLERECMEICSYEEVREIFEDDKTKYWTKY 84

RESULT 10
ID 088947 PRELIMINARY; PRT; 481 AA.
AC 088947.
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=96347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129SJ;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
DR EMBL; AF087644; AAC36345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KM Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481
SQ SEQUENCE 481 AA; 54018 MM; BAC09D5E5F9D271E CRC64;

```

Query Match          47.9%; Score 91; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 3e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 AANFLXXLRQGSIXRCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 44
DB 41 AANFLXXLRQGSIXRCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 84

RESULT 11
ID Q15253 PRELIMINARY; PRT; 100 AA.
AC Q15253;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Thrombin precursor (Fragment).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; PubMed=3471151;
RA MacGillivray R.T., Irwin D.M., Guinco E.R., Stone J.C.;
RT "Recombinant genetic approaches to functional mapping of thrombin.";
RL Ann. N. Y. Acad. Sci. 485:73-79(1996).
DR EMBL; M33031; AAA60220.1; -.
DR HSSP; P00735; 2PPI.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GSA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Signal.
FT SIGNAL. 1 43 POTENTIAL.
FT CHAIN 44 >100 POTENTIAL.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 11302 MW; FD055D0174E1FEFE CRC64;

Query Match          44.7%; Score 85; DB 4; Length 100;
Best Local Similarity 36.4%; Pred. No. 7.8e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 AANFLXXLRQGSIXRCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 44
DB 44 AANFLXXLRQGSIXRCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 87

RESULT 12
ID Q14316 PRELIMINARY; PRT; 456 AA.
AC Q14316;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-AUG-1999 (TRENBLREL. 11, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, Christmas disease, HEMOPHILIA B)) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Retsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,

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RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; 1CFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match          43.7%; Score 83; DB 4; Length 456;
Best Local Similarity 42.9%; Pred. No. 8.6e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 10 QGSLXRXCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 44
DB 52 QGSLXRXCKXKXQCSFYXAXEIXFKDAXRTKLFWISY 86

RESULT 13
ID Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RT Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.

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DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; G1a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolyase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 43.7%; Score 83; DB 6; Length 461;
Best Local Similarity 42.9%; Pred. No. 8.7e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Oy 10 OGSIXRXCXXQCSFXXAEXIFKDXRTKLFWISY 44
Db 57 QGNLERCEKCKSFEEAREVFENTERTEFWKQY 91

RESULT 14

ID Q95ND6 PRELIMINARY; PRT; 461 AA.

AC Q95ND6; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Saita Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; -
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; G1a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KM Hydrolyase; Serine protease.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 43.7%; Score 83; DB 6; Length 461;
Best Local Similarity 42.9%; Pred. No. 8.7e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Oy 10 OGSIXRXCXXQCSFXXAEXIFKDXRTKLFWISY 44
Db 57 QGNLERCEKCKSFEEAREVFENTERTEFWKQY 91

RESULT 15

ID Q95ME8 PRELIMINARY; PRT; 49 AA.

AC Q95ME8; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizlata M.N.; Amarel E.J.;
RT "Partial sequence of bovine F9 coding gene."
RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF394598; AK77556.1; -
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00594; G1a; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6023 MW; D15C6DE9CCBA4A14 CRC64;

Query Match 43.2%; Score 82; DB 6; Length 49;
Best Local Similarity 40.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Oy 10 OGSIXRXCXXQCSFXXAEXIFKDXRTKLFWISY 44
Db 14 RGNLERCEKCKSFEEAREVFENTERTEFWKQY 48

Search completed: March 19, 2003, 15:13:27
Job time : 59.3125 secs

AGE BLANK (USPTO)

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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 seconds
(without alignments)
132.780 Million cell updates/sec

Title: 10GLN28GLU

Perfect score: 190

Sequence: 1 ANAFLXLRQSLRQSLRXCKXX.....XAXEIFKDXRTKLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	85.3	44	3	US-08-955-636-26
2	161	84.7	44	3	US-08-955-636-30
3	160	84.2	44	3	US-08-955-636-27
4	159	83.7	44	3	US-08-955-636-3
5	159	83.7	406	1	US-08-293-778-24
6	159	83.7	406	1	US-08-295-411-5
7	159	83.7	406	1	US-08-955-471-5
8	159	83.7	406	5	PCT-US92-10242-5
9	159	83.7	444	1	US-08-475-845-2
10	159	83.7	444	2	US-08-327-650-2
11	159	83.7	444	2	US-08-660-289-2
12	159	83.7	444	2	US-08-537-807-2
13	159	83.7	444	2	US-08-871-003-2
14	159	83.7	444	2	US-08-464-233-2
15	159	83.7	444	4	US-09-189-607-2
16	159	83.7	444	4	US-09-378-907-2
17	159	83.7	444	5	PCT-US94-05779-2
18	159	83.7	466	1	US-07-882-202A-4
19	159	83.7	466	1	US-08-021-615A-4
20	159	83.7	466	1	US-08-321-777-4
21	159	83.7	466	4	US-09-009-217-14
22	159	83.7	466	4	US-09-009-656-14
23	159	83.7	466	5	PCT-US93-04493-4
24	156	82.1	44	3	US-08-955-636-28
25	153	80.5	44	3	US-08-955-636-29
26	144	75.8	41	1	US-08-229-280-4
27	123	64.7	44	3	US-08-955-636-4

28	108	56.8	139	1	US-08-330-978-2	Sequence 2, Appli
29	108	56.8	139	1	US-08-474-042-2	Sequence 2, Appli
30	108	56.8	139	1	US-08-484-558-2	Sequence 2, Appli
31	108	56.8	139	1	US-08-774-592-2	Sequence 2, Appli
32	108	56.8	437	1	US-08-487-037-2	Sequence 2, Appli
33	108	56.8	437	1	US-08-487-037-3	Sequence 3, Appli
34	108	56.8	448	1	US-08-487-037-1	Sequence 1, Appli
35	102	53.7	44	3	US-08-955-636-18	Sequence 18, Appli
36	102	53.7	487	2	US-08-469-486-53	Sequence 53, Appli
37	102	53.7	487	2	US-08-469-658-53	Sequence 53, Appli
38	102	53.7	487	2	US-08-469-486-2	Sequence 2, Appli
39	102	53.7	492	2	US-08-469-658-2	Sequence 2, Appli
40	101	53.2	44	3	US-08-955-636-24	Sequence 24, Appli
41	99	52.1	448	1	US-08-295-411-3	Sequence 3, Appli
42	99	52.1	448	2	US-08-955-471-3	Sequence 3, Appli
43	99	52.1	448	5	PCT-US92-10068-1	Sequence 1, Appli
44	99	52.1	448	5	PCT-US92-10242-3	Sequence 3, Appli
45	98	51.6	44	3	US-08-955-636-35	Sequence 35, Appli

ALIGNMENTS

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RESULT 1
US-08-955-636-26
Sequence 26, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Neissestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (0) ..(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match      85.3%; Score 162; DB 3; Length 44;
Best local Similarity 95.5%; Pred. No. 3.9e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXLRQSLRQSLRXCKXXCXCFXAXEIFKDXRTKLFWISY 44
Db 1 ANAFLXLRQSLRQSLRXCKXXCXCFXAXEIFKDXRTKLFWISY 44

RESULT 2
US-08-955-636-30
Sequence 30, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Neissestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30

Query Match 84.7%; Score 161; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 5, 7e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGLRXCKXXQCSFXXAEXIFPDAXRTKLFWISY 44
DB 1 ANAFLLXLRQGLRXCKXXQCSFXXAEXIFPDAXRTKLFWISY 44

RESULT 3
US-08-955-636-27

Sequence 27, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsaestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955, 636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match 84.2%; Score 160; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 8, 4e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGLRXCKXXQCSFXXAEXIFPDAXRTKLFWISY 44
DB 1 ANAFLLXLRQGLRXCKXXQCSFXXAEXIFPDAXRTKLFWISY 44

RESULT 4
US-08-955-636-3

Sequence 3, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsaestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955, 636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match 83.7%; Score 159; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 1, 2e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGLRXCKXXQCSFXXAEXIFPDAXRTKLFWISY 44
DB 1 ANAFLLXLRQGLRXCKXXQCSFXXAEXIFPDAXRTKLFWISY 44

RESULT 5
US-08-293-778-24

Sequence 24, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION:
APPLICANT: Nicolaesen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293, 778
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104, 509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434, 149
FILING DATE: 13-NOV-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
APPLICATION NUMBER: US 07/898, 248
FILING DATE: 12-JUN-1992

ATTORNEY/AGENT INFORMATION:
NAME: Agtib, Cheryl H.
REGISTRATION NUMBER: 34, 086
REFERENCE/DOCKET NUMBER: 3129, 224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123

TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-293-778-24

Query Match 83.7%; Score 159; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1, 2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGLRXCKXXQCSFXXAEXIFPDAXRTKLFWISY 44
DB 1 ANAFLLXLRQGLRXCKXXQCSFXXAEXIFPDAXRTKLFWISY 44

RESULT 6
US-08-295-411-5

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; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-295-411-5

Query Match      83.7%; Score 159; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Db 1 ANAFLLELRPGSLERCKEEOCSFEAREIFPDARTKLFWISY 44
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RESULT 7
US-08-955-471-5

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; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
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; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-955-471-5

Query Match      83.7%; Score 159; DB 2; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Oy 1 ANAFLXLRQGSILKRXCKXQCSFYXAXEIPFDARTKLFWISY 44
Db 1 ANAFLLELRPGSLERCKEEOCSFEAREIFPDARTKLFWISY 44
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RESULT 8
PCT-US92-10242-5

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; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
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: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/10242
: FILING DATE: 19921118
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/793,989
: FILING DATE: 18-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: SCRO472P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..152
: OTHER INFORMATION: /note="Factor VII Light Chain"
: FEATURE:
: NAME/KEY: Region
: LOCATION: 153..406
: OTHER INFORMATION: /note="Factor VII Heavy Chain"
: PCT-US92-10242-5

Query Match      83.7%; Score 159; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44
Db      1 ANAFLRLRPGSLRCKEQCSFEARLIFDKAERTKLFWISY 44

RESULT 9
US-08-475-845-2
: Sequence 2, Application US/08475845
: Patent No. 5788965
: GENERAL INFORMATION:
: APPLICANT: Berkner, Kathleen L.
: APPLICANT: Petersen, Lars C.
: APPLICANT: Hart, Charles E.
: APPLICANT: Hedner, Ulla
: APPLICANT: Bregengaard, Claus
: TITLE OF INVENTION: Modified Factor VII
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Stuart Street Tower
: CITY: San Francisco
: STATE: CA
: COUNTRY: U.S.A.
: ZIP: 94105-1492
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:

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: APPLICATION NUMBER: US/08/475,845
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/327,690
: FILING DATE: 24-OCT-1994
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/065,725
: FILING DATE: 21-MAY-1993
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 07/662,920
: FILING DATE: 28-FEB-1991
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Parmelee, Steven W.
: REGISTRATION NUMBER: 13952-8-4
: REFERENCE/DOCKET NUMBER: 31,990
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-467-9600
: TELEFAX: 415-543-5043
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 444 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-475-845-2

Query Match      83.7%; Score 159; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      1 ANAFLXXLRGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44
Db      39 ANAFLRLRPGSLRCKEQCSFEARLIFDKAERTKLFWISY 82

RESULT 10
US-08-327-690-2
: Sequence 2, Application US/08327690
: Patent No. 5817788
: GENERAL INFORMATION:
: APPLICANT: Berkner, Kathleen L.
: APPLICANT: Petersen, Lars C.
: APPLICANT: Hart, Charles E.
: APPLICANT: Hedner, Ulla
: APPLICANT: Bregengaard, Claus
: TITLE OF INVENTION: Modified Factor VII
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Stuart Street Tower
: CITY: San Francisco
: STATE: CA
: COUNTRY: U.S.A.
: ZIP: 94105-1492
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/327,690
: FILING DATE: 24-OCT-1994
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/065,725
: FILING DATE: 21-MAY-1993
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 07/662,920

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FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match 83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFPLXLRGSLRXCKXQCSFXAXEIFDAXRTKLFWISY 44
DB 39 ANAFLEELRPGSLERECKECCSFEEAREIFDAXRTKLFWISY 82

RESULT 11
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,289
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

Query Match 83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFPLXLRGSLRXCKXQCSFXAXEIFDAXRTKLFWISY 44
DB 39 ANAFLEELRPGSLERECKECCSFEEAREIFDAXRTKLFWISY 82

RESULT 12
US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFPLXLRGSLRXCKXQCSFXAXEIFDAXRTKLFWISY 44
DB 39 ANAFLEELRPGSLERECKECCSFEEAREIFDAXRTKLFWISY 82

RESULT 13
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.

APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 83.7%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXKQCSFXXAEXIFKDAKRTKLFWISY 44
DB 39 ANAFLELRPGSLERCKEQCSFEERARIFKDAERTKLFWISY 82

RESULT 14
US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match 83.7%; Score 159; DB 3; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXKQCSFXXAEXIFKDAKRTKLFWISY 44
DB 39 ANAFLELRPGSLERCKEQCSFEERARIFKDAERTKLFWISY 82

RESULT 15
US-09-189-607-2
Sequence 2, Application US/09189607
Patent No. 6168789
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,607
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,289
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:

Thu Mar 20 14:51:52 2003

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Page 7

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1      PRIOR APPLICATION DATA: 07/662,920
2      APPLICATION NUMBER: 07/662,920
3      FILING DATE: 28-FEB-1991
4      CLASSIFICATION:
5      ATTORNEY/AGENT INFORMATION:
6      NAME: Parmelee, Steven W.
7      REGISTRATION NUMBER: 31,990
8      REFERENCE/DOCKET NUMBER: 13952-8-4
9      TELECOMMUNICATION INFORMATION:
10     TELEPHONE: 206-467-9600
11     TELEFAX: 415-543-5043
12     INFORMATION FOR SEQ ID NO: 2:
13     SEQUENCE CHARACTERISTICS:
14     LENGTH: 444 amino acids
15     TYPE: amino acid
16     TOPOLOGY: linear
17     MOLECULE TYPE: protein
18     IS-09-189-607-2

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Query Match	83.7%	Score 159	DB 4	Length 444
Best Local	72.7%	Pred. No. 1.3e-18		
Matches 32	Conservative	0	Mismatches 12	Indels 0
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OM protein - protein search, using SW model

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(without alignments)
280.876 Million cell updates/sec

Title: 10Gln28Glu
Perfect score: 190
Sequence: 1 ANAFLLXLRQGSIXKXCKXK.....XXAEXIFDAXRTKLFWISY 44

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Gap 10.0, Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	101	53.2	419	US-10-182-263-6	Sequence 6, Appli
3	96	50.5	419	US-10-182-263-3	Sequence 3, Appli
4	96	50.5	419	US-10-182-263-4	Sequence 4, Appli
5	96	50.5	419	US-10-182-263-5	Sequence 5, Appli
6	85	44.7	419	US-10-182-263-1	Sequence 1, Appli
7	85	44.7	419	US-09-978-917A-4	Sequence 4, Appli
8	85	44.7	461	US-10-182-263-2	Sequence 2, Appli
9	85	44.7	461	US-09-978-917A-2	Sequence 2, Appli
10	83	43.7	415	US-09-118-748-2	Sequence 2, Appli
11	83	43.7	461	US-10-132-829-5	Sequence 5, Appli
12	83	43.7	461	US-09-884-901-3	Sequence 3, Appli
13	69.5	36.6	96	US-09-759-130B-313	Sequence 313, App
14	69.5	36.6	209	US-09-759-130B-112	Sequence 312, App
15	69.5	36.6	226	US-09-759-130B-110	Sequence 310, App
16	54.5	28.7	98	US-09-759-130B-356	Sequence 356, App
17	54.5	28.7	208	US-09-759-130B-355	Sequence 355, App
18	54.5	28.7	225	US-09-759-130B-353	Sequence 353, App
19	43	22.6	88	US-09-811-284-194	Sequence 194, App

20	43	22.6	273	9	US-09-764-868-968	Sequence 968, App
21	43	22.6	1266	9	US-09-931-969A-2	Sequence 2, Appli
22	43	22.6	1266	9	US-10-079-699-2	Sequence 2, Appli
23	43	22.6	1266	10	US-09-757-781-63	Sequence 63, Appli
24	43	22.6	1356	10	US-09-757-781-2	Sequence 2, Appli
25	42	22.1	608	10	US-09-908-664-5	Sequence 5, Appli
26	42	22.1	729	9	US-10-145-366-11	Sequence 11, Appli
27	42	22.1	1258	10	US-09-922-543-1	Sequence 1, Appli
28	42	22.1	1274	10	US-09-746-491-12	Sequence 12, Appli
29	41.5	21.8	440	9	US-09-910-186A-8	Sequence 8, Appli
30	41	21.6	447	10	US-09-815-242-13490	Sequence 13490, A
31	41	21.6	447	10	US-09-815-242-13612	Sequence 13612, A
32	41	21.6	447	10	US-09-735-564-2	Sequence 2, Appli
33	40.5	21.3	1149	10	US-09-969-528-5	Sequence 5, Appli
34	40	21.1	744	10	US-09-862-179A-1	Sequence 1, Appli
35	40	21.1	1337	10	US-09-757-781-62	Sequence 62, Appli
36	39	20.5	52	9	US-09-796-682-2179	Sequence 2179, App
37	39	20.5	52	9	US-09-796-682-2370	Sequence 2370, App
38	39	20.5	347	10	US-09-780-053-4	Sequence 4, Appli
39	39	20.5	730	9	US-10-145-396-12	Sequence 12, Appli
40	39	20.5	730	10	US-09-780-053-2	Sequence 2, Appli
41	39	20.5	873	9	US-10-200-154-2	Sequence 2, Appli
42	39	20.5	873	10	US-09-954-043-2	Sequence 2, Appli
43	38.5	20.3	49	10	US-09-764-864-1054	Sequence 1054, App
44	38.5	20.3	316	10	US-09-815-242-11911	Sequence 11911, A
45	38.5	20.3	348	10	US-09-982-610-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286 200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1
Query Match 83.7%; Score 159; DB 9; Length 406;
Best Local Similarity 95.5%; Pred. No. 1,1e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSIXKXCKXKOCSPFXAEXIFDAXRTKLFWISY 44
DB 1 ANAFLLXLRPGSLKRXCKXKOCSPFXAEXIFDAXRTKLFWISY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E

```

1 TITLE OF INVENTION: PROTEIN C DERIVATIVES
2
3 APPLICANT: Grinnell, Brian W
4
5 FILE REFERENCE: X-13611
6
7 CURRENT APPLICATION NUMBER: US/10/182,263
8
9 CURRENT FILING DATE: 2002-07-22
10
11 PRIOR APPLICATION NUMBER: 60/181948
12
13 PRIOR FILING DATE: 2002-02-11
14
15 PRIOR APPLICATION NUMBER: 60/189199
16
17 PRIOR FILING DATE: 2000-03-14
18
19 NUMBER OF SEQ ID NOS: 12
20
21 SOFTWARE: PatentIn version 3.1
22
23 SEQ ID NO 6
24
25 LENGTH: 419
26
27 TYPE: PRT
28
29 ORGANISM: Homo sapiens
30
31 US-10-182-263-6

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Query Match	53.2%;	Score 101;	DB 9;	Length 419;
Best Local Similarity	51.2%;	Pred. No. 3.3e-10;		
Matches 21; Conservative	3;	Mismatches 17;	Indels 0;	Gaps 0;

Qy 1 ANAFLLXLRQGSGLRXKCKKXQCGFXXAEIIFKQAKRRTLFW 411

D5 1 ANSFLLEERQGSJERECTIEICPFEEAKEIFEDVDTLAFW 411

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
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```

1  APPLICANT: Grinnell, Brian W
2  TITLE OF INVENTION: PROTEIN C DERIVATIVES
3
4  FILE REFERENCE: X-13611
5
6  CURRENT APPLICATION NUMBER: US/10/182,263
7  CURRENT FILING DATE: 2002-07-22
8  PRIOR APPLICATION NUMBER: 60/181948
9  PRIOR FILING DATE: 2002-02-11
10 PRIOR APPLICATION NUMBER: 60/189199
11 PRIOR FILING DATE: 2000-03-14
12 NUMBER OF SEQ ID NOS: 12
13 SOFTWARE: PatentIn version 3.1
14
15 SEQ ID NO 3
16
17 LENGTH: 419
18
19 TYPE: PRT
20
21 ORGANISM: Homo sapiens
22
23 US-10-182-263-3

```

Query Match	50.5%;	Score 96;	DB 9;	Length 419;
Best Local Similarity	48.8%;	Pred. No. 2.6e-09;		
Matches 20;	Conservative 3;	Mismatches 18;	Indels 0;	Gaps 0;

Oy

I ANAFLLXLRQSSLRXCKKXQCFFXXAEIIFKCAARXTLFW 411
||::| | | | | | | | | | | | | | | |
1 ANSFLEELRHGSLERECTIEICPFEEAEIFEDVDTLAFW 411

US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:

; CURRENT APPLICATION NUMBER: US/10/182,263
 ;
 ; CURRENT FILING DATE: 2002-07-22
 ;
 ; PRIOR APPLICATION NUMBER: 60/181948
 ;
 ; PRIOR FILING DATE: 2002-02-11
 ;

```

? PRIOR APPLICATION NUMBER: 60/168199
? PRIORITY DATE: 2000-03-14
? FILING DATE: 2000-03-14
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO. 4
? LENGTH: 419
? TYPE: prt
? ORGANISM: Homo sapiens
? OS-10-187-263-4
```

Query Match	50.5%;	Score 96;	DB 9;	Length 419;
Best Local Similarity	48.8%;	Pred. No. 2.6e-09;		
Matches	20;	Conservative	3;	Mismatches 18;
			Indels	0;
			Gaps	0;

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QY 1 ANAFLXXLRGSLXRXCCXXCCSFXAXEXIFDKARFTLFW 411
    ||:|||||:|||||
DB 1 ANSFLBELRHGSLERECTEIEICDFEAKEIFEVDDTLAFW 411

```

RESULT 5
US-10-182-263-5

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1 APPLICANT: Grinnell, Brian W
2 TITLE OF INVENTION: PROTEIN C DERIVATIVES
3 FILE REFERENCE: X-13611
4 CURRENT APPLICATION NUMBER: US/10/182,263
5 CURRENT FILING DATE: 2002-07-22
6 PRIOR APPLICATION NUMBER: 60/181948
7 PRIOR FILING DATE: 2002-02-11
8 PRIOR APPLICATION NUMBER: 60/189199
9 PRIOR FILING DATE: 2000-03-14
10 NUMBER OF SEQ ID NOS: 12
11 SOFTWARE: PatentIn version 3.1
12
13 SEQ ID NO 5
14     LENGTH: 419
15     TYPE: PRT
16 ORGANISM: Homo sapiens
17 US-10-182-263-5

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Query Match	50.5%;	Score 96;	DB 9;	Length 419;
Best Local Similarity	48.8%;	Pred. No. 2.6e-09;		
Matches 20; Conservative	3;	Mismatches 18;	Indels 0;	Gaps 0;

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Oy      1 ANAFLLXLRGGSLARXCKXKQCSFYXAEIIFDAXRTLLFW 411
        ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 ANSFLEELRHGSLRECELEICDFEAKEIFEVDDTLAFW 411

```

RESULT 6
US-10-182-263-1

```

1 TITLE OF INVENTION: PROTEIN C DERIVATIVES
2
3 FILE REFERENCE: X-13611
4
5 CURRENT APPLICATION NUMBER: US/10/182,263
6
7 PRIOR FILING DATE: 2002-07-22
8
9 PRIOR APPLICATION NUMBER: 60/181948
10
11 PRIOR FILING DATE: 2002-02-11
12
13 PRIOR APPLICATION NUMBER: 60/189199
14
15 PRIOR FILING DATE: 2000-03-14
16
17 NUMBER OF SEQ ID NOS: 12
18
19 SOFTWARE: PatentIn version 3.1
20
21 SEQ ID NO 1
22
23 LENGTH: 419
24
25 TYPE: PRT

```

ORGANISM: Homo sapiens
US-10-182-263-1

Query Match 44.7%; Score 85; DB 9; Length 419;
Best Local Similarity 43.9%; Pred. No. 2.5e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFIXLRQGSIXKXCKXQCSFYXAEIIFKDAKRTKLFW 41
Db 1 ANSFLELRHSSLRECEIEICDFEAKKEIFQNVDTLAFW 41

RESULT 7

US-09-978-917A-4
Sequence 4, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT

ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match 44.7%; Score 85; DB 9; Length 419;
Best Local Similarity 43.9%; Pred. No. 2.5e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFIXLRQGSIXKXCKXQCSFYXAEIIFKDAKRTKLFW 41
Db 1 ANSFLELRHSSLRECEIEICDFEAKKEIFQNVDTLAFW 41

RESULT 8
US-10-182-263-2

Sequence 2, Application US/10182263
Publication No. US20030022354A1

GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT

ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 44.7%; Score 85; DB 9; Length 461;
Best Local Similarity 43.9%; Pred. No. 2.8e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFIXLRQGSIXKXCKXQCSFYXAEIIFKDAKRTKLFW 41
Db 43 ANSFLELRHSSLRECEIEICDFEAKKEIFQNVDTLAFW 83

RESULT 9

US-09-978-917A-2
Sequence 2, Application US/09978917A
Publication No. US20030027299A1

GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u8310 - protein C
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 461
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(42)
FEATURE:
NAME/KEY: CHAIN
LOCATION: (43)...(461)
US-09-978-917A-2

Query Match 44.7%; Score 85; DB 9; Length 461;
Best Local Similarity 43.9%; Pred. No. 2.8e-07;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFIXLRQGSIXKXCKXQCSFYXAEIIFKDAKRTKLFW 41
Db 43 ANSFLELRHSSLRECEIEICDFEAKKEIFQNVDTLAFW 83

RESULT 10
US-09-118-748-2

Sequence 2, Application US/09118748A
Patent No. US20020031799A1

GENERAL INFORMATION:
APPLICANT: Stafford, Darrel W.
APPLICANT: Chang, Jinli
TITLE OF INVENTION: Factor IX Antithrombotic Factor with Increased Clotting
TITLE OF INVENTION: Activity
FILE REFERENCE: 5470-183
CURRENT APPLICATION NUMBER: US/09/118,748A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,571
EARLIER FILING DATE: 1997-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 415
TYPE: PRT

ORGANISM: Homo sapiens
US-09-118-748-2

Query Match 43.7%; Score 83; DB 10; Length 415;
Best Local Similarity 42.9%; Pred. No. 5.8e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 10 QGSLRXCKXKXQCSFYXAEIIFKDAKRTKLFWISY 44
Db 11 QGNLERECMEKCSFEARVEVENTERTTTEFWKQY 45

RESULT 11
US-10-132-829-5

Sequence 5, Application US/10132829
Publication No. US20030044982A1

GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
TITLE OF INVENTION: with vesicle vector
FILE REFERENCE: 6627-P41170

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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          43.7%; Score 83; DB 9; Length 461;
Best Local Similarity 42.9%; Pred. No. 6.5e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 10 QGSLXRXCKXKQCSFXAXEKFMDAXRTKLFWISY 44
DB 57 QGNLRECEMEKCSFPEARVFENTERTEFFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOPW-1-17386
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRF
; ORGANISM: Homosapien
US-09-884-901-3

Query Match          43.7%; Score 83; DB 10; Length 461;
Best Local Similarity 42.9%; Pred. No. 6.5e-07;
Matches 15; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 10 QGSLXRXCKXKQCSFXAXEKFMDAXRTKLFWISY 44
DB 57 QGNLRECEMEKCSFPEARVFENTERTEFFWKQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
```

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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match          36.6%; Score 69.5; DB 9; Length 96;
Best Local Similarity 36.4%; Pred. No. 3.3e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY 2 NAF-LXXLRQSLXRXCKXKQCSFXAXEKFMDAXRTKLFWISY 44
DB 36 NRPDLFLTPGNLRECEMEKCSFPEARVFENTERTEFFWKQY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 312
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-1308-312

Query Match 36.6%; Score 69.5; DB 9; Length 209;
Best Local Similarity 36.4%; Pred. No. 7.6e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

OY 2 NAF-LXXLRQSLXRXCKXOCFFXXAEXIFKDXRTKLFWISY 44
DB 36 NRPDLFTPGNLERECNEBELCNYEAREIFVDEDTIAFWQY 79

RESULT 15

US-09-759-1308-310
Sequence 310, Application US/09759130B
Publication No. US2003002279A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirst, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Meyers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
FILE REFERENCE: MP100-5350M1M
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 310
LENGTH: 226
TYPE: PRT

ORGANISM: Homo sapiens
US-09-759-1308-310

Query Match 36.6%; Score 69.5; DB 9; Length 226;
Best Local Similarity 36.4%; Pred. No. 8.3e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

OY 2 NAF-LXXLRQSLXRXCKXOCFFXXAEXIFKDXRTKLFWISY 44
DB 53 NRPDLFTPGNLERECNEBELCNYEAREIFVDEDTIAFWQY 96

Search completed: March 20, 2003, 13:30:08
Job time : 10.375 secs

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